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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:38:22 ; Search time 27.2998 Seconds
(without alignments)
2821.919 Million cell updates/sec

Title: US-10-656-394A-4
Perfect score: 5255
Sequence: 1 MAETVLSMARSLVGSALSKA.....SQVITLTNDSEIGTAQAG 1032

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgm2_6/ptodata/1/1aa/5A COMB.pcp.*
2: /cgm2_6/ptodata/1/1aa/5B COMB.pcp.*
3: /cgm2_6/ptodata/1/1aa/6A COMB.pcp.*
4: /cgm2_6/ptodata/1/1aa/6B COMB.pcp.*
5: /cgm2_6/ptodata/1/1aa/PTCUS COMB.pcp.*
6: /cgm2_6/ptodata/1/1aa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	20.9	1205	3	US-09-330-330-1
2	977	18.6	928	3	US-08-930-996A-8
3	676.5	12.9	928	4	US-09-336-946B-2
4	676.5	12.9	928	4	US-09-993-170-58
5	662.5	12.6	928	4	US-09-336-946B-4
6	633	12.0	1240	3	US-08-930-996A-4
7	622.5	11.8	1402	3	US-09-004-838-11
8	615.5	11.7	905	3	US-09-360-186-3
9	615.5	11.7	905	4	US-09-864-680A-3
10	598.5	11.4	1220	3	US-08-930-996A-2
11	575	10.9	1824	2	US-08-680-327-3
12	575	10.9	1824	3	US-09-228-246-2
13	568	10.8	1255	3	US-08-947-823-3
14	557	10.6	1206	4	US-09-245-928A-19
15	557	10.6	1243	4	US-09-245-928A-17
16	557	10.6	1257	4	US-09-245-928A-18
17	553	10.5	1247	4	US-09-803-286A-2
18	551	10.5	1257	3	US-08-947-823-5
19	545	10.4	784	3	US-09-004-838-12
20	476	9.1	553	3	US-09-004-838-16
21	422	8.0	909	2	US-08-310-912A-142
22	422	8.0	909	3	US-09-301-085-142
23	422	8.0	909	5	PCT-US95-04589-142
24	416.5	7.9	885	2	US-08-310-912A-2
25	416.5	7.9	885	3	US-08-841-089-2
26	416.5	7.9	885	3	US-09-301-085-2
27	416.5	7.9	885	5	PCT-US95-04570-2

28 416.5 7.9 885 5 PCT-US95-04589-2 Sequence 2, Appli
29 414 7.9 907 3 US-08-930-996A-7 Sequence 7, Appli
30 384 7.3 1854 3 US-09-004-838-108 Sequence 108, App
31 362.5 6.9 247 4 US-09-803-286A-9 Sequence 9, Appli
32 356 6.8 232 4 US-09-803-286A-6 Sequence 6, Appli
33 340 6.5 1074 3 US-09-004-838-111 Sequence 111, App
34 338.5 6.4 1323 3 US-09-004-838-90 Sequence 90, Appli
35 336.5 6.4 1066 3 US-09-004-838-24 Sequence 24, Appli
36 336.5 6.4 1143 2 US-08-310-912A-108 Sequence 108, App
37 336.5 6.4 1143 3 US-09-301-085-108 Sequence 108, App
38 336.5 6.4 1143 5 PCT-US95-04589-108 Sequence 108, App
39 336.5 6.4 1144 1 US-08-261-663A-2 Sequence 2, Appli
40 336.5 6.4 1144 1 US-08-261-663A-4 Sequence 4, Appli
41 336.5 6.4 1144 3 US-08-930-996A-9 Sequence 9, Appli
42 336.5 6.4 1144 3 US-09-357-206A-3 Sequence 3, Appli
43 336.5 6.4 1144 4 US-09-813-742A-3 Sequence 3, Appli
44 336.5 6.4 1144 5 PCT-US95-07754A-2 Sequence 2, Appli
45 336.5 6.4 1144 5 PCT-US95-07754A-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-330-330-1
; Sequence 1, Application US/09330330
; Patent No. 6274789
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; APPLICANT: Iwamoto, Masao
; APPLICANT: Katayose, Yuichi
; APPLICANT: Sasaki, Takuji
; APPLICANT: Wang, Zi-Xuan
; APPLICANT: Yamanouchi, Utako
; APPLICANT: Ishimaru, Lisa
; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,330
; FILING DATE: 11-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 10-181455
; FILING DATE: 12-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/032001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1205 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-330-330-1

Query Match 20.9%; Score 1100; DB 3; Length 1205;
Best Local Similarity 27.2%; Pred. No. 1.8e-85;

164 VGFSDSKRLEEMIDTNDANDGPAK-VICVWGMGLGKTALSRKIFSEEDIRKNFPCNAW 222
172 VGIDAPKGLIGRL---LSPEQRIVAVWGMGSGKTTLSANIFKS-QSVRRHFESYAW 227
223 ITVSQSFRHIELLMDIROLQPSLSLOLLHLELOKVQVQVHHLS-----BYLIEELKEK 277
228 VTISKY-----VIEDVFRMT-----IKEFYKEADTQIPAEYLSIGYRELVEKUYEQSK 278
278 RYFVVLDDTLIHDWNWINEIAPKNNKSGSRIVITRNVDLAE-KCATAVLVHLDPLQ 336
279 RYIVVLDVWTGLWREIS-IALP-DGIYGRVWMTTRDMNVASFPYIGISTKEIELLK 336
337 MNDAILLLRTKNHEDMESNMKNQKVERIVNKGRLPLAIIITIGAVLATKQV-SEWE 395
337 EDEAWLFSNKAFFASLEQCRQNTONLEPTARKLVERCG-LPLAIASLGSMMSTKFESEWK 395
396 KFYEQLSLEINSLAERWVLGVNHLPSHLKPCFLYLSIFPEFQORNLVGRWI 455
396 KVSTLAWELNNHKLIVRSIMFLSFNDLPYLRKRCFLYCSLPFVNYRMKRLIRMMW 455
456 AEGVVRKVGWMTTKOVGESYNELINRSMIQSRVGTAGIKTKRIHDIIRDITVSISRQ 515
456 AORFVEPIRGKAEVADSYNELVYRNMLQVILWNPGRPKAFKMDVIEIALSVKL 515
516 ENF-VLLPMGDGSDLVQ--EN--TRHIAFGHSMCKTGLDWSIIRSLAIFGDRPKSLAH 569
516 ERFCDVNDSDGDDAAETMENYGRHLCIKEMT-PDSIRATNLHSLVCSAKHNM-- 572
570 AVCPDQRLMRVLEDEVTFLITOKDFRIALLCHLXVLSIGYSSSYSLPRSGKLOGL 629
573 ELLP-SLNLRALDLESSI---SKLPCLVTMFLNLYLNL-SKQKELPKNPHKLVLN 627
630 QTLNMSITYAALPSEISKLOCLTLRCIRELEFDNFSLNHPMKCIWTICLPKVFTPLV 689
628 ETLNKHSKEELPLGHWKLKLYLITFRNE----- 660
690 SRDNRAKQIAEFHMATKFSNSESFGVKPGIGKRLDQVLEYVDIIRTSRAIKELGOL 749
661 -----GHSDSNMYVLGTRVVPKIWLQKDLQVMDCFN---EDELINLGCN 702
750 SKLRKLAIVTGSTKECKIYAAIEKLSLSQSLYMAALLSDIETLECLDSISSPPPLL 809
703 TQLTRSLVM--VRRERGRDLCDSINKIKIR--FLSLTSDSEEPLE-IDDLATAS--I 755
810 RTGLGSLSEMPNWIOLTHLKKFNWSSKKEGKNMILGALPNLMFLSLYHNSYLGE 869
756 EKLFLAKLERVPSWFTLQNLTYLGLGSQLQENA-ILSIQTLPLRVWLISFY-NATMGP 813
870 KLVFKTGAPNRLTLVIFNLQDLREIRPEDGSSPQLEKIEISCCR-LESIGIIGHLPRL 928
814 RLRFAGQ-FQNLKILEIVQMKHLTEVVIEDGAMFELQKLYVRACKGLEYPVPRGIENLNL 872
929 KEISLEYKSK--VARLQKGEVNTHPNRPVLR 959
873 QELHLHVSNLQVERI-RGEGSVDSRVHIPAK 904

RESULT 3

US-09-336-946B-2
; Sequence 2, Application US/09336946B
; Patent No. 649731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryant, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A PI-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 2

; LENGTH: 928

; TYPE: PR1

; ORGANISM: Oryza sativa

US-09-336-946B-2

Query Match 12.9%; Score 676.5; DB 4; Length 928;

Best Local Similarity 24.9%; Pred. No. 4.1e-49;

Matches 262; Conservative 164; Mismatches 366; Indels 261; Gaps 37;

Qy 1 MAEIVLSMARSLVCSAISKAS-----AAANETSLLLGVEKDIWYKDELKTM--Q 49
Db 1 MAPAVIASQGVIMRSLTSKLSLLQPPPPPPAPQPSLRKGRKKILLRGLRHLDD 60
Qy 50 AFTRA---AEVWKKDELLKVAEQIRDLSYDIDSDEKPVHI----- 90
Db 61 YLLVBPSPDAPPDSTAACAKEVRELSVDVDFDELTTQLLHRRGGDGGSTAGAK 120
Qy 91 --ESQTLFROLKLRERHRIAIRIHNLSRVEVSSRNTRYNLVPEISSG---TEDDMS 145
Db 121 KMISSMIARLRLGELNRRRIADEVTLFRARVKEAIRRHESYHLGRRTSSRPBDDDD 180
Qy 146 YAEIRNQSR-----NVDEA-----ELVSPDSKRLLEMDITNANDGP-AKVICVGM 194
Db 181 REDSAGNERRRFLSLTFGMDDAAVHGQVAGRDISMQKLVRL---ADGEPKLKVASIVGS 237
Qy 195 GGLGKTALSRKIPSE-EDIRKNPFCNAWITVSQSFHRIELDKMIROLLOPSSLDQLH 253
Db 238 GGVKTTLATFYLHGRRLDAPDFCAFAVTPRPKPDWTKILTDMSQ-----RQMH 290
Qy 254 ELQKVVVQVHLSYELIEELKEKRYFVLDLWILHDWNWINEIAPKNNKSGSRIVIT 313
Db 291 QHOSDVWEVDRLLETIRTHLODKRYFIIEDLWASSMWDIVSR-GLPDNN-SCSRILIT 348
Qy 314 TRNVDLAEKATASLVHLDPLQNDALISLLRKNHEDMESNMKNQKVERIVNKG 373
Db 349 TEIEPVALACGVNSEHIKIDPLGDDVSSQLFSGVVGQGNFPGHLTEVSHDMKKCG 408
Qy 374 RLPLAITIGAVLATKQ---VSEWKFYEOL-PSELEINPSLEALRMVTLGVNHLPSH 428
Db 409 GLPLAI-TIYARHPKSQLLDGMQWNNHIQSLTTSNLKKNPTLOGMROVLNLYNLPHC 467
Qy 429 LKPCFLYLSIFPEDFEIQRNLVGRWIAEGFVRPKVGMWTKOVGESYNELINRSMIQRS 488
Db 468 LKACLLYLSIVKEDIIRKANLRQWMAEGFINSIENKMWEEVAGNYFDELVGRGLVQPV 527
Qy 489 RVGTAGIKTCRIHDIIRDITVSISROENP-VLLPMGDGSDLVQENTHIAFHGSMCKT 547
Db 528 DVNCKNEVLSCVHHMVLNFIKCSIBENFSITLDHSQTTVVRHADKVRRLSLHFSNAHDT 587
Qy 548 ---GLDWSIIRSLAIFGDRPKSLAHAVCPDQ---BMLRVL-----DLEDVTFLITQK 594
Db 588 TPLAGRLSQVRSWAFPG-----QVKCMPSIADYRLRLVLIICFWADQKTSY----- 635
Qy 595 DFDRIALLCHLKYLSIGYSSSYSLPRSIGKLOGLQTLNMSSTYIAALPSSIKLQCLHT 654
Db 636 DLTSIFELLQRLYLKITGNITV-KLPEKIQGLQHLQTLLEADARATAVL-LDIVHTQCLH 693
Qy 655 LRCIRELEFNFSLNHPMKCIWTICLPKVFTPLVSRDNRAKQIAEFHMATKFSWSESFG 714
Db 694 LRLVL-LDL---LPH-----CHRYIPT----- 711
Qy 715 VKVPKIGIKRLDQVLEYVDIIRTSRAIKELGOLSKLRKLAIVTGSTKECKIYAAI 774
Db 712 -SIPKWTGKLNLRILNI-----AVMQISO----- 735
Qy 775 EKLSSLOSLYMAALLSDIETLECLDSISSPPPLRTITGLNGSLEEMPNWIEQLTHLKKF 834
Db 736 -----DDLOTLKGSLTALSLLVRTAPAQRIV----- 763
Qy 835 NLWSSKUKKEGNMILGALPNLMFLSLYHNSYLGEKLVFKTGAPNRLTLVI-FNLQDLR 893

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Db 764 -----AANEG-----FGLSKYFMFVC-----TAPCMTFVEGAMPSVQRLNLRNANEFK 807
Qy 894 EIRPEDGSSPOLEKIEISCCELESIGI IHLPRKKEISLEYKSKVARLG----- 943
Db 808 Q-----YDSKETGLEHLVALAEBIS-----ARIGGTDDDESNTK 840
Qy 944 ----QLKEVNTHPNRVLRMDSRRDRHDLGAE 972
Db 841 EVESALRTAIRKHPTPTSLMVDIQWVDWIFGAE 873

RESULT 4
US-09-993-170-58
; Sequence 58, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: BB1385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/246,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 58
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-993-170-58

Query Match 12.9%; Score 676.5; DB 4; Length 928;
Best Local Similarity 24.9%; Pred. No. 4.1e-49;
Matches 262; Conservative 164; Mismatches 366; Indels 261; Gaps 37;

Qy 1 MAETVLSMARSLVGSATSKAAS-----AANETSLLGVKDIWYKDELKTM--Q 49
Db 1 MAPAVIASQGVIMRSLTSKLDLSLLQPPPPAPQSSLRKGERKKILLRGLRHLDD 60
Qy 50 AFLRA---AEVWKCKDELLKVAEQIRDSLYDIEDSLDEPKVHI----- 90
Db 61 YLLVEPSPDAPPDSTAAWKEVRELSVDVDFDELDTQLLHRRGGGSGSTAGAK 120
Qy 91 --ESQTLFRQVLKLRHRIAIRIHNLSKRYVEVSSRNTRYNLVEPISSG---TEDDMS 145
Db 121 KMISSMIARLKGELNRRRIADEVTLFRARVKEAIRRHESYHLGRTSSSRPREEDDDDD 180
Qy 146 YAEIRNQSAR-----NVDEA----ELVGSDSKRLLEMDTNDGPAKVLCVGM 194
Db 181 REDSAGNERRFLSLTFGMDDAVHGQVLGRDLSMQKLVRLW---ADGEPKLVASIVGS 237
Qy 195 GGLKATLSARKIFESE-EDIRKNFPCNAWITVQSOFHRIELLDKMIQQLGPPSLDQLLH 253
Db 238 GGUKTILATEFYRLHGRDLDPDCRAFVTPKPDWTKILTDMLSQL-----RPQH 290
Qy 254 ELQGVVVQVHHLSEYLIIEELKEKRYFVVLDDLWLHDWMNINEIAPPNNKKGSRIVIT 313
Db 291 QHQSDDVWEVDRLETTIRTHLODKRYFIIEEDLWASSMWDIVSR-GLPDNN-SCSRILIT 348
Qy 314 TRNVDLAEKATASLVLDPLQWDAISLLLRKTNKHEDMESKMKQKQVRIWVKCG 373
Db 349 TEIEFVALACGYNSEHIIKIDPLGDDVSSQLFFSGVVVQGNFPGHLTEVSHMDIKKCG 408
Qy 374 RLPLAITIGAVLATKO---VSEWKEFYEOL-PSELEINPSLEALRRMWTGLVGNHLP 428
Db 409 GLPLAI-TYIARHFQSLLDGQGNHNIQKSLTTSNLKKNPTLQGMQVNLINLPHC 467
Qy 429 LKPCFLYLSIPPEFETQRNLVGRWIAEAGFVRPKVGMGTTKDVGESYFNELINRSMTQRS 488
Db 468 LKACLLYLSIKEDYIIRKANLVRQWMAEGFINSIENKVMEEVAGNYPDELVGRGLVQPV 527
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Qy 489 RVGTAGKIKTCRIHDIIRDITVTSISROENF-VLLPMGDGSDLVQENTRHHIAFHGSMSCKT 547
Db 528 DVNCKNEVLSCVHVHVLNPIRCKSIEENFSITLDHSQTTVRHADKVRRLSLHFSNAHDT 587
Qy 548 ----GLDWSIIRSLAIFGDRPKSLAHAVCPDQL---RMLRVL-----DLBDVFLITQK 594
Db 588 TPLAGRLSQRVRSMAFFG-----QVKCMPSIADYRLLRVLILCFWADQEKTSY----- 635
Qy 595 DFDRIALLCHLYLSIGYSSSIYSLPRSIGKLOGLQTLNMSSTYIAALPSISIKLOCLHT 654
Db 636 DLTSIFELLQLRLYKLTGNITV-KLPEKIQGLQHLQLEADARATAVL-LDIVHTQCLLH 693
Qy 655 LRCIRELEFDNFSNLNHPMKCITNTICLPKVTPLVSRDNRAKQIAEFHMAATKSFWSSEFG 714
Db 694 LRLVL-LDL---LPH-----CHRYLFT----- 711
Qy 715 VKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGOLSKLRKLAIVITKGTKECKKILYAAI 774
Db 712 -SIPKWTGKLNLRILNI-----AVMQISQ----- 735
Qy 775 EKLSSLOSLYNNAALLSDIETLECLDSISSPPPLRLTLGLNGSLEEMPNIETQTLTKKF 834
Db 736 -----DLDLTKGLSLTALSALVRTAPQRIV----- 763
Qy 835 NLWSSKLKEGKNMLILGALPNLMFSLYHNSYLGEKLVFKTGAPPNLRTLVI-FNLQDLR 893
Db 764 ----AANEG-----FGLSKYFMFVC-----TAPCMTFVEGAMPSVQRLNLRNANEFK 807
Qy 894 EIRPEDGSSPOLEKIEISCCELESIGI IHLPRKKEISLEYKSKVARLG----- 943
Db 808 Q-----YDSKETGLEHLVALAEBIS-----ARIGGTDDDESNTK 840
Qy 944 ----QLKEVNTHPNRVLRMDSRRDRHDLGAE 972
Db 841 EVESALRTAIRKHPTPTSLMVDIQWVDWIFGAE 873

RESULT 5
US-09-336-946B-4
; Sequence 4, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A P1-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-336-946B-4

Query Match 12.6%; Score 662.5; DB 4; Length 928;
Best Local Similarity 24.8%; Pred. No. 6.7e-48;
Matches 262; Conservative 163; Mismatches 364; Indels 267; Gaps 38;

Qy 1 MAETVLSMARSLVGSATSKAAS-----AANETSLLGVKDIWYKDELKTM--Q 49
Db 1 MAPAVIASQGVIMRSLTSKLDLSLLQPPPPAPQSSLRKGERKKILLRGLRHLDD 60
Qy 50 AFLRA---AEVWKCKDELLKVAEQIRDSLYDIEDSLDEPKVHI----- 90
Db 61 YLLVEPSPDAPPDSTAAWKEVRELSVDVDFDELDTQLLHRRGGGSGSTAGAK 120
Qy 91 --ESQTLFRQVLKLRHRIAIRIHNLSKRYVEVSSRNTRYNLVEPISSG-TEDDMSYA 147
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Db 121 KMSMTARLNGELNRRRRIADEVTLFSARVKEAIRROESYHLGRTSSSRPRBEVD--- 177
Qy 148 EDIRNQARN-----VDEA-----ELVGFSDSKRLLEMDITNANDGP-AKVICV 191
Db 178 DDDREDSAGNERRPLSLTFGMDDAHVHQLVGRDISMQKLVRL--ADGEPKLVASI 234
Qy 192 VGMGGLGKTALSRKIFESE-EDIRKNPPCNAMITVSGSFHRIELKMIROLGLPSSLDQ 250
Db 235 VSGGVGKTTLTATFYLHGRRLDAPDCRAFAVTRPKPDMTKILTDMLSQL-----R 287
Qy 251 LLHLEQKVVVQVHLSYLLLEEKEKYFVVLDDMLLHDMNINEIAFPKNNKGSRI 310
Db 288 PQHQSSDWEVORLLETTIHTLODKRYFIIEEDLWASSMWDIVSR-GLPDNN-SCSRI 345
Qy 311 VITTRNDVLAEKCATASIVYHLDELQMDAISLLRLKTNKHEDMESKNNQKQVRIIV 370
Db 346 LITTEIEPVALLCCGYNSEHIIKIDPLGDDVSSQLPFGVGQGNPPGHLTEVSHDMIK 405
Qy 371 KCGRLPLAILTIGAVLATKQ-----VSEWEKPYEQI-PSELEINPSLEALRMVTLGYNHL 425
Db 406 KCGGLPLAI-TITARHFKSQLLDGNQWNNHITKSLTISNLKKNPTLQGMROVLNLIYNL 464
Qy 426 PSHLKPCLYLSIPPEDEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYENELINRSMI 485
Db 465 PHCLKACLLYLSIYKEDIIRKANLVROMMAEGFINSIENKVMEEVAGNYFDELVGRGLV 524
Qy 486 QRSVGTAGIKTKCRIHDIIRDITVTSISROENF-VLLPMGDSGLDVBENTRHIAFHGMS 544
Db 525 QPVDVNCQNEVLSVWHHVLNFRCKSIEENFSLDHSQTTVRHADKVRRLSLHPSNA 584
Qy 545 CKT-----GLWSIIRSLAIFGDRPKSLAHAVCPQOL---RMLRVL-----DLSDVTLFI 591
Db 585 HDITPLAGRLSLQVRSNAFFG-----QVKCMPSIADYRLRLVILCFWADQKTSY-- 635
Qy 592 TQKDFDRIALLCHLYLSIGVSSISYSLPRSIGKLOGLOTLMNSTVIAALPSSIKLOC 651
Db 636 ---DLTSIFELLQRLYLKITGNITV-KLPEKIQGLQHLQTLLEADARATAVL-LDIVHTQC 690
Qy 652 LHTRCIRELEFDNFSLNHPMKCTNTTICLPKVTPVLSRDNRAKQIAEFHMAFKSWSE 711
Db 691 LLHLRLVL-LDL-----LPH-----CHRYIF----- 711
Qy 712 SFGVKVPKIGKRLDLQVLEYVDIRRTSSRAIKELGQLSKRLKLAIVITKGSTKECKILY 771
Db 712 ---SIPKWTGKLNRLINI-----AVMQISQ----- 735
Qy 772 AAIEKLSLSLYNNAALLSDIETLECLDSISSPPPLRTLTGLNGSLEEMPNWIEQLTHL 831
Db 736 -----DDLDTLKGLSLTALSLVVRTAPAQRIV----- 763
Qy 832 KKFNLWSSKLKEGKNMLITLGPALNLMFLSLVHNSYLGKLVFKTGAPPNLRTLVI-FNLD 890
Db 764 -----ANEG-----FGSLKYFMFVC-----TAPCMTFVEGAMPSVORLNLRNAN 804
Qy 891 QLRBEIRFDGSSPQLEKIEISCRLSEGIIGIHLPRLKEISLBYKSKVARLG----- 943
Db 805 EFKQ-----YDSKETGLEHLVALAEIS-----ARIGGTDDDES 837
Qy 944 -----QLKEVTHPNRPVLRMSDRDRDHDLGAE 972
Db 838 NKTEVESALRTAIRKHPTTPTSLMVDIQWDMIFGAE 873
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RESULT 6

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US-08-930-996A-4
; Sequence 4, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
```

```
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-4

Query Match 12.08; Score 633; DB 3; Length 1240;
Best Local Similarity 24.7%; Pred. No. 3.8e-45;
Matches 247; Conservative 190; Mismatches 379; Indels 184; Gaps 40;

Qy 3 ETVLMSARSLVGSISAASAAANETSLLLGVEKDIIWIKDELTKMQAFRAAEVYMKKD 62
Db 2 EIGLVAGAFSSALNVLPDLAPNGDLLNFRKHQHVK-LLKKLQMTLRGIQIVLSDA 60
Qy 63 ELLKWAQIRDLSDYDIEDSLDEPKVHIESOTLFRQLVLRERHRIARIH----- 113
Db 61 ENKQASNPVRDMLNELRDVDAENLIEVYNEALRLKVEGQHNFSETSNQOVSDRFF 120
Qy 114 -NLKSRVEVSSRTRNYLVLPIS-SCTEDDMSVADIRNQSARNVDDEALVCFSDSKK 171
Db 121 LNIKKDLDE--TIETLKQEQIGLGLKEYFDSYTKLETRTPSLIDEPDIFG---RQS 175
Qy 172 RLLEMDITNANDGPA----KVICVGMGGLGKTALSRRKIFESBEDIRKNPPCNAMITVSQ 227
Db 176 EIEDLIDRLLESEGASGNLTVVPVGVGGLGKTTAKAVY-NDESVKNHFDLKAFCVSE 234
Qy 228 SFHRIELKMIROLGLPSSLDQLLHLELQGVVQVHLSYLLLEEKEKYFVVLDDLM 287
Db 235 AYNAFRITKGLQIGISIDLVDDNLNLQVQK-----LKERLKEKEFLIVLDDVM 283
Qy 288 --ILHDNWNINEIAFPKNNKGSRIIVITRNVLDLAEKCATASLVYHLDPLOMDAISLLL 345
Db 284 NDNYNEWDELNRNVPV--QGDIGSKIIVTRKDSVALMMGNEQI--SMGNLSTEASWSLFQ 339
Qy 346 RKTGNKHEDMESKNNQKQVRIVKNCGRLPLAILTIGAVLATK-QVSEWEKPYEQLPSE 404
Db 340 RHAFENDDPM-GHSELEEVGQIAACKGKPLALKTLAGMLRSKSEVEWKILRSEIWE 398
Qy 405 LEINPSLEALRMVTLGYNHLPSHLKPCFLYLSITPPEDFEIQRNRLVGRWIAEGFVRPKV 464
Db 399 LRDNILPAL-----MLSYNDLPAHLKRCFCSCAIFPKDYPFRKQVHILWIANGLV-PVE 453
Qy 465 GMTTKDVGESYFNELINRSMIQRSVGTAGIKTC-RIHDIIRDITVTSISQENFVLLPM 523
Db 454 DEITQDLGNQFFLELSRSRSLFVRPNPSEGNKELFLMHLVNDL-AQLASSKLCIRLEE 512
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QY 524 GDGSDLVQENTRHTAFHGSCKTGLD-----WSIIRSLA-----IFGDRPKSLA 568
Db 513 SQGSHML-EQCRHLSY---SMGYDGFEXKLPLYKLEQLRLLPTCSSVNFYFNPLTKRVL 569
QY 569 HAVCPDQRLMRVLDELBDVFLITQKDFDRIALCHLYKLSIGYSSSIYSLPRSIGKLOQ 628
Db 570 HNILP-TLRSIRALSLSH--YKMEELPNDLFIKLLRFLDIS-RTNKRPLPDSICVLYN 625
QY 629 LOTLNMSTVIAALPSISKLOCHLTLRCIRELEFDFNLSNHPMKCITNITICLPKVFTPL 688
Db 626 LETLLSSCKLEELPQWEXLINL-----RHLDISN----- 656
QY 689 VSRDNRAQIAEFHMTKFSWSESGVGVKPGKIGKLRDLQVLE-----YVDIRRTSSRAIK 744
Db 657 -----FWHLKMPHLHLSKLSLQVCAKFLVGWR-----ME 688
QY 745 ELGQSLK-LRKLAVI-----TKGSTKERCKILYAAIEKLSLSQSLYMNAAALLSD 792
Db 689 DLGEAQLYGSLSVVKLENVVDREAVKPKWREKNHVEQLSLEWSESISA--DNSQTERD 746
QY 793 IETLECLDSTSSPPPL--LRTLGLNGSLEMPNIEQIHLKKNLWSSKLEKGNMLIL 850
Db 747 I-----LDELPRHKNIQEVKIIGYRG--NPPNVVADPLFLKVKLSLRNCKDCYSLPAL 799
QY 851 GALPNLFLSLYHNSYLGEKLVFKTGAPPNLRVLVLENLDOLREIFED----- 899
Db 800 GQUPCLFLSV--KMGHIGRVTEE--FYGRUSSKKPNC--LEKLEFEDMTWKQWHAIG 854
QY 900 -GSSPOLEKIEISCRLESIGIIGIHLPRK-EISLEYKS 937
Db 855 IGEPTLEK-----LSIINCPELSLEIPIQFSS 882

RESULT 7

US-09-004-838-11
; Sequence 11, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelson, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Confering Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1402 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..1402
; OTHER INFORMATION: /note= "RLG1a amino acids"
; US-09-004-838-11

Query Match 11.8%; Score 622.5; DB 3; Length 1402;
Best Local Similarity 23.4%; Pred. No. 3.7e-44;
Matches 245; Conservative 178; Mismatches 353; Indels 269; Gaps 40;

QY 1 MAETVLSMARSLVCSAISKAASAAANETSLLLGVKEKDIWIKDELKTMQAFLRAEVMKK 60
Db 367 MAETVLSAFLTVV---FEKLAEALKKIVRSKRISSELKKLKETLDIQDILLNDASQKVR 423
QY 61 KDELLKVWAEQIRLSDYDIEDSLDEFKVIH-----ESQTLFRQV-----KLRER 105
Db 424 TNEAVKRWLNDLQHLAYDIDDLDDXATEAVRRELTTEGGASSSWVRKLIIPSCCTSPQS 483
QY 106 HRIAIRHNLSRVVE--VSSRNTRYNLVPEPISSCTEDDMDSYAEIIRNQSARNVDEABLV 164
Db 484 NRMHAKLDDIATRLQELVEAKN--NLGLSVITYEKPRIERY-----EASLVDESQTV 533
QY 165 GFSDSKKRLLEMDITNDANDGPAK---VICVVGMGGLKLTALSRKIPSEEDIRKNFPCNA 221
Db 534 GREDDKKKLEKLGDKDESGNQFSFVPIVGMGVGKTTIARLLYD-EKKVKOHFELRA 592
QY 222 WITVQSQFRIEILKMDIROLGSPSLDQLLHLEQGVQVQVHLSLEYLIEELKEKRYFV 281
Db 593 WVCVSDSEFSVPNTSRVIYQSVTG-----EKKEFEDNLQLQEALEKLRNQLFLI 641
QY 282 VLDDLTWLHDWNWINEIAFPKNNKKGSRIVITTRNVDLAEKCATASLYVH---LDLFQMN 338
Db 642 VLDDVWSESYGDMWEKLVGPPFLAGSPGSRITWTTRKEQLLRKLGFS---HQDPLEGLSQD 697
QY 339 DALSLLRKTNNKH-----EDMESNNQMKQKVERIVNKGRLPLAILITIGAVLANQVSEW 394
Db 698 DALSLEFAQ-----HAFGVNPFDSHTLRPHGELFVKKCDGLPLALRTLGLRLRTK--TDE 750
QY 395 EKPYEQLPSEL-----EINPSLEALRMVTLGYNHLPKPCFYLSIFPDDFEQIR 447
Db 751 EQWKELLDSEIWRGLKSDIEIVPALR-----LSYNDLSAKLLKLLFAYCSLFPKDYEDK 803
QY 448 NRLVGRWIAEGFV-RPKVGMTTKDVGSYFNELINRSMIQSRVGTAGIKTKRI-HDII 505
Db 804 EELILLWAEGLFHQPTKNSKQRLGLEYPKXELLSRSFFQH-----APNKKSLFVMDHLM 858
QY 506 RDI-----VSISRQENFVLLPMGDSGLVQENTHIA-----FHG 541
Db 859 NDLATFVAGEFFSRDLDEMKEKFRMXSL-----EKHRMSFVCEYIYKKEPFRG 910
QY 542 SMSCKTGL-----DWSIIRSLAIFGDRPKSLAHAVCPDQLR---MLRVLDLEDVTF 590
Db 911 AKNLRTFLALSVGVVEDWKF-----YLSNKVLDXLDQLPLLRVLXL----- 953
QY 591 ITQKDFDRIALCHLYKLSIGYSSSIYSLPRSIGKLOGLQTLNMSSTVIAALPSISKLO 650
Db 954 -----IXL-----XIXXVPKXVGMXHLRYLNLSTXITHLPEXXCNLY 992
QY 651 CLHTLRCIRELEFDFNLSNHPMKCITNITICLPKVFTPLVSRDNRAQIAEFHMTKFSWS 710
Db 993 NLQTL-----IVSGCYXVLPLKPTFSXL-----KNLXHDFMRXTPXK 1030
QY 711 ESFGVKVPKIGIKLRDLQVL-EYVDIRRTSSRAIKEL-----GOLSKRLKLAIVITGST 763
Db 1031 -----NMPLXIGELKXIQTLFXNIGIAITELKNLXNHLGKXCIGLGGWENAVGCTLSEL 1085
QY 764 KEK-----CKILYAAIEKLSQSLYMNAAALLSIETLECLDSTSSPPPL 808


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Db 147 -----KVKN-----NMVRDQRKQLLEDL-TRSYSGPKVPIVGMGGIGKTTLA 191
Qy 204 RKIPESIEDIRKPNPCNAWITVSQSFRIELDKMIRQLLGPSSLDQLLHQLQKVVQV 263
Db 192 KEVY-NDSEILCRFDVHAWATISQOHNKKEILLGLLHSTIKMDDRVKXIGEAE-----243
Qy 264 HHLSEYLIIEELKEKRYFVWLDLWILHDMWNWINEIAPPKNKKGSRIVITTRNVDLAEKC 323
Db 244 --LADMLQSLKRYKRYLIVLDDIISCEVWDGVR-CPFTEDNAGSRILLITRNDVACYA 300
Qy 324 ATASLVYHLDFLOMNDALISLLRKTNNKHEDMESNMQMKQVERIVNKKCRPLPLAITIG 383
Db 301 GVENFSLRMFMDDQDEWS-LFKSAAPSSALP--YEFETVGKQIADCEHGLPLTVVVA 357
Qy 384 AVLATKO-VSEWEKFEQLPSELINPSLEALRMWTLGYNHLPSHLKPCFLYLSIPED 442
Db 358 GLLSKRKTIEDWKTVAKDVKFSVTNDPD-ERCSRVGLSYDHLTSDLTKCLLHGFIPED 416
Qy 443 FEIQORNLVGRWIAEGFVRPKVGMVTTKDVGESYFENELINRSMI---QKSRVGTAGTKTC 499
Db 417 SDIPVKMLMSWMAEGFL--KLENDLEGEVEKCLQELVDRLCLVLVSKSRDGT--KIRSC 472
Qy 500 RIHDIIRDITVISIRQENFVLLPMGDGSDLV-----QENTRHHIAFHGMS 544
Db 473 KVHDLIYDLCVREQENIFIM-----NDIVLVSYPECSYLCVMKQPPKRVGTGDEINY 527
Qy 545 KTGOLDWSII-----RSLAIFQDRPKSLAHAVCPD--QURMLRVLDLE 585
Db 528 CPYGLYRALLTPVNRQLRDHNNLKRTHSVFSFHLPELYLVYLKSEVHFVKLAKVLELR 587
Qy 586 DVTFLITQKDP-----RIALLCHLYLSIGVSSIYSLPRSIGKQLQLOT--LNMSSYI 639
Db 588 -----HRQIDGPPREILSLIWRYLSL-PSYGNFDPVPEICRLWNLQTFIVORPSDI 639
Qy 640 AALPSEISKLOCLHTLRCIREFDNFSLNHPMKCIITNTICLPKVFTPLVSRDNRAQIA 699
Db 640 IIPAEIIEWLMQLRHLK-----LPRFYLTP-----663
Qy 700 EFHMTKSFWSSESQVKVPKG-IGKLR-----DLOVLEYVDVIRTSSRAIKELQOLSKLR 753
Db 664 -----DCPSGSVDKGRHLDFSNIQTISYLSPRCCTKEVI--MG-IQNVK 704
Qy 754 KLAIVITGSTKEKILYAAIEKLSLQSLVMAALLSDIETLECLDSISSPPPLRLTLG 813
Db 705 KLGI---SGNKDDYKSRFS-----GLENNLVYLOQLIELSLISVDYSLLPVVIS--751
Qy 814 LNSLEEMPWNWIEQLTHLKKFNLWSKLEKGNMMLILGALPNLMFLSLYHNSYLGEKLVF 873
Db 752 ---SAKAPPATLKKGLERTYLSWS-----YLDIITAELENLEVLKMDDACCGEWHP 801
Qy 874 KTGAFPNLRTLVIFNLQDLREIRFEDGSSPOLEKIEISCCR-----LESIGIHLPR 927
Db 802 IVMGFNRLKLLLI-KYSFLKFWKATNDNFPVLERIMIRSCNKLKEIPFIEADITHLQIE 860
Qy 928 LKEISLEYKSVARLGOLKGVNTHP-----NRPVLRMDSRRDH 967
Db 861 LRECPKLGESAARIQKEQEDLGNPVDVIRISNPLKESDSDEEH 905

RESULT 10
US-08-930-996A-2
; Sequence 2, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; NUMBER OF SEQUENCES: 12
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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-2

Query Match 11.4%; Score 598.5; DB 3; Length 1220;
Best Local Similarity 24.3%; Pred. No. 3.5e-42;
Matches 237; Conservative 189; Mismatches 349; Indels 201; Gaps 44;

Qy 43 DELTKMQAFRAAEVMMKKDELLKVAEQIR---DLSYDIEDSLDEPKVHIESOTLPRQL 99
Db 48 DILLSLQIVLSDAENKKASQFVSQWLHLQTAADAAENLIEQVNYEALRLKVTSSQQV 107
Qy 100 VKLERHRIAIR---IHNLSRVEEVSSRNTRYNLVPEISS-----GTEDDMSYAEIR 151
Db 108 SDL-----NCLSDSDFFLNIKKLEDTIK-----LEVLEKQIGRLGKEHFITKQETR 157
Qy 152 NQSAARNYDEAELGFDSDSK-----RLLEMIDTNANDGPAKVICVVMGGLGKTALSRIKIF 207
Db 158 TPSTSLVDDSGIFGRKNEIENLVGRLLSM-DTKRKN--LAVVPVGVGGMGKTTAKAVY 214
Qy 208 ESEBDIRKNFPCNAWITVSQSFRIELDKMIRQLLGPSSL--DQLHLELQKVVV--QV 263
Db 215 -NDRVQKHFGLTAWFCVSEAYDAFRIPKGLQSE-IGSTDLKADDNLNLQVLKADNDL 272
Qy 264 HHLSEYLIIEELKEKRYFVWLDLW--ILHDWNWINEIAPPKNKKGSRIVITTRNVDLAE 321
Db 273 NQLQVKLKEKNGKRFVLVLDVWVNDNYPEDDRLNLF--QGDIGSKIIVTTKESVAL 330
Qy 322 KCATASLVYHLDFLOMNDALISLLRKTNNKHEDMESNMQMKQVERIVNKKCRPLPLAIT 381
Db 331 MMDSGAI--YMGILSSEDSWA-LPKRHSLEHKDPKEHPEPEVGVKQIADCKGLPLAKA 387
Qy 382 IGAVLATK-QVSEWEKFEQLPSEL-EINPSLEALRMWTLGYNHLPSHLKPCFLYLSIP 439
Db 388 LAGMLRSKSEVDEWRNI---LRSEIWELPSCSGNILPALMLSYNDLPALHKOCLAYCAIY 444
Qy 440 PEDFEIQORNLVGRWIAEGFVRPKVGMVTTKDVGESYFENELINRSMIORSRVGTAGTKTC 499
Db 445 PKYQFRKEQVHLWNIANGLVH-----QPHSGNQYFIELSRSLFEMASPFSDVEEF 498
Qy 500 RIHDIIRDITVISIRQENFVLLPMGDGSDLVQENTRHHIAFHGMSCKTGLDWSIIRSLAI 559
Db 499 LMHDLVNDL-AQIASSNHCIRLEDNKGSHML-EQCRH-----MSYIGQDGEFEKLKSL 550
Qy 560 FGDR-----PKSLAHAVCPDQOLRMRLVLDLEDVTFITQKO-FDRIA 600
Db 551 FKSEQLRTLLPIDIQFHYSKKLSKRVLHNLTP-LTSLRALSLSHYQIEVLNPLDFIKLK 609
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Qy 601 LLCHKYLSIGYSSISYLSRPSIGKLOGLOTLNMS--TYIAALPSEISKLOCLTLRCIR 659
Db 610 L---LRFELDS-ETSITKLPDSIFVLNLETLLSSCEYLEELPLOWEKLNL-----R 659
Qy 660 ELEPDNFSLNHPMKCIYNTICLPCVFTPLVSRDNRKQIAEFHMAKSFWSSEFGVKVPK 719
Db 660 HLD-----ISNTRL-----KIPL 673
Qy 720 GIGKRLDQVL-----BYVDIRTSRAIKELGOLSKRLKLAIVI-----TKGS 762
Db 674 HLSRLKSLQVLVGAFLVGGWMEYL-----GEAPNLVGLSILELENVDRREAVKAK 727
Qy 763 TKECKKLYAAIEKLSLSQSLYMAALLSDIETLECLDSISSPPPLRTGLNGLS-LEM 821
Db 728 MREKQHEQSLSEWSEISA---DNSQTERDI-----LDEL-RPHKNIKAVEITGYRGTF 779
Qy 822 PNWTEQLTHLKKFNLWSSKLEKGNMLITIGALPNLPLSLYHNSVLGKLVFKTGAPENL 881
Db 780 PNWVADPLFVKLVHLYLENCKDCYSLPALGQPLCLEFLSI---RGWGIYRVTEE-FYGR 836
Qy 882 RTLVIPLNDQIREIRPED-----GSSPOLEKIEISCCRLSESGIIGIHLPLK 929
Db 837 SSKKPFN--SLVKLRFEDPMPKQWHTLIGEGFPLEKLSIKNC-----P 879
Qy 930 EISLEYKSKVARLQOL 945
Db 880 ELSLEIPIQFSSKRL 895

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RESULT 11

US-08-680-327-3

; Sequence 3, Application US/08680327

; Patent No. 5859321

; GENERAL INFORMATION:

; APPLICANT: Staskawicz, Brian S., Oldroyd, Giles Edward,

; APPLICANT: Salmeron, John M., Rommens, Caius

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS: PATHOGEN RESISTANCE

; ADDRESSEE: Klarquist Sparkman Campbell Leigh &

; ADDRESS: Whinston

; STREET: One World Trade Center

; STREET: 121 S.W. Salmon Street

; CITY: Portland

; STATE: Oregon

; COUNTRY: United States of America

; ZIP: 97204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3-1/2 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/680,327

; FILING DATE: July 11, 1996

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/310,912

; FILING DATE: September 22, 1994

; CLASSIFICATION: 800

; APPLICATION NUMBER: 08/227,360

; FILING DATE: April 13, 1994

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Alan. E.

; REGISTRATION NUMBER: 35,123

; REFERENCE/DOCKET NUMBER: 5151-45038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-3446

; INFORMATION FOR SEQ ID NO: 3:

;

;

;

;

;

;

;

;

;

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1824 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-680-327-3

Query Match 10.9%; Score 575; DB 2; Length 1824;

Best Local Similarity 23.8%; Pred. No. 7.1e-40;

Matches 249; Conservative 188; Mismatches 378; Indels 230; Gaps 46;

17 ISKAASAAANETSLLGVEKDIWIKDELKTMQAFI-RAAEVWKKCDLKKVMAEIRDL 75

Qy 959 LGKLEELLRLSKLDLIIDKHQIESVKEGLLCIRSFIDHFSYDEHDEACGLIA-RVSM 1017

Db 76 SYDIEDSLDE-----PKV-----HIESQTLFRQLV-KLRRHRHRAIRHNLKSRVE 120

Qy 1018 AYKAEYVIDSLAYSHPLWYKVLVSEVLNI-KLVNKVGTCTERRNIEVTVHEV----- 1072

Db 121 EVSSRNTRYNLVEPISSGTEDDMDSYAEIDIRNQARNVDEAEIVGFSGSKRGLLEMDTN 180

Qy 1073 ---AKTTY--VAP-----SFSAYTQRANE-----EMEGFQDT---IDELKDKL 1108

Db 181 ANDGP-AKVICVVGMGIGKTALSRIKIPESSEDIRKNPPPCNAWITVSQSEHRIELDKMI 239

Qy 1109 LGGSPFELDVISIVGMPGLGKTTAKKIY-NDPEVTSRFDVHAQCQVVTQLISRWRELLTIL 1167

Db 240 RQLIGSSLDQLLHLEQKVVVQVHHLSSEYLIBELKEKRYFVVLDDWLHLDWMINBIA 299

Qy 1168 NDVLEPSDRNE---KEDGEIADELRRF-----LLTKRFLIIDDVDWYKVDNLCWCF 1217

Db 300 PPKNKKGSRIVITTRNVDLAEKCATASLVTHLDFLQWNDALISLLRTKNQNHEDMESNK 359

Qy 1218 SDVSNR--SRILITRLNDVAEYVKCESDPHHLFRDDESWTLLQKEV---FQGESCPP 1272

Db 360 NMOKMVERIVNKGRLPLAILTIGAVLATKQ--VSEWEKPYEQLPSELEINPSLEALRM 417

Qy 1273 ELEDVGFEISKRCGLFSLVVLVAGVLKQKKKTLDSW-KVVEQSLSSORIG-SLEESISI 1330

Db 418 VTGYNHLPShLPCFLYLSIPPEDFEIRQNRNLVGRVIAEGFVRPKVGMITKDVGESYFN 477

Qy 1331 IGPSYKNLPHYLKPCFLYFCGFLQKDIHVSMMKLMVAEGFVQANNEKQEDTAQGFLD 1390

Db 478 ELINRSMIQSRVGTAGKIYTCRIHDIIRDTIVSISQENFVLLPMGDGSDLVQENTR-- 535

Qy 1391 DLIGRNVVMAKEKRPNTKVTCTRIHDLHLKFCMEKAKQEDP-LLQINSGEVGFPERLEEY 1449

Db 536 HIAPHGSMCKTGLD-W-----SIIRSLAIFGDRPKSLAHAVCPDOL-----R 577

Qy 1450 RLFVH---SYODEIDLWRPSRSNRVSL-----LFNAIDPDNLLWPRDISIFESFK 1497

Db 578 MLRVLDLEDVTLITQKDFDRIALLCHLVLSIGYSSSIYSLPRSIGKLOGLQTL---NM 634

Qy 1498 LVKVLDEL--SFNIGGTFPTEIQVLIQMKYFAA--QTDANSIPSSIAKLENLEFVVVRL 1553

Db 635 SSTYIAALPSEISKLOCLHLTCIRELEFPNFSLNHPMKCITNTICLPKVFTPLVSRNR 694

Qy 1554 GGEMI--LPCSLLKQV---KLRIHVANDRVSGFLHNMVDLTGNSQLPNL----- 1598

Db 695 AKQIAEFHMAKTSFWSSEFGVKVPGKIGKLRDLQVLEVVDIRRTSSRAIKELGOLSKLRK 754

Qy 1599 -----ETTFSTFRLPYGKD-----AELVLRKMPKURK 1624

Db 755 LAVITKGS-----TKECKKILYAAIEKLSLQSLYMAALLSDIETLECLDSISSPPPL 808

Qy 1625 LSCIFSGTFCYGRKLGRC-VRPRLDFLSHLSLK-----LVNSNSYPAKL 1669

Db 809 LRTGLNGSLEEMPNTWIEQTLTHLKKFNL-WSSKLKEGKNMLILGALPNMLFSLYHNSYL 867

Qy 1670 PHKF-----NFPQSRLRELTSKFRPLMT-----QISIIAELPNLVILKLLRAFE 1714

Db 868 GEKLVPTKTAGPNLRLTAVIPLNDOLREIRP--EDGSSPOLEKIEISCCRLESGIIGIHL 925

Qy 1715 GDHWEVKDSBFLKYL---KLDNLKVQVMSISDADFPKLEHLVLTCK----- 1760

Db

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 22:05:25 ; Search time 1041.76 Seconds
(without alignments)
17609.842 Million cell updates/sec

Title: US-10-656-394A-3
Perfect score: 3099
Sequence: 1 atggcgagacgtgtctgag.....gcacagctcaagctgctga 3099

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3099	100.0	3099	12	Adm72240 O. minuta
2	2977	96.1	3096	12	Adi57171 Oryza min
3	2953.2	95.3	3090	12	Adm72250 O. minuta
4	2910.2	93.9	3099	12	Adm72244 O. minuta
5	2862	92.4	76272	12	Adi57166 Oryza min
6	2842.2	91.7	3276	12	Adi57175 Oryza min
7	2359.8	76.1	2997	12	Adm72248 O. minuta
8	1591.8	51.4	3220	12	Adi57173 Oryza min
9	1571.8	50.7	2940	12	Adi57167 Oryza min
10	1563	50.4	2982	12	Adm72238 O. minuta
11	1491.4	48.1	2422	12	Adm72252 O. minuta
12	1156.2	37.3	2982	12	Adi57169 Oryza min
13	1053.2	34.0	4147	12	Adm72242 O. minuta
14	949.2	30.6	2265	12	Adi57179 Oryza min
15	854.2	27.6	2351	12	Adi57180 Oryza min
16	555.8	17.9	1355	12	Adi57177 Oryza min
17	374.6	12.1	1214	12	Adm72251 O. minuta
18	372.2	12.0	1389	12	Adm72246 O. minuta
19	184	5.9	2862	3	Aaz58295 Sorghum r
20	176.8	5.7	2954	3	Aaz58294 Sorghum r

21	176.8	5.7	6760	3	Aaz58293	Sorghum r
22	131	4.2	4125	8	Ada70202	Rice gene
23	129	4.2	3925	3	Aaz46679	Blatt dis
24	129	4.2	4514	3	Aaa11350	CDNA for
25	128.4	4.1	2877	4	ABL50546	Mla1 nucl
26	125.6	4.1	2871	4	ABL50537	Barley M1
27	125.6	4.1	2871	4	ABL50547	Mla6 nucl
28	125.6	4.1	3717	4	ABL50538	Barley M1
29	125.4	4.0	2739	3	Aaz50262	Coding re
30	125.4	4.0	2817	3	Aaz50652	Coding re
31	125.4	4.0	2833	4	ABL50549	Rghibcd n
32	125.4	4.0	10329	3	Aaz50653	Genomic D
33	125.4	4.0	10329	3	Aaz50264	Genomic D
34	124	4.0	3434	4	ABL50541	Barley M1
35	121	3.9	2851	4	ABL50548	Mla6 nucl
36	118.8	3.8	2904	4	ABL50550	Rghia nuc
37	115.4	3.7	3989	4	ABL50551	Mla1 nucl
38	115.4	3.7	7900	4	ABL50542	Barley M1
39	115	3.7	2745	12	ADJ39841	Plant CDN
40	114.2	3.7	3683	4	AAS03713	DNA encod
41	113.2	3.7	2613	10	ADD29383	Potato Me
42	112.6	3.6	3066	2	Aaz37154	Partial n
43	112.6	3.6	5820	2	Aaz37153	DNA seque
44	112.2	3.6	4052	4	ABL50554	Mla conse
45	111.8	3.6	3976	4	ABL50552	Mla6 nucl

ALIGNMENTS

RESULT 1
ADMT72240
ID ADM72240 standard; CDNA; 3099 BP.
XX
AC ADM72240;
XX
DT 03-JUN-2004 (first entry)
XX
DE O. minuta NBS2 polypeptide encoding CDNA.
XX
KW P12; NBS2; plant protectant; gene therapy; rice; disease resistance;
KW gene; 88.
XX
OS Oryza minuta.
XX
FH Key Location/Qualifiers
FT CDS 1..3099
FT /*tag= a
FT /product= "NBS2"
XX
FN WO2004022715-A2.
XX
PD 18-MAR-2004.
XX
PF 08-SEP-2003; 2003WO-US027913.
XX
PR 09-SEP-2002; 2002US-0409216P.
PR 18-MAR-2003; 2003US-0455713P.
PR 05-SEP-2003; 2003US-00656394.
XX
(OHIS) UNIV OHIO STATE.
XX
Wang G;
XX
WPI; 2004-257576/24.
DR P-PSDB; ADM72241.
XX
PT New rice P12-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX
PS Claim 1; SEQ ID NO 3; 120pp; English.
XX

CC The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA
CC encoding a rice NBS2 polypeptide.
XX
SQ

Sequence 3099 BP; 965 A; 607 C; 725 G; 802 T; 0 U; 0 Other;	
Query Match	100.0%; Score 3099; DB 12; Length 3099;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 3099; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGCGGAGACGGTCTGAGCATGCGAGGTGCTGGTGGCAGTGCATCAGCAAGGCC 60
Db	1 ATGCGGAGACGGTCTGAGCATGCGAGGTGCTGGTGGCAGTGCATCAGCAAGGCC 60
Qy	61 GCCTCTGCGCTGCCAATGAGACGAGCCTCTGCTCGCGCTCGAAGGACATCTGGTAT 120
Db	61 GCCTCTGCGCTGCCAATGAGACGAGCCTCTGCTCGCGCTCGAAGGACATCTGGTAT 120
Qy	121 ATCAAGATGAGCTTAAACCAATGACGACATTTCTTAGAGCTGCTGAAGTTATGAAAAAG 180
Db	121 ATCAAGATGAGCTTAAACCAATGACGAGCATTCCTTAGAGCTGCTGAAGTTATGAAAAAG 180
Qy	181 AAAGATGAATATTAAAGGTTTGGGCAGAGCAAAATACGTGACCTGTGCTATGACATTGAA 240
Db	181 AAAGATGAATATTAAAGGTTTGGGCAGAGCAAAATACGTGACCTGTGCTATGACATTGAA 240
Qy	241 GATTCCTTGTATGAATTTAAAGTTCATATTGAAGCCAAACCTATTTCGTCAGTTGGTG 300
Db	241 GATTCCTTGTATGAATTTAAAGTTCATATTGAAGCCAAACCTATTTCGTCAGTTGGTG 300
Qy	301 AAACCTAGAGAGCGCACCGATCGTATCGTATCCAGCAACCTCAAAATCAAGAGTTGAA 360
Db	301 AAACCTAGAGAGCGCACCGATCGTATCGTATCCAGCAACCTCAAAATCAAGAGTTGAA 360
Qy	361 GAAGTGAATAGCAGGAACACACGCTACAAATTTAGTCGAGCCTATTTCCTCGGCACAGAG 420
Db	361 GAAGTGAATAGCAGGAACACACGCTACAAATTTAGTCGAGCCTATTTCCTCGGCACAGAG 420
Qy	421 GATGACATGGATTCCTATGAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAA 480
Db	421 GATGACATGGATTCCTATGAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAA 480
Qy	481 GCTGAGCTTGTGGTTTTCTGACTCCAAAGAAAAGGCTGCTTGAAATGATCGATACCAAT 540
Db	481 GCTGAGCTTGTGGTTTTCTGACTCCAAAGAAAAGGCTGCTTGAAATGATCGATACCAAT 540
Qy	541 GCTAATGATGTCGGGCCAAGGTAATCTGTGTTGTTGGGATGGGTGTTTAGGCAAGACA 600
Db	541 GCTAATGATGTCGGGCCAAGGTAATCTGTGTTGTTGGGATGGGTGTTTAGGCAAGACA 600
Qy	601 GCTCTTCGAGGAAGATCTTTGAAAGGGAAGAGACATTAGGAAGAACTTCCCTTGGCAAT 660
Db	601 GCTCTTCGAGGAAGATCTTTGAAAGGGAAGAGACATTAGGAAGAACTTCCCTTGGCAAT 660
Qy	661 GCTTGGATACAGTGTCAATCATTTTACAGGATTCAGCTACTTAAAGATATCATACGC 720
Db	661 GCTTGGATACAGTGTCAATCATTTTACAGGATTCAGCTACTTAAAGATATCATACGC 720
Qy	721 CAACCTCTTGGTCCAGTTCTCTGGATCAACTCTTGTGATGAATTCGAGGGAAGGTGGTG 780
Db	721 CAACCTCTTGGTCCAGTTCTCTGGATCAACTCTTGTGATGAATTCGAGGGAAGGTGGTG 780
Qy	781 GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGGCTCAAGAGAGAGGTACTTTT 840
Db	781 GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGGCTCAAGAGAGAGGTACTTTT 840
Qy	841 GTTGTCTTAGATGATCTATGATTTTACATTTGGAATTCGATAAATGAAATTCGATTT 900
Db	841 GTTGTCTTAGATGATCTATGATTTTACATTTGGAATTCGATAAATGAAATTCGATTT 900
Qy	901 CCTAAGAACATAAGAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCG 960

Db	901 CCTAAGAACATAAGAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCG 960
Qy	961 GAGAAGTGTGCCACAGCCTCACTGGTGACACCTTGATTTCTTGCGAGATGAACGATGCC 1020
Db	961 GAGAAGTGTGCCACAGCCTCACTGGTGACACCTTGATTTCTTGCGAGATGAACGATGCC 1020
Qy	1021 ATTTCAATGCTTACCTGAGAAAAACAAATAAAAAATCATGAAGACATCGAATCAATAAAAAAT 1080
Db	1021 ATTTCAATGCTTACCTGAGAAAAACAAATAAAAAATCATGAAGACATCGAATCAATAAAAAAT 1080
Qy	1081 ATGCAAAAGATGTTGAACGAATTTGTAATAAATGTGGTCTCTACCAATAGCAATACTTT 1140
Db	1081 ATGCAAAAGATGTTGAACGAATTTGTAATAAATGTGGTCTCTACCAATAGCAATACTTT 1140
Qy	1141 ACAATAGAGCTGTGCTTGCACCTAAACAGGTGTCAGATGGGAGAAATTCATGAACAA 1200
Db	1141 ACAATAGAGCTGTGCTTGCACCTAAACAGGTGTCAGATGGGAGAAATTCATGAACAA 1200
Qy	1201 CTTCTTTCAGAACTAGAAATAAACCCCAAGCCTGGAAGCTTTGAGAGAAATGGTGACCCCTA 1260
Db	1201 CTTCTTTCAGAACTAGAAATAAACCCCAAGCCTGGAAGCTTTGAGAGAAATGGTGACCCCTA 1260
Qy	1261 GGTTCACCAACCTTACCATCCATCTGAAACCATGCTTTTGTATCTAAGATPATCTTTCCCT 1320
Db	1261 GGTTCACCAACCTTACCATCCATCTGAAACCATGCTTTTGTATCTAAGATPATCTTTCCCT 1320
Qy	1321 GAGGATTTTGAATACAAAGGAATCGTCTAGTAGGTAGATGATGACAGAGGGTTGGTT 1380
Db	1321 GAGGATTTTGAATACAAAGGAATCGTCTAGTAGGTAGATGATGACAGAGGGTTGGTT 1380
Qy	1381 AGACAAAGGTTGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGCTAATC 1440
Db	1381 AGACAAAGGTTGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGCTAATC 1440
Qy	1441 AACCGAAGTATGATTTCAACGATCAAGAGTGCGCACAGCAGGAAAAATTAAGACTTGTGCA 1500
Db	1441 AACCGAAGTATGATTTCAACGATCAAGAGTGCGCACAGCAGGAAAAATTAAGACTTGTGCA 1500
Qy	1501 ATCCATGATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATTA 1560
Db	1501 ATCCATGATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATTA 1560
Qy	1561 TTACCAATGGAGATGGCTCTGATTTAGTTTCAAGAAAAACACTCGCCACATAGCATTCCTAT 1620
Db	1561 TTACCAATGGAGATGGCTCTGATTTAGTTTCAAGAAAAACACTCGCCACATAGCATTCCTAT 1620
Qy	1621 GGGAGTATGTCCTGCAAAAACAGGATTTGGAAGCAATTTATTCGATCATTTAGCTATTTT 1680
Db	1621 GGGAGTATGTCCTGCAAAAACAGGATTTGGAAGCAATTTATTCGATCATTTAGCTATTTT 1680
Qy	1681 GGTGACAGCCCAAGAGCTTAGCACATGCTGCTGAGTTCAGATCAATTTGAGGATGTTACGG 1740
Db	1681 GGTGACAGCCCAAGAGCTTAGCACATGCTGCTGAGTTCAGATCAATTTGAGGATGTTACGG 1740
Qy	1741 GTCTTGGATCTTGAAGATGTGACATCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
Db	1741 GTCTTGGATCTTGAAGATGTGACATCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
Qy	1801 TTGTTGTGCCACTTGAATAACTTTGAGTATTTGGATTTTCGTCATCCATATATTCTACTTCCC 1860
Db	1801 TTGTTGTGCCACTTGAATAACTTTGAGTATTTGGATTTTCGTCATCCATATATTCTACTTCCC 1860
Qy	1861 AGATCCATTTGGTAAACTACAGGGGCTTACAGCTTTGAACATGTCAAGCACATACATTGCA 1920
Db	1861 AGATCCATTTGGTAAACTACAGGGGCTTACAGCTTTGAACATGTCAAGCACATACATTGCA 1920
Qy	1921 GCATACCAAGTGAATCACTCAATGCTGATATCTCTTCTGTTGTTAAGAGAG 1980
Db	1921 GCATACCAAGTGAATCACTCAATGCTGATATCTCTTCTGTTGTTAAGAGAG 1980
Qy	1981 CTTGAAATTCGACAACTTTAGTCTAAATCACCCCAATGAAGTGCATTAACACAAATATGC 2040
Db	1981 CTTGAAATTCGACAACTTTAGTCTAAATCACCCCAATGAAGTGCATTAACACAAATATGC 2040

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Db 1981 CTTGAAATTGCAACTTTAGTCTCTAAATCACCACCAATGAAGTCATCACTAACACAAATATGC 2040
Qy 2041 CTGCTAAAGTATTTACACCTTTTATGTTAGTTCGCGATATATCGTGCAAAACAAATTTGCTGAA 2100
Db 2041 CTGCTAAAGTATTTACACCTTTTATGTTAGTTCGCGATATATCGTGCAAAACAAATTTGCTGAA 2100
Qy 2101 TTTTCATGCGCCACCAAAAGTTTCTGGTCTCTGAATCATTCGGTGTGAAGGTACCCCAAGGA 2160
Db 2101 TTTTCATGCGCCACCAAAAGTTTCTGGTCTCTGAATCATTCGGTGTGAAGGTACCCCAAGGA 2160
Qy 2161 ATAGTAAAGTTGCGAGACTTACAGGTTCTAGATATGTAGATATCAGGCGACCAAGTAGT 2220
Db 2161 ATAGTAAAGTTGCGAGACTTACAGGTTCTAGATATGTAGATATCAGGCGACCAAGTAGT 2220
Qy 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTAGCTGTGATACAAAA 2280
Db 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTAGCTGTGATACAAAA 2280
Qy 2281 GGCTCGACAAAGGAAATGTAAAGTACTTTATGCGCCATTGAGAGCTCTCTCCCTC 2340
Db 2281 GGCTCGACAAAGGAAATGTAAAGTACTTTATGCGCCATTGAGAGCTCTCTCCCTC 2340
Qy 2341 CAATCTCTATATGAATGCTGCGTTATATCAGATATTGAAACACTTTGAGTGCCTAGAT 2400
Db 2341 CAATCTCTATATGAATGCTGCGTTATATCAGATATTGAAACACTTTGAGTGCCTAGAT 2400
Qy 2401 TCTATTTTCATCTCTCCCTCTACTGAGGACACTCGGTTGGAATGGAAGTCTTTGAAGAG 2460
Db 2401 TCTATTTTCATCTCTCCCTCTACTGAGGACACTCGGTTGGAATGGAAGTCTTTGAAGAG 2460
Qy 2461 ATGCTTAATCTGGATGAGCAGCTCACTCAGCTGAAGAGTTCAACTTATGAGTAGTAAA 2520
Db 2461 ATGCTTAATCTGGATGAGCAGCTCACTCAGCTGAAGAGTTCAACTTATGAGTAGTAAA 2520
Qy 2521 CTTAAGGAAGTAAAAACATCTGATCTTGGGCGACTGCCCAACCTCATCTCTCTTCT 2580
Db 2521 CTTAAGGAAGTAAAAACATCTGATCTTGGGCGACTGCCCAACCTCATCTCTCTTCT 2580
Qy 2581 CTTTATCATATTTCTTATCTTTGGGAGAGTAGTATTTCAAAACGGGAGCAATTCCTCAAT 2640
Db 2581 CTTTATCATATTTCTTATCTTTGGGAGAGTAGTATTTCAAAACGGGAGCAATTCCTCAAT 2640
Qy 2641 CTTAGAACATTTGATTTCAATTTGATCAGCTAAGAGAGATCAGATTTGAGGACGGC 2700
Db 2641 CTTAGAACATTTGATTTCAATTTGATCAGCTAAGAGAGATCAGATTTGAGGACGGC 2700
Qy 2701 AGCTCACCCAGTTGGAAGATAGAAATCTTCTGCTGAGGTTGGAATCAGGATTTAT 2760
Db 2701 AGCTCACCCAGTTGGAAGATAGAAATCTTCTGCTGAGGTTGGAATCAGGATTTAT 2760
Qy 2761 GGTATCATTTCACTTTCCAAAGGCTCAAGGAGATTTCACTTGAATCAAAAGTAAAGTGCT 2820
Db 2761 GGTATCATTTCACTTTCCAAAGGCTCAAGGAGATTTCACTTGAATCAAAAGTAAAGTGCT 2820
Qy 2821 AGGCTTGCTAGCTGAAGGAGAGTGAACACACACCAATCGCCCGTCTCGAATG 2880
Db 2821 AGGCTTGCTAGCTGAAGGAGAGTGAACACACACCAATCGCCCGTCTCGAATG 2880
Qy 2881 GACAGTACCAAGGATCAGACTGGGCTGAGCCGAGGATCTTCTATAGAGTG 2940
Db 2881 GACAGTACCAAGGATCAGACTGGGCTGAGCCGAGGATCTTCTATAGAGTG 2940
Qy 2941 CAAACAGCAGATCTGTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGGAGCAACG 3000
Db 2941 CAAACAGCAGATCTGTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGGAGCAACG 3000
Qy 3001 GATCCCTTCCGACGAGGAGAGCTCGCAGTCCGAGGTGATCAGTTGACGACG 3060
Db 3001 GATCCCTTCCGACGAGGAGAGCTCGCAGTCCGAGGTGATCAGTTGACGACG 3060
Qy 3061 AATGATAGCAGAGATAGGACACAGCTCAAGCTGGCTGA 3099
Db 3061 AATGATAGCAGAGATAGGACACAGCTCAAGCTGGCTGA 3099
```

RESULT 2

```
ADI57171
ID ADI57171 standard; DNA; 3096 BP.
XX
AC ADI57171;
XX
DT 22-APR-2004 (first entry)
XX
DE Oryza minuta P19 locus nucleotide binding site (NBS) gene #3.
XX
KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
XX plant breeding; transgenic plant; plant; gene; ds.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JAN-2003; 2003US-00352179.
XX
PR 25-JAN-2002; 2002US-0352106P.
XX
PR 01-FEB-2002; 2002US-0353304P.
XX
(WANG/) WANG G.
PA
(LIU/) LIU G.
XX
Wang G, Liu G;
XX
WPI; 2004-121064/12.
DR
P-PSDB; ADI57172.
XX
Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
and NBS3, useful for producing plants resistant to Magnaporthe grisea
infection.
XX
Claim 3; SEQ ID NO 88; 136pp; English.
XX
The invention comprises the amino acid and coding sequences of nucleotide
binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
blight and rice blast resistance genes). The DNA sequences may be used as
markers for resistance to infection with Magnaporthe grisea in plant
breeding programs. The present DNA sequence represents an NBS gene from
the Oryza minuta P19 locus.
XX
Sequence 3096 BP; 960 A; 506 C; 730 G; 800 T; 0 U; 0 Other;
Query Match 96.1%; Score 2977; DB 12; Length 3096;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 3013; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 1 ATGCGGAGAGCGGTGCTGAGCATGGCGAGTGGCTGCTGGCGAGTCCATCAGCAAGGCC 60
Db 1 ATGCGGAGAGCGGTGCTGAGCATGGCGAGTGGCTGCTGGCGAGTCCATCAGCAAGGCC 60
Qy 61 GCCTCTCGCTGCCAATGAGACGAGCTCTCTGCTCGCGCTCGAGAGGACATCTGGTAT 120
Db 61 GCCTCTCGCTGCCAATGAGACGAGCTCTCTGCTCGCGCTCGAGAGGACATCTGGTAT 120
Qy 121 ATCAAGATGAGCTTAAACCAATGACAGGCAATTCCTTAGAGCTGCTGAAGTTATGAAGAAG 180
Db 121 ATCAAGATGAGCTTAAACCAATGACAGGCAATTCCTTAGAGCTGCTGAAGTTATGAAGAAG 180
Qy 181 AAAGATGAATTAAGAGTTTGGGCGAGCAATACTGACCTGCTGATGACATTTGAA 240
Db 181 AAAGATGAATTAAGAGTTTGGGCGAGCAATACTGACCTGCTGATGACATTTGAA 240
Qy 241 GATTCCCTTCATGAATTTAAAGTCCATATTGAAGCCAAACCTATTTCGTCAGTTGGTG 300
Db 241 GATTCCCTTCATGAATTTAAAGTCCATATTGAAGCCAAACCTATTTCGTCAGTTGGTG 300
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Qy 301 AAACCTTAGAGAGCCACCAGGATCGCTATCCGTATCCA CAACCTCAAATCAAGAGTTGAA 360
Db |||||
Qy 301 AAACCTTAGAGAGCCACCAGGATCGCTATCCGTATCCA CAACCTCAAATCAAGAGTTGAA 360
Db |||||
Qy 361 GAAGTAGTAGCAGGAACACACGCTACAAATTTAGTCGAGCCTATTTCCCTCGGCACAGAG 420
Db |||||
Qy 361 GAAGTAGTAGCAGGAACACACGCTACAAATTTAGTCGAGCCTATTTCCCTCGGCACAGAG 420
Db |||||
Qy 421 GATCAGATGGATTCCTATGCAAGAGACANTCGCAATCAATCAGCTCGAAATGTCGATGAA 480
Db |||||
Qy 421 GATCAGATGGATTCCTATGCAAGAGACANTCGCAATCAATCAGCTCGAAATGTCGATGAA 480
Db |||||
Qy 481 GCTGAGCTTGTGGGTTTTCTGACTCCAAGAAAAAGGCTGCTTGAATGATCGATACCAAT 540
Db |||||
Qy 481 GCTGAGCTTGTGGGTTTTCTGACTCCAAGAAAAAGGCTGCTTGAATGATCGATACCAAT 540
Db |||||
Qy 541 GCTAATGATGTCGCGCCCAAGGTAATCTGTGTTGTTGGGATGGGTGGTTTAGGCAAGACA 600
Db |||||
Qy 541 GCTAATGATGTCGCGCCCAAGGTAATCTGTGTTGTTGGGATGGGTGGTTTAGGCAAGACA 600
Db |||||
Qy 601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACACATTAGGAAGAACTTCCCTTGCAAT 660
Db |||||
Qy 601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACACATTAGGAAGAACTTCCCTTGCAAT 660
Db |||||
Qy 661 GCTTGGATTACAGTGTCACAATCAATTTACAGGATTTGAGCTACTTAAAGATATGATACGC 720
Db |||||
Qy 661 GCTTGGATTACAGTGTCACAATCAATTTACAGGATTTGAGCTACTTAAAGATATGATACGC 720
Db |||||
Qy 721 CAACCTTCTGTCGCCAGTTCCTGGATCAACTCTTGGANTGAATTTGCAAGGAAAGGTGGTG 780
Db |||||
Qy 721 CAACCTTCTGTCGCCAGTTCCTGGATCAACTCTTGGANTGAATTTGCAAGGAAAGGTGGTG 780
Db |||||
Qy 781 GTGCAAGTACATCATCTTCTGAGTACTGATAGAGGCTCAAGGAGAGAGGTACTTT 840
Db |||||
Qy 781 GTGCAAGTACATCATCTTCTGAGTACTGATAGAGGCTCAAGGAGAGAGGTACTTT 840
Db |||||
Qy 841 GTTCTTCTAGATGATCTATGGAATTTACATGATTTGGAATTTGGAATTTGGAATTTGCAATTT 900
Db |||||
Qy 841 GTTCTTCTAGATGATCTATGGAATTTACATGATTTGGAATTTGGAATTTGGAATTTGCAATTT 900
Db |||||
Qy 901 CCTAAGAACAAATAGAGAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCG 960
Db |||||
Qy 901 CCTAAGAACAAATAGAGAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCG 960
Db |||||
Qy 961 GAGAAGTGTGCCACAGCTCACTGGGTGACACCTTGATTTCTTGCAAGATGAACGATGCC 1020
Db |||||
Qy 961 GAGAAGTGTGCCACAGCTCACTGGGTGACACCTTGATTTCTTGCAAGATGAACGATGCC 1020
Db |||||
Qy 1021 ATTTTCATTGCTACTGAGAAAAACAAATAAAATCATGAAGACATGGAATCAAAATAAAAT 1080
Db |||||
Qy 1021 ATAACTATGCTACTGAGAAAAACAAATAAAATCATGAAGACATGGAATCAAAATAAAAT 1080
Db |||||
Qy 1081 ATGCAAAAGATGGTTGAAACGAATTTGTAATAAATGTCGTGCTTACCAATTAGCAATACTT 1140
Db |||||
Qy 1081 ATGCAAAAGATGGTTGAAACGAATTTGTAATAAATGTCGTGCTTACCAATTAGCAATACTT 1140
Db |||||
Qy 1141 ACAATAGAGCTGCTGTCGAACTAACAAGGTGTCAGATGGGAGAAATTTCTATGAAACA 1200
Db |||||
Qy 1141 ACAATAGAGCTGCTGTCGAACTAACAAGGTGTCAGATGGGAGAAATTTCTATGAAACA 1200
Db |||||
Qy 1201 CTTCTCTTCAGAACTAGAAAAATAAACCCAGCTGGAAGCTTTGAGGAGAAATGGTGACCCCTA 1260
Db |||||
Qy 1201 CTTCTCTTCAGAACTAGAAAAATAAACCCAGCTGGAAGCTTTGAGGAGAAATGGTGACCCCTA 1260
Db |||||
Qy 1261 GGTTACAAACCTTACATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCT 1320
Db |||||
Qy 1261 GGTTACAAACCTTACATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCT 1320
Db |||||
Qy 1321 GAGGATTTTGAATACAAAGGAATCGTCTAGTAGTAGTGAATGATGAGAGGTTGTT 1380
Db |||||
Qy 1321 GAGGATTTTGAATACAAAGGAATCGTCTAGTAGTAGTGAATGATGAGAGGTTGTT 1380
Db |||||
Qy 1381 AGACCAAAGGTTGGGATGACGACTAAGGATGTCGGAAGAAAGTTACTTTTAATGAGCTAATC 1440

Db |||||
Qy 1381 AGACCAAAGGTTGGGATGACGACTAAGGATGTCGGAAGAAAGTTACTTTTAATGAGCTAATC 1440
Db |||||
Qy 1441 AACCGAAGTAGTAAACGATCAAGAGTGGGACACAGGAAAAATTTAGACTTTGCGA 1500
Db |||||
Qy 1441 AACCGAAGTAGTAAACGATCAAGAGTGGGACATAGGAAAAATTTAAGACTTTGTCGA 1500
Db |||||
Qy 1501 ATCCATCATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATTA 1560
Db |||||
Qy 1501 ATCCATCATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATTA 1560
Db |||||
Qy 1561 TTACCAATGGAGATGCTCTGATTTAGTTTACAGAAAAACACTCGCCACATAGCAATTCAT 1620
Db |||||
Qy 1561 TTACCAATGGAGATGCTCTGATTTAGTTTACAGAAAAACACTCGCCACATAGCAATTCAT 1620
Db |||||
Qy 1621 GGGAGTAGTCTCGCAAAAACAGGATTTGGATTTGGAGCATTTTCGATCATTTAGCTATTTT 1680
Db |||||
Qy 1621 GGGAGTAGTCTCGCAAAAACAGGATTTGGATTTGGAGCATTTTCGATCATTTAGCTATTTT 1680
Db |||||
Qy 1681 GGTGACAGACCCCAAGAGTCTAGCACATGTCAGATTTGTCCAGATCAATTTGAGGATGTTACGG 1740
Db |||||
Qy 1681 GGTGACAGACCCCAAGAGTCTAGCACATGTCAGATTTGTCTAGATCAATTTGAGGATGTTACGG 1740
Db |||||
Qy 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTGACCCGATTTGCA 1800
Db |||||
Qy 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTGACCCGATTTGCA 1800
Db |||||
Qy 1801 TTGTTGTGCCACTTGAATTAATTAATTAATTTGGATTTGGTCAATTAATTTCACTTTCCC 1860
Db |||||
Qy 1801 TTGTTGTGCCACTTGAATTAATTAATTAATTTGGATTTGGTCAATTAATTTCACTTTCCC 1860
Db |||||
Qy 1861 AGATCCATTCGGTAAACTTACAGGGCTACAGACTTTGAAACATGTCAAGCACATACATTTGCA 1920
Db |||||
Qy 1861 AGATCCATTCGGTAAACTTACAGGGCTACAGACTTTGAAACATGTCAAGCACATACATTTGCA 1920
Db |||||
Qy 1921 GCATACCAAGTGAAGTACAGTAAACTCCAAATGTCTGATATCTCTTCGTTGTFATAAGAGAG 1980
Db |||||
Qy 1921 GCATACCAAGTGAAGTACAGTAAACTCCAAATGTCTGATATCTCTTCGTTGTFATAAGAGAG 1980
Db |||||
Qy 1981 CTTGAATTTGACAACTTTAGTCTAAATCACCCCAATGAAGTGCATTAACATACACAAATATGC 2040
Db |||||
Qy 1981 TTTGTTTTATGACAACTTTAGTCTAAACACCCCAATGAAGTGCATTAACATACAAATATGC 2040
Db |||||
Qy 2041 CTGCTAAAGTATTTCACACCTTTAGTTAGTCGGATTAATCGTGCAAAACAAATTTGCTGAA 2100
Db |||||
Qy 2041 CTGCTAAAGTATTTCACACCTTTAGTTAGTCGGATTAATCGTGCAAAACAAATTTGCTGAA 2100
Db |||||
Qy 2101 TTTTCATGTCGCCACCAAAAGTTCGCTGCTGAATCAATTCGGTGTGAAGGTACCCAAAGGA 2160
Db |||||
Qy 2101 TTTTCATGTCGCCACCAAAAGTTCGCTGCTGAATCAATTCGGTGTGAAGGTACCCAAAGGA 2160
Db |||||
Qy 2161 ATAGTAAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATACAGCGGACCAAGTAGT 2220
Db |||||
Qy 2161 ATAGTAAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATACAGCGGACCAAGTAGT 2220
Db |||||
Qy 2221 AGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGTTGAGGAAAAATTTAGCTGTGATACAAAA 2280
Db |||||
Qy 2221 AGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGTTGAGGAAAAATTTAGCTGTGATACAAAA 2280
Db |||||
Qy 2281 GGCTCGCAAAAGGAAAAATGTAAGATACTTTTATGACCCCAATTTGAGAAAGCTCTCTTCCCTC 2340
Db |||||
Qy 2281 GGCTCGCAAAAGGAAAAATGTAAGATACTTTTATGACCCCAATTTGAGAAAGCTCTCTTCCCTC 2340
Db |||||
Qy 2341 CAATCTCTATATGAATGCTGGGTATTAATCAGATATTGAAACACTTTGAGTGCCTAGAT 2400
Db |||||
Qy 2341 CAATCTCTATATGAATGCTGGGTATTAATCAGATATTGAAACACTTTGAGTGCCTAGAT 2400
Db |||||
Qy 2401 TCTATTTTCATCTCTCTCTCCCTACTGAGGACACTCGGGTTGTAATGGAAGTCTTTGAAGAG 2460
Db |||||
Qy 2401 TCTATTTTCATCTCTCTCTCCCTACTGAGGACACTCGGGTTGTAATGGAAGTCTTTGAAGAG 2460
Db |||||
Qy 2461 ATGCTTAACCTGGATTGAGCAGCTCACTCACCTGAAGAAAGTTCACTTATGAGGATGATAA 2520
Db |||||

Db 2461 ATGCTAACTGGATTGACGAGCTCACTCACCTGAAGAGATCTACTATTTCAGGAGCNA 2520
Qy 2521 CTAAGGAAGGTAAACATCTGATCTACTTGGGCACTGCCCAACCTCATGTTCTTTCT 2580
Db 2521 CTAAGGAAGGTAAACATCTGATCTTGGGCACTTGGCCCAACCTCATGTTCTTTAT 2580
Qy 2581 CTTTATCATTAATCTTATCTTGGGAGAGCTAGTATTCAAAACGGGAGCATTCCTCAAT 2640
Db 2581 CTTTATTTGGAATGCTTACCTTGGGAGAGCTAGTATTCAAAACGGGAGCATTCCTCAAT 2640
Qy 2641 CTTAGAACACCTTGATGATTTTCAATTTGGATCAGCTAAGAGAGATCAGATTTGAGACGGC 2700
Db 2641 CTTAGAACACCTTCGATTTTACGAATTTGGATCAGCTAAGAGAGATGAGATTTGAGATGGC 2700
Qy 2701 AGCTCACCCAGTTGGAAAGATAGAAATCTTCTGCTGAGGTTGGAATCAGGATATT 2760
Db 2701 AGCTCACCCCTGTTGGAAAGATAGAAATCTTCTGCTGAGGTTGGAATCAGGATATT 2760
Qy 2761 GGTATCATTCACCTTCAGGCTCAAGGAGATTTTCACTTGAATCAAAAGTAAAGTGGCT 2820
Db 2761 GGTATCATTCACCTTCCAAGGCTCAAGGAGATTTTCACTTGAATCAAAAGTAAAGTGGCT 2820
Qy 2821 AGGCTTGGTCACTGAGGAGAGAGTGAACACACACCAATCGCCCGTCTGCGAATG 2880
Db 2821 AGGCTTGGTCACTGAGGAGAGAGTGAACACACACCAATCGCCCGTCTGCGAATG 2880
Qy 2881 GACAGTACCCGAAGGGATCAGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTG 2940
Db 2881 GACAGTACCCGAAGGGATCAGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTG 2940
Qy 2941 CAAACAGCAGATCCTGTTCTGTATGCCCAAGGATCAGTCACTGTAGCAGTGGGAAGCAAG 3000
Db 2941 CAAACAGCAGATCCTGTTCTGTATGCCCAAGGATCAGTCACTGTAGCAGTGGGAAGCAAG 3000
Qy 3001 GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCACCTTCAGCAGC 3060
Db 3001 GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCACCTTCAGCAGC 3060
Qy 3061 AATGATACGGAAG 3073
Db 3061 AACGATAGTCAAG 3073

RESULT 3

ID ADM72250
XX ADM72250 standard; DNA; 99090 BP.
XX AC ADM72250;
XX DT 03-JUN-2004 (first entry)
XX DE O. minuta P12 region contiguous sequence.
XX KW P12; NBS1; plant protectant; gene therapy; rice; disease resistance;
XX KW gene; ds.
XX OS Oryza minuta.
XX PN WO2004022715-A2.
XX PD 18-MAR-2004.
XX PF 08-SEP-2003; 2003WO-US027913.
XX PR 09-SEP-2002; 2002US-0409216P.
XX PR 18-MAR-2003; 2003US-0455713P.
XX PR 05-SEP-2003; 2003US-00656394.
XX PA (OHIS) UNIV OHIO STATE.
XX PI Wang G;
XX DR WPI; 2004-257576/24.

XX New rice P12-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX Example 3; SEQ ID NO 13; 120pp; English.
PS The invention relates to novel broad-spectrum resistance gene P12 and the
XX NBS(1-6) genes present in the P12 gene cluster region. The rice P12-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a P12
CC region contiguous sequence
XX
SQ Sequence 99090 BP; 28990 A; 20403 C; 21246 G; 28450 T; 0 U; 1 Other;
Query Match 95.3%; Score 2953.2; DB 12; Length 99090;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2955; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 116 GGTATATCAAGATGAGCTAAACAAATGCAAGGCAATTCCTTAGAGCTGCTGAAGTATGA 175
Db 51390 GGTATATCAAGATGAGCTAAACAAATGCAAGGCAATTCCTTAGAGCTGCTGAAGTATGA 51449
Qy 176 AAAAGAAAGATGAACTATTAAAGGTTTGGGAGAGCAAAATACGACCTGCGTATGACA 235
Db 51450 AAAAGAAAGATGAACTATTAAAGGTTTGGGAGAGCAAAATACGACCTGCGTATGACA 51509
Qy 236 TTGAAGATTCCTTGTATGAATTTAAAGTCCATATTGAAGCCAAACCTATTTCTGTCAGT 295
Db 51510 TTGAAGATTCCTTGTATGAATTTAAAGTCCATATTGAAGCCAAACCTATTTCTGTCAGT 51569
Qy 296 TGGTGAACCTTAGAGAGCGGCACCGGATCGGTATCCGATATCCAACTCAAAATCAAGAG 355
Db 51570 TGGTGAACCTTAGAGAGCGGCACCGGATCGGTATCCGATATCCAACTCAAAATCAAGAG 51629
Qy 356 TTGAAGAGTGGTAGGAGGAGACACGCTACATTTAGTCGAGCCTATTTCTCCCGCA 415
Db 51630 TTGAAGAGTGGTAGGAGGAGACACGCTACATTTAGTCGAGCCTATTTCTCCCGCA 51689
Qy 416 CAGAGGATGATATGGATTTCCTATGCAGAAGACATTCGCAATCAATCAGCTCGAAATGTGG 475
Db 51690 CAGAGGATGATATGGATTTCCTATGCAGAGACATTCGCAATCAATCAGCTCGAAATGTGG 51749
Qy 476 ATGAAGCTGAGCTTTGGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATA 535
Db 51750 ATGAAGCTGAGCTTTGGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATA 51809
Qy 536 CCAATGCTATGATGGTCCGCGCAAGGTAACTCTGTGTTGGGATGGTGGTTAGGCA 595
Db 51810 CCAATGCTATGATGGTCCGCGCAAGGTAACTCTGTGTTGGGATGGTGGTTAGGCA 51869
Qy 596 AGACAGCTCTTTTCAGGAAGATCTTTGAAGCGAAGAGACATTTAGGAAGAACTTCCCTT 655
Db 51870 AGACAGCTCTTTTCAGGAAGATCTTTGAAGCGAAGAGACATTTAGGAAGAACTTCCCTT 51929
Qy 656 GCAATGCTTGGATTACAGTGTACAAATCATTTTCAAGGATTTGAGCTACTTAAAGATATGA 715
Db 51930 GCAATGCTTGGATTACAGTGTACAAATCATTTTCAAGGATTTGAGCTACTTAAAGATATGA 51989
Qy 716 TACGCCAACTTCTTGGTCCCGAGTTCTCTGGATCAACTCTTGCATGAAATGCAAGGGAAG 775
Db 51990 TACGCCAACTTCTTGGTCCCGAGTTCTCTGGATCAACTCTTGCATGAAATGCAAGGGAAG 52049
Qy 776 TGGTGGTGCAGATACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGT 835
Db 52050 TGGTGGTGCAGATACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGT 52109
Qy 836 ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATAAAATTG 895
Db 52110 ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATAAAATTG 52169
Qy 896 CATTTCCTAGAAACAATAAGAGGCGAGTCAATAGTAATTAACCACTCGGAATGTTGATC 955

Db	52170	CATTTCCTAAGACAAATAAGAGGCGAGTCGAAATAGTATTAATACCACCTCGGAATGTTGATC	52229
Qy	956	TAGCGGAGAGTGTGCCACAGCCTCACCTGGTGTATCCACCTTTGATTTCTTTCGAGATGAACG	1015
Db	52230	TAGCGGAGAGTGTGCCACAGCCTCACCTGGTGTATCCACCTTTGATTTCTTTCGAGATGAACG	52289
Qy	1016	ATGCCATTTTCATTCTACTGAGAAAAAACAATAAAAAATCATGAAGACATGGAAATCAATA	1075
Db	52290	ATGCCATTTTCATTCTACTGAGAAAAAACAATAAAAAATCATGAAGACATGGAAATCAATA	52349
Qy	1076	AAATATGCAAAAGATGGTTCGAACGAATTTGAATAAATGTTGGTCTACCATTAAGCAA	1135
Db	52350	AAATATGCAAAAGATGGTTCGAACGAATTTGAATAAATGTTGGTCTACCATTAAGCAA	52409
Qy	1136	TACTTACAATAGGAGCTGTCTTGCACATAACAGGTGTGAGATGGAGAAAATCTCTATG	1195
Db	52410	TACTTACATAGGAGCTGTCTTGCACATAACAGGTGTGAGATGGAGAAAATCTCTATG	52469
Qy	1196	AACAACCTTCCTCAGAACTAGAAATAAACCCAAAGCCTGGAAAGCTTTGAGGAGAAATGGTGA	1255
Db	52470	AACAACCTTCCTCAGAACTAGAAATAAACCCAAAGCCTGGAAAGCTTTGAGGAGAAATGGTGA	52529
Qy	1256	CCCTAGGTTACAACCACTACCATCCCATCTGAAAACGATGCTTTTGTATCTAAGTATCT	1315
Db	52530	CCCTAGGTTACAACCACTACCATCCCATCTGAAAACGATGCTTTTGTATCTAAGTATCT	52589
Qy	1316	TTCTCGAGGATTTTGAATAACAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAGGGT	1375
Db	52590	TTCTCGAGGATTTTGAATAACAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAGGGT	52649
Qy	1376	TTGTTAGACCAAAAGGTTGGGATGACGACTAAGGATGTGGGAGAAAGTTACTTTTAATGAGC	1435
Db	52650	TTGTTAGACCAAAAGGTTGGGATGACGACTAAGGATGTGGGAGAAAGTTACTTTTAATGAGC	52709
Qy	1436	TAATCAACCGAAGTATGATTCACGATCAAGATGGGCAACGAGGAGAAAATTAAGACTT	1495
Db	52710	TAATCAACCGAAGTATGATTCACGATCAAGATGGGCAACGAGGAGAAAATTAAGACTT	52769
Qy	1496	GTCCAAATCCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTG	1555
Db	52770	GTCCAAATCCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTG	52829
Qy	1556	TATTAATACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAAACACTCGCCACATAGCAT	1615
Db	52830	TATTAATACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAAACACTCGCCACATAGCAT	52889
Qy	1616	TCCATGGGAGTATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATAGCTA	1675
Db	52890	TCCATGGGAGTATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATAGCTA	52949
Qy	1676	TTTTTGTGTGACAGACCCAAAGTCTAGCACATGCAGTTTGTCCAGATCAATTTGAGGATGT	1735
Db	52950	TTTTTGTGTGACAGACCCAAAGTCTAGCACATGCAGTTTGTCCAGATCAATTTGAGGATGT	53009
Qy	1736	TACGGGTCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTGACCCGTA	1795
Db	53010	TACGGGTCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTGACCCGTA	53069
Qy	1796	TTGCAATTTGTGCGCCTTGAATPACTTTGAGTATTTGGATATTCGTCAATCATATATTCAAC	1855
Db	53070	TTGCAATTTGTGCGCCTTGAATPACTTTGAGTATTTGGATATTTGCTCATATATTTCAC	53129
Qy	1856	TTCCCGATCCATTTGGTAAATACAGGGCCTACAGACTTTTGAACATGTCAGGACATACA	1915
Db	53130	TTCCCGATCCATTTGGTAAATACAGGGCCTACAGACTTTTGAACATGTCAGGACATACA	53189
Qy	1916	TTGACGACCTACCAAGTGAGATCAGTAAATCTCCAAATGTCTGCATPACTCTTCGTTGTATAA	1975
Db	53190	TTGACGACCTACCAAGTGAGATCAGTAAATCTCCAAATGTCTGCATPACTCTTCGTTGTATAA	53249
Qy	1976	GAGAGCTTGAATTTGACAACTTTTAGTCTAAATCAACCAATGAAGTGCATTAACACAA	2035
Db	53250	GAGAGCTTGAATTTGACAACTTTTAGTCTAAATCAACCAATGAAGTGCATTAACACAA	53309

Qy	2036	TATGCTGCTTAAAGTATTCACACCTTTAGTTAGTCGCGATAAATCGTGCAAAAACAAATTTG	2095
Db	53310	TATGCTGCTTAAAGTATTCACACCTTTAGTTAGTCGCGATAAATCGTGCAAAAACAAATTTG	53369
Qy	2096	CTGAATTTTCATGCGGCCACCAAAAGATTTCTGGTCTGAATCAATTCGGTGTGAAGTACCCA	2155
Db	53370	CTGAATTTTCATGCGGCCACCAAAAGATTTCTGGTCTGAATCAATTCGGTGTGAAGTACCCA	53429
Qy	2156	AAGGAATAGGTAAAGTTCGGGAGACTTACAGGTCTCAGAGTATGTAGATATCAGGCGGACCA	2215
Db	53430	AAGGAATAGGTAAAGTTCGGGAGACTTACAGGTCTCAGAGTATGTAGATATCAGGCGGACCA	53489
Qy	2216	GTAGTAGAGCAATCAAAAGAGCTGGGGCAGTTAAAGCAAGTTGAGGAAAATTAAGTCTGTATAA	2275
Db	53490	GTAGTAGAGCAATCAAAAGAGCTGGGGCAGTTAAAGCAAGTTGAGGAAAATTAAGTCTGTATAA	53549
Qy	2276	CAAAAGGCTCGACAAAGGAAAAATGTAAGATACATTTTATGAGCACTTGAAGAGCTCTCTT	2335
Db	53550	CAAAAGGCTCGACAAAGGAAAAATGTAAGATACATTTTATGAGCACTTGAAGAGCTCTCTT	53609
Qy	2336	CCCTCCAATCTCTATATGAATGCCTGGTATTTATCAGATATTTGAAACACTTGAGTGCC	2395
Db	53610	CCCTCCAATCTCTATATGAATGCCTGGTATTTATCAGATATTTGAAACACTTGAGTGCC	53669
Qy	2396	TAGATTCTATTTTCACTCTCTCCTCCCTACTGAGGACACTCGGGTTGAAATGAAAAGTCTTGT	2455
Db	53670	TAGATTCTATTTTCACTCTCTCCTCCCTACTGAGGACACTCGGGTTGAAATGAAAAGTCTTGT	53729
Qy	2456	AAGAGATGCTAACTGGAATGAGCAGCTCACTCACTGGAAGAGTTCAACTTATGAGAGTA	2515
Db	53730	AAGAGATGCTAACTGGAATGAGCAGCTCACTCACTGGAAGAGTTCAACTTATGAGAGTA	53789
Qy	2516	GTAAACTAAAGGAGGTAAACCATGCTGATCTTGGGGCACTGCCCCAACCCTCATGTTC	2575
Db	53790	GTAAACTAAAGGAGGTAAACCATGCTGATCTTGGGGCACTGCCCCAACCCTCATGTTC	53849
Qy	2576	TTTCTCTTTTATCAATAATCTTATCTTGGGAGAGCTAGTATTTCAAAACCGGAGCATTTCC	2635
Db	53850	TTTCTCTTTTATCAATAATCTTATCTTGGGAGAGCTAGTATTTCAAAACCGGAGCATTTCC	53909
Qy	2636	CAAACTTTAGAACTTTGTGCAATTTTCAATTTGGATCAGCTAAGAGAGATCAGATTTGAGG	2695
Db	53910	CAAACTTTAGAACTTTGTGCAATTTTCAATTTGGATCAGCTAAGAGAGATCAGATTTGAGG	53969
Qy	2696	ACGCGAGCTCACCCAGTTGGAAGAGATAGAAATCTCTTCTGCTGAGCTTGGAAATCAGGGA	2755
Db	53970	ACGCGAGCTCACCCAGTTGGAAGAGATAGAAATCTCTTCTGCTGAGCTTGGAAATCAGGGA	54029
Qy	2756	TTATTTGTATCATTTCACTTTCAAGGCTCAAGGAGATTTTCACTTGAATACAAAAGTAAAG	2815
Db	54030	TTATTTGTATCATTTCACTTTCAAGGCTCAAGGAGATTTTCACTTGAATACAAAAGTAAAG	54089
Qy	2816	TGCTAGGCTTTGCTCAGCTGAAAGGAGAGTGAACACACCCAAATGCCCCCTGCTGC	2875
Db	54090	TGCTAGGCTTTGCTCAGCTGAAAGGAGAGTGAACACACCCAAATGCCCCCTGCTGC	54149
Qy	2876	GAATGGACGTGACCGAAGGATCAACACTTGGGGCTGAAGCCGAGAGTCTTCTATAG	2935
Db	54150	GAATGGACGTGACCGAAGGATCAACACTTGGGGCTGAAGCCGAGAGTCTTCTATAG	54209
Qy	2936	AAGTGCAAAACAGCAGATCTCTTCTGATGCCAAGGATCAGTCACTGTAGCAGTGAAG	2995
Db	54210	AAGTGCAAAACAGCAGATCTCTTCTGATGCCAAGGATCAGTCACTGTAGCAGTGAAG	54269
Qy	2996	CAACGGATCCCTTCCGACGACGAGGAGAGAGTCCGAGTCCGAGGTGATCAGTTGA	3055
Db	54270	CAACGGATCCCTTCCGACGACGAGGAGAGAGTCCGAGTCCGAGGTGATCAGTTGA	54329
Qy	3056	CGAGGATGATAGGAG 3073	
Db	54330	CGAGGATGATAGGTCAG 54347	

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RESULT 4
ADM72244
ID ADM72244 standard; cDNA; 3099 BP.
XX AC
XX ADW72244;
XX
DT 03-JUN-2004 (first entry)
XX
DE O. minuta NBS4 polypeptide encoding cDNA.
XX
KW pi2; NBS4; plant protectant; gene therapy; rice; disease resistance;
KW gene; ss.
XX
OS Oryza minuta.
XX
FH Key Location/Qualifiers
FD CDS 1..3099
FT /*tag= a
FT /product= "NBS4"
XX
XX WO2004022715-A2.
XX
XX 18-MAR-2004.
XX
XX 08-SEP-2003; 2003WO-US027913.
XX
XX 09-SEP-2002; 2002US-0409216P.
XX
XX 18-MAR-2003; 2003US-0455713P.
XX
XX 05-SEP-2003; 2003US-00656394.
XX
XX (OHIS ) UNIV OHIO STATE.
XX
XX Wang G;
XX
XX WPI; 2004-257576/24.
XX
XX P-PSDB; ADM72245.
XX
XX New rice pi2-like disease resistance nucleic acid molecule that confers
XX disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.
XX
XX Claim 1; SEQ ID NO 7; 120pp; English.
XX
XX The invention relates to novel broad-spectrum resistance gene pi2 and the
XX NBS(1-6) genes present in the pi2 gene cluster region. The rice pi2-like
XX disease resistance nucleic acid molecules are useful for enhancing
XX disease resistance in plants. The present sequence represents a cDNA
XX encoding a rice NBS4 polypeptide.
XX
XX Sequence 3099 BP; 954 A; 613 C; 743 G; 789 T; 0 U; 0 Other;
XX
Query Match 93.9%; Score 2910.2; DB 12; Length 3099;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY 1 ATGGCGGAGACGGTGTCTGAGCATGCGGAGGTGCGTGTGGCAGTGCATCAGCAAGGCC 60
DB 1 ATGGCGGAGACGGTGTCTGAGCATGCGGAGGTGCGTGTGGCAGGCCATCAGCAAGGCC 60
QY 61 GCCTCTGCGGTGCGCAATAGACGAGCCTCTGCTGGCGGTGCGAGAGCAATCTGGTAT 120
DB 61 GCCTCTGCGGTGCGCAGCAGACCGCCTCTGCTGGCGGTGCGAGAAAGACATCTGGTAT 120
QY 121 ATCAAGATGAGCTAAACAACTCAGGCATTCCTTAGAGCTGCTGAGTTATGAAAAG 180
DB 121 ATCAAGATGAGCTAAACAACTCAGGCATTCCTTAGAGCTGCTGAGTTATGAAAAG 180
QY 181 AAAGATGAATATTAAAGGTTTGGCAGAGCAAAATACGTGACCTGTCTATGACATTGAA 240
DB 181 AAAGATGAATATTAAAGGTTTGGCAGAGCAAAATACGTGACCTGTCTATGACATTGAA 240
QY 241 GATTCCCTTGATGAATTTTAAAGTCCATATTGAAAGCCAAACCTTATTTTCGTAGTGGTG 300
DB 241 GATTCCCTTGATGAATTTTAAAGTCCATATTGAAAGCCAAACCTTATTTTCGTAGTGGTG 300
QY 301 AAATCTAGAGAGCCCAACCGGATCGCTATCGTATCCAACTCAACCTCAAGAGTTGAA 360
DB 301 AAATCTAGAGAGCCCAACCGGATCGCTATCGTATCCAACTCAACCTCAAGAGTTGAA 360
QY 361 GAAGTGAAGTACGAGCAACACGCTACAAATTTAGTCGAGCCTATTTCTCGGCACAGAG 420
DB 361 GAAGTGAAGTACGAGCAACACGCTACAAATTTAGTCGAGCCTATTTCTCGGCACAGAG 420
QY 421 GATCAGATGATTCCTATGCAAGAGACATTCGCAATCAATCAGCTCGAAATGTGATGAA 480
DB 421 ATTGACATGATTCCTATGCAAGAGACATTCGCAATCAATCAGCTCGAAATGTGATGAG 480
QY 481 GCTGAGCTTGTGGGTTTTCTGACTCCAAGAAAAGGCTTGAATGATGATACCAAT 540
DB 481 GCTGAGCTTGTGGGTTTTCTGACTCCAAGAAAAGGCTTGAATGATGATACCAAT 540
QY 541 GCTAATGATGTCGGGCAAGGTAATCTGTGTTGGGATGGGTGGTTTAGGCAAGACA 600
DB 541 GCTAATGATGTCGGGCAAGGTAATCTGTGTTGGGATGGGTGGTTTAGGCAAGACA 600
QY 601 GCTCTTTCGAGGAGATCTTTTGAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 660
DB 601 GCTCTTTCGAGGAGATCTTTTGAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 660
QY 661 GCTTGGATTACAGTGTCAATCAATTTTCAAGGATTCAGCTTAAAGATATGATACGC 720
DB 661 GCTTGGATTACAGTGTCAATCAATTTTCAAGGATTCAGCTTAAAGATATGATACGC 720
QY 721 CAATCTTGTGTCAGTCTCTGAGTCACTTTCGATGAAATTCGAAAGGAAAGGTGGTG 780
DB 721 CAATCTTGTGTCAGTCTCTGAGTCACTTTCGATGAAATTCGAAAGGAAAGGTGGTG 780
QY 781 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAAAGGTGACTTT 840
DB 781 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAAAGGTGACTTT 840
QY 841 GTTCTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATTTGGAATTTG 900
DB 841 GTTCTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATTTGGAATTTG 900
QY 901 CCTAAGAACATAAGAGGGCAGTCGAAATAGTAATACCACTCGGAATGTTGATCAGCG 960
DB 901 CCTAAGAACATAAGAGGGCAGTCGAAATAGTAATACCACTCGGAATGTTGATCAGCG 960
QY 961 GAGAGTGTGCCAGAGCTCACTGGTGTACACCTTGAATTTCTTTCGAGATCAACGATGCC 1020
DB 961 GAGAGTGTGCCAGAGCTCACTGGTGTACACCTTGAATTTCTTTCGAGATCAACGATGCC 1020
QY 1021 ATTTTCATTGCTACTGAGAAAAAACAATAAATAATCATGAAGACATGGAATCAATAAATAAT 1080
DB 1021 ATTAACATTTGCTACTGAGAAAAAACAATAAATAATCATGAAGACATGGAATCAATAAATAAT 1080
QY 1081 ATGCAAAAGATGTTGAACGAAATTTGTAATTTAAATTTGTTGCTCTACCAATAGCAATCTT 1140
DB 1081 ATGCAAAAGATGTTGAACGAAATTTGTAATTTAAATTTGTTGCTCTACCAATAGCAATCTT 1140
QY 1141 ACATAGAGCTGTGCTTGCNACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAAACA 1200
DB 1141 ACATAGAGCTGTGCTTGCNACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAAACA 1200
QY 1201 CTTCTCTTCAGAACTAGAAATAAACCCAGCTGGAAGCTTTGAGGAGAAATGGTGACCCCTA 1260
DB 1201 CTTCTCTTCAGAACTAGAAATAAACCCAGCTGGAAGCTTTGAGGAGAAATGGTGACCCCTA 1260
QY 1261 GGTTCACACCACTTACCATCCCACTGAAACCACTTTTTTTTGTATCTAAGTATCTTTCCCT 1320
DB 1261 GGTTCACACCACTTACCATCCCACTGAAACCACTTTTTTTTGTATCTAAGTATCTTTCCCT 1320
QY 1321 GAGGATTTTGAATATACAAAGGAATCGTCTAGTAGTATGATGATGAGGAGGTTGTTT 1380
DB 1321 GAGGATTTTGAATATACAAAGGAATCGTCTAGTAGTATGATGATGAGGAGGTTGTTT 1380
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Db 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGATGGATAGCAGAAAGGGTTTGGT 1380
Qy 1381 AGACCAAGGTTGGGATGACCACTAAGGATGTCGGAGAAAGTTACTTTAAATGAGCTAATC 1440
Db 1381 AGACCAAGGTTGGGATGACCACTAAGGATGTCGGAGAAAGTTACTTTAAATGAGCTAATC 1440
Qy 1441 AACCAGAGTATGATTTCAACGATCAAGAGTGGGCAAGCAGGAGAAAATTAAGACTTGTGGA 1500
Db 1441 AACCAGAGTATGATTTCAACGATCAAGAGTGGGCAAGCAGGAGAAAATTAAGACTTGTGGA 1500
Qy 1501 ATCCATGATATCATCCGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTGTATTA 1560
Db 1501 ATTCATGATATCATCCGATATCACAGTTTCAATCTCGAGACAGGAAAATTTTGTATTA 1560
Qy 1561 TTACCAATGGGAGATGGCTGTGATTTAGTTTCAAGAAACACTCGCCACATAGCAATTCAT 1620
Db 1561 TTACCAATGGGAGATGGCTGTGATTTAGTTTCAAGAAACACTCGCCACATAGCAATTCAT 1620
Qy 1621 GGGAGTATGTCCTGCAAAACAGGATGGATTTGGAGCAATTAATTCGATCATTAAGCTATTTT 1680
Db 1621 GGGAGTATGTCCTGCAAAACAGGATGGATTTGGAGCAATTAATTCGATCATTAAGCTATTTT 1680
Qy 1681 GGTGACAGCCAGAGCTTAGCAGATGCGAGTTTGTCCAGATCAATTTGAGGATGTTACGG 1740
Db 1681 GGTGACAGCCAGAGCTTAGCAGATGCGAGTTTGTCCAGATCAATTTGAGGATGTTACGG 1740
Qy 1741 GTCTTTGGATCTTGAAGATGACATCTTAACTCACTCAAAAAGATTTGACCGTATTGCA 1800
Db 1741 GTCTTTGGATCTTGAAGATGACATCTTAACTCACTCAAAAAGATTTGACCGTATTGCA 1800
Qy 1801 TTGTTGTGCCACTTGAATTAATCTTGAGTATTTGGATTAATTCGTCATCATATATTCATTTCCC 1860
Db 1801 TTGTTGTGCCACTTGAATTAATCTTGAGTATTTGGATTAATTCGTCATCATATATTCATTTCCC 1860
Qy 1861 AGATCCATTTGTAATCTACAGGGCTACAGACTTTGAAACATGTCAGACATACATATGCA 1920
Db 1861 AGATCCATTTGTAATCTACAGGGCTACAAACTTTGAAACATGTCGCGAGCACATACATGCA 1920
Qy 1921 GCATACCAAGTGAATCAGTAAACTCCAATGTCGATCTCTGTCATCTCTGTTGTATAAGAGAG 1980
Db 1921 GCATACCAAGTGAATCAGTAAACTCCAATGTCGATCTCTGTCATCTCTGTTGTATAAGAGAG 1980
Qy 1981 CTTGAAATTTGCAACTTTAGTCTAAATCACCCATGAAGTGCATACTAATACACAAATATGC 2040
Db 1981 TTTTCATTAATGACAACTTTAGTCTAAACCAACCAATGAAGTGCATACTAATACACAAATATGC 2040
Qy 2041 CTGCTAAAGTATTCACACCTTTAGTTAGTGGCGATGATCGTGCAAAACAAATTTGCTGAA 2100
Db 2041 CTGCTAAAGTATTCACACCTTTAGTTAGTGGCGATGATCGTGCAAAACAAATTTGCTGAA 2100
Qy 2101 TTTTCATATGCGCAACCAAAAGTTTCTGGTCTGAATCATTTCCGTTGGAAGGTACCCAAAGGA 2160
Db 2101 TTTTCATATGCGCAACCAAAAGTTTCTGGTCTGAATCAATTCGTTGGAAGGTACCCAAAGGA 2160
Qy 2161 ATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGGACCAAGTAGT 2220
Db 2161 ATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGGACCAAGTAGT 2220
Qy 2221 AGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGTTGAGGAAAATTAAGCTGTGATACAAA 2280
Db 2221 AGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAAATTAAGCTGTGATACAAA 2280
Qy 2281 GGGTCGACAAAGGAAAATTAAGATATCTTATGACAGCAATTTGAGAGCTCTCTCCCTC 2340
Db 2281 GGGTCGACAAAGGAAAATTAAGATATCTTATGACAGCAATTTGAGAGCTCTCTCCCTC 2340
Qy 2341 CAATCTCTATATGAATGCTGCTTATTAATCAGATATTTGAAAACACTTTGAGTGCCTAGAT 2400
Db 2341 CAATCTCTCCATGTTGGATGTCGACAGGAATCTCAGATGTTGGAACACTTTGAGTGCCTAGAT 2400
Qy 2401 TCTATTTTCATCTCTCTCCCTACTGAGGACACTCGGGTTGAATGGAAGTCTTTGAAGAG 2460
Db 2401 TCTATTTTCATCTCTCTCCCTACTGAGGACACTCGTGTGTTGGATGGAATTTCTTGAGGAG 2460

Qy 2461 ATGCTTAACCTGGATTTGAGCAGCTCACTCACCTGAAGAAGTTCAACTTATGAGTAGTAAA 2520
Db 2461 ATGCTTAACCTGGATTTGAGCAGCTCACTCACCTGAAGAAGATCTACTTATTTAGGAGCAAA 2520
Qy 2521 CTTAAAGGAAGTAAAAACATGCTGATACCTTGGGGCAGCTGCCCAACCTCATGTTCTTTCT 2580
Db 2521 CTTAAAGGAAGTAAAAACATGCTGATACCTTGGGGCAGCTGCCCAACCTCATGTTCTTTCT 2580
Qy 2581 CTTTATCATATTTCTTATCTTTGGGGAAGCTAGTATTTCAAAACGGGAGCAATTTCCCAAT 2640
Db 2581 CTTTATCGGAATGCTTTACCTTTGGGGGAAGCTAGTATTTCAAAACAGGAGCAATTTCCCAAT 2640
Qy 2641 CTTAGAACACCTTTGATTTTCAATTTGGATCAGCTAAGAGAGATTCAGATTTTGAGGACGGC 2700
Db 2641 CTTAGAACACCTTTGATTTTCAATTTGGATTTGATTTGATTTGAGAGATCAGATTTTGAGGACGGC 2700
Qy 2701 AGCTCACCCAGTTGGAAAAAGATAGAAAATCTTTGCTGCAGGTTTGGAAATCAAGGATTAAT 2760
Db 2701 AGCTCACCCCTGTTGGAAAAAGATAGAAAATAGGCGAGTGCAGTTTGAATCTGGGATTAAT 2760
Qy 2761 GGTATCATTTCACTTCCCAAGGCTCAAGGAGATTTCACTTGAATACAAAAGCTAAAGTCGCT 2820
Db 2761 GGTATCATTTCACTTCCCAAGGCTCAAGGAGATTTCACTTGAATACAAAAGCTAAAGTCGCT 2820
Qy 2821 AGGCTTGGTCAAGTGAAGGAGAGTGAACACACACCAAAATCCGCCGCTGCTGCGAATG 2880
Db 2821 GGGCTTGGTCAAGTGAAGGAGAGTGAACACACACCAAAATCCGCCGCTGCTGCTAATG 2880
Qy 2881 GACAGTGACCGAAGGATACAGACCTGGGGGCTGAAGCCGAAAGATCTTCTATAGAAAGTG 2940
Db 2881 TACAGTGACCGAAGGATACAGACCTGGGGGCTGAAGCCGAAAGATCTTCTATAGAAAGTG 2940
Qy 2941 CAACAGCAGATCTGTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAACG 3000
Db 2941 CAACAGCAGATCTGTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAACG 3000
Qy 3001 GATCCCCCTTCCGAGCAGGAGGAGAGCTCGCAGTTCGAGGTGATCAAGTTGACCAACG 3060
Db 3001 GATCCCCCTTCCGAGCAGGAGGAGAGCTCGCAGTTCGAGGTGATCAAGTTGACCAACG 3060
Qy 3061 AATGATAGCGAAGAGATAGGACAGCTCAAGCTGGCTGA 3099
Db 3061 AATGATAGCGAAGAGATAGGACAGCTCAAGCTGGCTGA 3099

RESULT 5

ADIS7166

ID ADIS7166 standard; DNA; 76272 BP.

XX AC ADIS7166;

XX XX

XX DT 22-APR-2004 (first entry)

XX XX

XX DE Oryza minuta Pig locus genomic DNA sequence.

XX XX nucleotide binding site; NBS; Pig; bacterial blight; rice blast;

XX KW plant breeding; transgenic plant; plant; ds.

XX OS Oryza minuta.

XX XX

XX PN US2004006788-A1.

XX XX

XX PD 08-JAN-2004.

XX XX

XX PF 27-JAN-2003; 2003US-00352179.

XX XX

XX PR 25-JAN-2002; 2002US-0352106P.

XX PR

XX PR 01-FEB-2002; 2002US-0353304P.

XX XX

XX PA (WANG/) WANG G.

XX PA (LIUG/) LIU G.

XX XX

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PI Wang G, Liu G;
XX WPI; 2004-121064/12.
DR
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
PT
XX Disclosure; SEQ ID NO 83; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta p19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents the Oryza minuta
CC P19 locus.
XX
SQ Sequence 76272 BP; 22112 A; 16049 C; 16316 G; 21795 T; 0 U; 0 Other;
Query Match 92.4%; Score 2862; DB 12; Length 76272;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2898; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 116 GGTATATCAAGATGAGCTAAACAAATGACAGGCAATCCCTTAGAGCTGCTGAAGTTATGA 175
DB 39202 GGTATATCAAGATGAGCTAAACAAATGACAGGCAATCCCTTAGAGCTGCTGAAGTTATGA 39261
QY 176 AAAAGAAAGATGAACCTATTAAAGGTTTGGGACAGACAAATACGTCGCTGATGACA 235
DB 39262 AAAAGAAAGATGAACCTATTAAAGGTTTGGGACAGACAAATACGTCGCTGATGACA 39321
QY 236 TTGAAGATTCCTTGATGAATTTAAAGTCCATATTGAAGCCAAACCTATTTCGTCAGT 295
DB 39322 TTGAAGATTCCTTGATGAATTTAAAGTCCATATTGAAGCCAAACCTATTTCGTCAGT 39381
QY 296 TGGTGAACCTTAGAGAGCGCCACCGATCGCTATCGTATCCAACTCAAAATCAAGAG 355
DB 39382 TGGTGAACCTTAGAGAGCGCCACCGATCGCTATCGTATCCAACTCAAAATCAAGAG 39441
QY 356 TTGAAGAAAGTGAAGTAGCAGGAAACACACGCTACAATTTAGTCGACCTATTTCCTCCGGCA 415
DB 39442 TTGAAGAAAGTGAAGTAGCAGGAAACACACGCTACAATTTAGTCGACCTATTTCCTCCGGCA 39501
QY 416 CAGAGATGATCGATTCCTATCGAAGACATTCGCAATCAATCAAGCTGCAAAATGTGG 475
DB 39502 CAGAGATGATCGATTCCTATCGAAGACATTCGCAATCAATCAAGCTGCAAAATGTGG 39561
QY 476 ATGAAGCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGGCTGCTGCAATGATCGATA 535
DB 39562 ATGAAGCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGGCTGCTGCAATGATCGATA 39621
QY 536 CCAATGCTAATGATGGTCCGGCCAAAGGTAAATCTGTGTTGGGATGGGTGTTTAGGCA 595
DB 39622 CCAATGCTAATGATGGTCCGGCCAAAGGTAAATCTGTGTTGGGATGGGTGTTTAGGCA 39681
QY 596 AGACAGCTCTTTGAGGAAGATCTTTGAAAGCGAAGACATTTAGAAAGCAATTCCTT 655
DB 39682 AGACAGCTCTTTGAGGAAGATCTTTGAAAGCGAAGACATTTAGAAAGCAATTCCTT 39741
QY 656 GCAATGCTTGGATTTACAGTGTCAATCAATTTTCAAGATTTGAGCTTAAAGATATGA 715
DB 39742 GCAATGCTTGGATTTACAGTGTCAATCAATTTTCAAGATTTGAGCTTAAAGATATGA 39801
QY 716 TACGCCAACTTTTGGTCCAGTTCTCTGGATCAACTCTTTCATGAATTTGCAAGGGAAGG 775
DB 39802 TACGCCAACTTTTGGTCCAGTTCTCTGGATCAACTCTTTCATGAATTTGCAAGGGAAGG 39861
QY 776 TGGTGGTGAAGTACATCTTTCTGAGTACCTGATAGAGAGCTCAAGAGAGAGGT 835
DB 39862 TGGTGGTGAAGTACATCTTTCTGAGTACCTGATAGAGAGCTCAAGAGAGAGGT 39921
QY 836 ACTTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGATAAATGAAATTTG 895
DB 4002 TTGAGCAGCTACCAAGTGAGTCAAGTAAATCTCCAAATGCTGTCATCTTCTGTTGTAGTA 41061
DB 39922 ACTTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGATAAATGAAATTTG 39981
QY 896 CATTTCTTAAGAACAAATAAGAGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATC 955
DB 39982 CATTTCTTAAGAACAAATAAGAGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATC 40041
QY 956 TAGCGGAGAGTGTGCCACAGCCTCACTGGTGTACCACTTGATTTCTTGCAGATGAACG 1015
DB 40042 TAGCGGAGAGTGTGCCACAGCCTCACTGGTGTACCACTTGATTTCTTGCAGATGAACG 40101
QY 1016 ATGCCATTTCTTACTACTGAGAAAAACAAATAAAAAATCATGAAGACATGGAATCAAAATA 1075
DB 40102 ATGCCATTAACATTTCTTACTGAGAAAAACAAATAAAAAATCATGAAGACATGGAATCAAAATA 40161
QY 1076 AAAATATGCAAAAGATGGTTGAACGAATTTGAATAAATGTGTCGTCTACCATTAGCAA 1135
DB 40162 AAAATATGCAAAAGATGGTTGAACGAATTTGAATAAATGTGTCGTCTACCATTAGCAA 40221
QY 1136 TACTTACANTAGGAGCTGCTTTCGAACCTAAACAGGTGTCAGATGGGAGAAATCTATG 1195
DB 40222 TACTTACANTAGGAGCTGCTTTCGAACCTAAACAGGTGTCAGATGGGAGAAATCTATG 40281
QY 1196 AACAACTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTGAGGAGAAATGGTGA 1255
DB 40282 AACAACTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTGAGGAGAAATGGTGA 40341
QY 1256 CCCTAGGTTTCAACCACTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCT 1315
DB 40342 CCCTAGGTTTCAACCACTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCT 40401
QY 1316 TTCTGAGGATTTTGAATACAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 1375
DB 40402 TTCTGAGGATTTTGAATACAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAG 40461
QY 1376 TTGTTAGCACAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTTTACTTTTAAATGAGC 1435
DB 40462 TTGTTAGCACAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTTTACTTTTAAATGAGC 40521
QY 1436 TAATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCACAGCAGGAAAAATTAAGACTT 1495
DB 40522 TAATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCACAGCAGGAAAAATTAAGACTT 40581
QY 1496 GTCGAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTG 1555
DB 40582 GTCGAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTG 40641
QY 1556 TATTATTACCAGTGGGAGATGGCTCTGATTTTAGTTTCAAGGAAAAACACTCGCCACATAGCAT 1615
DB 40642 TATTATTACCAGTGGGAGATGGCTCTGATTTTAGTTTCAAGGAAAAACACTCGCCACATAGCAT 40701
QY 1616 TCCATGGGAGTATGTCCTCGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATTAGCTA 1675
DB 40702 TCCATGGGAGTATGTCCTCGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATTAGCTA 40761
QY 1676 TTTTGTGTGACAGACCCCAAGCTTAGCAATGACAGTTTGTTCAGATCAATTTGAGGATGT 1735
DB 40762 TTTTGTGTGACAGACCCCAAGCTTAGCAATGACAGTTTGTTCAGATCAATTTGAGGATGT 40821
QY 1736 TAGGGGTCTTGGATCTTGAAGATGTGACATTTTAACTCACTCAAAAAGATTTCCGACCGTA 1795
DB 40822 TAGGGGTCTTGGATCTTGAAGATGTGACATTTTAACTCACTCAAAAAGATTTCCGACCGTA 40881
QY 1796 TTGCATTTGTTGTCCTGCACTTGAATACTTTGAGTATTTGATATTCGTCAATATATATTCAC 1855
DB 40882 TTGCATTTGTTGTCCTGCACTTGAATACTTTGAGTATTTGATATTCGTCAATATATATTCAC 40941
QY 1856 TTCCAGATCCATTTGTTAAACTACAGGGCCCTACAGACTTTGAAACATGTCAGACACATACA 1915
DB 40942 TTCCAGATCCATTTGTTAAACTACAGGGCCCTACAGACTTTGAAACATGTCAGACACATACA 41001
QY 1916 TTGCAGCACTACCAAGTGAGTCAAGTAAATCCAAATGCTGTCATCTTCTGTTGTATTA 1975
DB 41002 TTGCAGCACTACCAAGTGAGTCAAGTAAATCCAAATGCTGTCATCTTCTGTTGTATTA 41061
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Db 534 TGAAGAGTGTAGTACAGAGACACACGCTACAGTTTGTCAAGCCTATTTCTCTGGCAC 593
Qy 417 AGAGGATGACATGGATTCCTATGCAAGAGACATTCGCAATCAATCAGCTCGAAATGTGGA 476
Db 594 AGAGATTGACATGGATTCCTATGCAAGAGACATTCGTAATCAGTCAGCTCGCAATGTGA 653
Qy 477 TGAAGCTGAGCTGTGTGGGTTTCTGACTCGAAGAAAGGCTGCTTGAATGATCGATAC 536
Db 654 TGAAGCTGAGCTGTGTGGGTTTCTGACTCGAAGAAAGGTTGCTTGAATGATCGATAC 713
Qy 537 CAATCTAATGATGTCCGGCCAAAGCTAATCTGTCTGTGTGGATGGGTGGTTAGGCAA 596
Db 714 CAATGCTAATGATGTCCGGCCAAAGTAACTGTGTGTGGATGGGTGGTTAGGCAA 773
Qy 597 GACAGCTCTTTGAGGAAGATCTTTGAAAGCGAAGACATTAAGAAAGAACTTCCCTTG 656
Db 774 GACAGCTCTTTGAGGAAGATCTTTGAAAGCGAAGACATTAAGAAAGAACTTCCCTTG 833
Qy 657 CAATGCTTGGATTACAGTGTCAAAATCAATTTTCAAGGATTTGAGCTACTTTAAGATATGAT 716
Db 834 CAATGCTTGGATTACAGTGTCAAAATCAATTTTCAAGGATTTGAGCTACTTTAAGATATGAT 893
Qy 717 ACGCCAACTCTTGTGCTCCAGTTCTCTGATCAACTCTTTGCAATGAATTCGAAGGAAGGT 776
Db 894 ACGCCAACTCTTGTGCTCCAAATTTCTGAAACAACTTTGCAAGAAATTCGAAGGAAGGT 953
Qy 777 GGTGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGAGCTTCAAGGAGAGAGGTA 836
Db 954 GGTGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTTCAAGGAGAGAGGTA 1013
Qy 837 CTTTGTGCTTCTAGATGATCTAAGATTTTATCATGATTTGAATTTGAATTAAGATTAAGTGC 896
Db 1014 CTTTGTATTTCTAGATGATCTATGATTTTATCATGATTTGAATTTGAATTAAGATTAAGTGC 1073
Qy 897 ATTTCTTAAGACATTAAGAGGAGCTGCAATAGTATTAATCACTCGAATGTGATCT 956
Db 1074 ATTTCTTAAGAACATTAAGAGGAGCTGCAATAGTATTAATCACTCGAATGTGATCT 1133
Qy 957 AGCGGAGAGTGTGCAAGCTCTACTGCTGTATCAACCTTGATTTCTTGCAGATGAACGA 1016
Db 1134 AGCGGAGAGTGTGCAAGCTCTACTGCTGTATCAACCTTGATTTCTTGCAGATGAACGA 1193
Qy 1017 TGCCATTTCTTGTGCTAGAGAAACAAATAAATAATCATGAAGACATGGAATCAATPAA 1076
Db 1194 TGCCATAAATGCTACTTAAGAAACAAATAAATAATCATGAAGACATGGAATCAATPAA 1253
Qy 1077 AAATATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGCTGCTACCATTTAGCAAT 1136
Db 1254 AAATATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGCTGCTACCATTTAGCAAT 1313
Qy 1137 ACTTACAATAGAGCTGTGCTTGCATTAACAGGCTGCAGAAATGGGAGAAATTTCTATGA 1196
Db 1314 ACTTACAATAGAGCTGTGCTTGCATTAACAGGCTGCAGAAATGGGAGAAATTTCTATGA 1373
Qy 1197 ACAACTTCTTTCAGAACTAGAAATAAACCCAGCTTGAAGCTTTGAGGAGATGGTGAC 1256
Db 1374 ACAGCTTCTTTCAGAACTAGAAATAAACCCAGCTTGAAGCTTTGAGGAGATGGTGAC 1433
Qy 1257 CCTAGGTTACAACCACTTACCCTTCCATCTGAAACCATGCTTTTGTATCTTAAGTATCTT 1316
Db 1434 CCTAGGTTACAACCACTTACCCTTCCATCTGAAACCATGCTTTTGTATCTTAAGTATCTT 1493
Qy 1317 TCCTGAGGATTTTGAATTAACAAAGAAATCGTCTAGTAGTATGATGATAGCAGAGGGTT 1376
Db 1494 TCCTGAGGATTTTGAATTAACAAAGAAATCGTCTAGTAGTATGATGATAGCAGAGGGTT 1553
Qy 1377 TGTAGACCAAGGTTGGGATGACGACTAAGGATGTCGAGAGAAAGTTACTTTAATGAGCT 1436
Db 1554 TGTAGACCGGAGGTTGGGATGACGACTAAGGATGTCGAGAGAAAGTTACTTTAATGAGCT 1613
Qy 1437 AATCAACGAGTATGATTTCAACGATCAAGAGTGGGCAAGCAGAGGAAATTTAAGACTTG 1496

Db 1614 AATCAGCCGAAGTATGATTTCAACGATCAAGAGTGGGCATATCAGGAAATTTAAGACTTG 1673
Qy 1497 TCGAATCCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAATTTTGT 1556
Db 1674 TCGAATCCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAATTTTGT 1733
Qy 1557 ATTATTACCAATGGAGATGGCTCTGATTTAGTTTCAGGAAACACTCGCCACATAGCAAT 1616
Db 1734 ATTGTACCATGGAGATGGCTCTGATTTAGTTTCAGGAAACACTCGCCACATAGCAAT 1793
Qy 1617 CCATGGGAGTATGCTCTGCAAAACAGGATTCGATTTGAGAGCAATTTCCATCATTTAGCTAT 1676
Db 1794 CCATGGGAGTATGCTCTGCAAAACAGGATTCGATTTGAGAGCAATTTCCATCATTTAGCTAT 1853
Qy 1677 TTTTGGTGACAGACCCCAAGAGCTAGACATGCGAGTTTGTCCAGATCAATTTGAGAGTGT 1736
Db 1854 TTTTGGTGACAGACCCCAAGAGCTAGACATGCGAGTTTGTCTAGATCAATTTGAGAGTGT 1913
Qy 1737 ACGGGTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGAGATTTTCGACCGTAT 1796
Db 1914 ACGGGTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGAGATTTTCGACCGTAT 1973
Qy 1797 TGCATTTGTGTCACACTTGAATACTTGGATTTGGATATTCGTCATCCATATTTCACT 1856
Db 1974 TGCATTTGTGTCACACTTGAATACTTGGATTTGGATATTCGTCATCCATATTTCACT 2033
Qy 1857 TCCAGATTCATTTGGTAAACTACAGGGCTTACAGATTTTGAACATGTCAGACACATACAT 1916
Db 2034 TCCAGATTCATTTGGTAAACTACAGGGCTTACAGATTTTGAACATGTCAGACACATACAT 2093
Qy 1917 TGCAGACTACCAAGTGAGATCAGTAAACTCCAATCTGTCATCTCTGTTGTATTAAG 1976
Db 2094 TGCAGACTACCAAGTGAGATCAGTAAACTCCAATCTGTCATCTCTGTTGTATAGTAG 2153
Qy 1977 AGAGCTTGAATTTTGCACAACTTTAGTCTTAAATCACCCTAAGTGCATTAACACACAT 2036
Db 2154 AAAGTTTGTATGACAACTTTAGTCTTAAACCCCAATGAAGTGCATTAACACACAT 2213
Qy 2037 ATGCTGCTTAAAGTATTTACACCTTTTAGTTAGTTCGGATTAATCGTGCAAAACAAATTCG 2096
Db 2214 ATGCTGCTTAAAGTATTTACACCTTTTAGTTAGTTCGGATTAATCGTGCAAAACAAATTCG 2273
Qy 2097 TGAATTTACATGCGCACCAAAAGTTTCTGCTGTAATTCATTTGCTGTGAAGGTACCCAA 2156
Db 2274 TGAATTTGACATGCGCACCAAAAGTTGCTGCTGTAATCATTTGCTGTGAAGGTACCCAA 2333
Qy 2157 AGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAATATACAGCGACCCAG 2216
Db 2334 AGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAATATACAGCGACCCAG 2393
Qy 2217 TAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGTTTGAAGAAATTTAGCTGTGATTAAC 2276
Db 2394 TAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGTTTGAAGAAATTTAGCTGTGATTAAC 2453
Qy 2277 AAAAGGCTCGACAAAGGAAATGTAAAGTACTTTATGACGCCATTTGAGAGCTCTCTTC 2336
Db 2454 AAAAGGCTCGACAAAGGAAATGTAAAGTACTTTATGACGCCATTTGAGAGCTCTCTTC 2513
Qy 2337 CCTCCAATCTCTCTATTAAGTGTGCTTATTAATCAGATATTTGAACACATTTGAGTGCCT 2396
Db 2514 CCTCCAATCTCTCTATTAAGTGTGCTTATTAATCAGATATTTGAACACATTTGAGTGCCT 2573
Qy 2397 AGATTTCTATTTCACTCTCTCTCTCTACTGAGGACACTCGGGTTGAATTTGAAGTCTTGA 2456
Db 2574 AGATTTCTATTTCACTCTCTCTCTCTACTGAGGACACTCGGGTTGAATTTGAAGTCTTGA 2633
Qy 2457 AGAGATGCTTAATCTGATTTGAGAGCTCACTCACTGAAAGAGTTTCAACTTATGAGTAG 2516
Db 2634 AGAGATGCTTAATCTGATTTGAGAGCTCACTCACTGAAAGAGTCTACTTATTTGAGGAG 2693
Qy 2517 TAAACTAAGGAGGTAAGAAACATGCTGATTTGGGGCACTGGCCCAACCTCATGTTCT 2576
Db 2694 CAAACTAAGGAGGTAAGAAACATGCTGATTTGGGGCACTGGCCCAACCTCATGTTCT 2753

Qy 2577 TTCTCTTTATCATTAATCTTATCTTGGGGAAGCTAGTATTTCAAAACGGGAGCATTTCCC 2636
Dy 2754 TTAATCTTATGGAACTGCTTACCTTGGGGAAGCTAGTATTTCAAAACGGGAGCATTTCCC 2813
Qy 2637 AAATCTTAGAACACTTGTGATTTTCAATTTGGATCAGCTAAGAGAGATTCAGATTTGAGGA 2696
Dy 2814 AAATCTTAGAACACTTGTGATTTTCAATTTGGATCAGCTAAGAGAGATTCAGATTTGAGGA 2873
Qy 2697 CGGAGCTACCCAGTGTGGAAGATAGAAATCTTCTGCTGAGGTGGGAATCAGGAT 2756
Dy 2874 TGGAGCTACCCCTGTGTGGAAGATAGAAATCTTCTGCTGAGGTGGGAATCAGGAT 2933
Qy 2757 TATTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCACTTGAATACAAAAGTAAAGT 2816
Dy 2934 TATTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCACTTGAATACAAAAGTAAAGT 2993
Qy 2817 GGCTAGGCTTGGTCAAGTGAAGGAGAGTGAACACACACCAATCGCCCGCTGCTGCG 2876
Dy 2994 GGCTAGGCTTGGTCAAGTGAAGGAGAGTGAACACACACCAATCGCCCGCTGCTGCG 3053
Qy 2877 AATGGACGTACCGAAGGATCAGACCTGGGGGCTGAAGCCGAAGATCTTCTATAGA 2936
Dy 3054 AATGGACGTACCGAAGGATCAGACCTGGGGGCTGAAGCCGAAGATCTTCTATAGA 3113
Qy 2937 AGTCAACACAGCAGATCTCTGTCTGTATGCCCAAGGATCAGTCACTGTAGCAGTGGAAAGC 2996
Dy 3114 AGTCAACACAGCAGATCTCTGTCTGTATGCCCAAGGATCAGTCACTGTAGCAGTGGAAAGC 3173
Qy 2997 AACGGATCCCCCTCCGAGCAGGAGGAGAGAGCTCGCAGTFCGAGGTGATCACTGTGAC 3056
Dy 3174 AACGGATCCCCCTCCGAGCAGGAGGAGAGAGCTCGCAGTFCGAGGTGATCACTGTGAC 3233
Qy 3057 GACCAATGATAGCGAAGATAGGCACAGCTCAAGCTGGCTGA 3099
Dy 3234 GACCAATGATAGCGAAGATAGGCACAGCTCAAGCTGGCTGA 3276

RESULT 7

ADW72248
ID ADW72248 standard; cDNA; 2997 BP.
XX AC ADW72248;
XX AC
DT 03-JUN-2004 (first entry)
XX DE
XX DE O. minuta NBS6 polypeptide encoding cDNA.
XX P12; NBS6; plant protectant; gene therapy; rice; disease resistance;
XX KW gene; ss.
XX OS
XX OS Oryza minuta.
XX FH Key Location/Qualifiers
XX CDS 1. .2997
FT /*tag= a
FT /product= "NBS6"
XX PN W02004022715-A2.
XX PD
XX PD 18-MAR-2004.
XX PF 08-SEP-2003; 2003WO-US027913.
XX PR 09-SEP-2002; 2002US-0409216P.
XX PR 18-MAR-2003; 2003US-0455713P.
XX PR 05-SEP-2003; 2003US-00656394.
XX PA (OHIS) UNIV OHIO STATE.
XX FI Wang G;
XX DR WPI; 2004-257576/24.

DR P-PSDB; ADM72249.
XX New rice P12-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX Claim 1; SEQ ID NO 11; 120pp; English.
XX The invention relates to novel broad-spectrum resistance gene P12 and the
CC NBS(1-6) genes present in the P12 gene cluster region. The rice P12-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA
CC encoding a rice NBS6 polypeptide.
XX SQ Sequence 2997 BP; 874 A; 607 C; 723 G; 793 T; 0 U; 0 Other;
Query Match 76.1%; Score 2359.8; DB 12; Length 2997;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
Qy 427 ATGGATTCTTATGCAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAG 486
Dy 202 ATAGATTCTTATGCAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAG 261
Qy 487 CTGTGTTGGGTTTCTGACTCCAGAAAAGGCTGCTTGAAATGATCGATACCAATGCTAAT 546
Dy 262 CTGTGTTGGGTTTCTGACTCCAGAAAAGGCTGCTTGAAATGATCGATACCAATGCTAAT 321
Qy 547 GATGTTCCGGCAAGGTAATCTGTGTTGGGATGGGTGTTTGGGCAAGACAGCTCTT 606
Dy 322 GATGTTCCGGCAAGGTAATCTGTGTTGGGATGGGTGTTTGGGCAAGACAGCTCTT 381
Qy 607 TCAGAGGAAGATCTTTGAAAGCGAAGACATTAAGGAAGAACTTCCCTTGCAATGCTTGG 666
Dy 382 TCAGAGGAAGATCTTTGAAAGCGAAGACATTAAGGAAGAACTTCCCTTGCAATGCTTGG 441
Qy 667 ATTACAGTGTCACAATCATTTTCAGGATTCAGCTACTTAAAGATATGATACGCCAATTT 726
Dy 442 ATTACAGTGTCACAATCATTTTCAGGATTCAGCTACTTAAAGATATGATACGCCAATTT 501
Qy 727 CTGTGTTCCAGTTCTCTGGATCAACTCTTGCATGAATTCAGGGAAGGTGGTGGTCAA 786
Dy 502 CTGTGTTCCAGTTCTCTGGATCAACTCTTGCATGAATTCAGGGAAGGTGGTGGTCAA 561
Qy 787 GTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGTACTTTGTTGTTT 846
Dy 562 GTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGTACTTTGTTGTTT 621
Qy 847 CTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATAAATGAAATTCGATTTTCTTAAG 906
Dy 622 CTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATAAATGAAATTCGATTTTCTTAAG 681
Qy 907 AACAAATGAAGGCGAGTCGAATAGTAATTAACCACTCGGAATGTTGATCTAGCGGAGAAG 966
Dy 682 AACAAATGAAGGCGAGTCGAATAGTAATTAACCACTCGGAATGTTGATCTAGCGGAGAAG 741
Qy 967 TGTGCCACAGCTCACCTGTTGACCTTGTGATTTCTTGAGATGAACGATGCGCATTTCA 1026
Dy 742 TGTGCCACAGCTCACCTGTTGACCTTGTGATTTCTTGAGATGAACGATGCGCATTTCA 801
Qy 1027 TTGCTACTGAGAAAAACAAAATAAAAAATCATGAAGACATGGAATCAAAATAAAAAATATGCAA 1086
Dy 802 TTGCTACTGAGAAAAACAAAATAAAAAATCATGAAGACATGGAATCAAAATAAAAAATATGCAA 861
Qy 1087 AAGATGTTGAACGAATTTGAAATAAATGTTGTTGCTGCTACCATTTAGCAATTAATTAATA 1146
Dy 862 AAGATGTTGAACGAATTTGAAATAAATGTTGTTGCTGCTACCATTTAGCAATTAATTAATA 921
Qy 1147 GGAGCTGTGCTTGCACACTAAACAGGTGTCAGATGGGAGAAAATTTCTATGAACACTTCTCT 1206
Dy 922 GGAGCTGTGCTTGCACACTAAACAGGTGTCAGATGGGAGAAAATTTCTATGAACACTTCTCT 981
Qy 1207 TCAGAACTAGAAAAATAAACCAAGCTGGAAGCTTTTGGAGGAATGGTGAACCTTAGGTTAC 1266

XX Wang G, Liu G;
XX WPI; 2004-121064/12.
DR P-PSDB; ADI51714.
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
XX Claim 3; SEQ ID NO 90; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta p19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents an NBS gene from
CC the Oryza minuta p19 locus.
XX
SQ Sequence 3220 BP; 990 A; 616 C; 747 G; 867 T; 0 U; 0 Other;

Query Match 51.4%; Score 1591.8; DB 12; Length 3220;
Best Local Similarity 73.2%; Pred. No. 0;
Matches 2179; Conservative 0; Mismatches 752; Indels 46; Gaps 9;

Qy 1 ATGGCGGAGCGGTGCTGAGCATGCGGAGGTGCGTGTGGCGAGTGCCTCAGCAAGGCC 60
Db 1 ATGGCGGATACAGTACTCGCATGTCGAAGTCCCTGTGGGAGTGTCTGTAAAGAGTT 60
Qy 61 GCCTCTGCGGTGCCAATGAGACGAGCCTCTGCTCGGCGTGCAGAGGACATCTGTTAT 120
Db 61 GCTTCGGTTGCGGACACAGATGATCATGCTGCTGGGAGTGCAGAGGAGATGTTTC 120
Qy 121 ATCAAGATGAGCTAAACAAATGAGGATTCCTTAGAGCTGCTGAGAGTTATGAAGAAG 180
Db 121 ATCAAGATGAGCTACAAACGATCAAGCATTTTGTGTTGCTGCCGAG---CATCAAG 177
Qy 181 AAAGATGAATATTAAAGTTTGGCGAGCAAAATACGTGACCTGCTGTATGACATTGAA 240
Db 178 AAAGATGATCTATTGAAGTTTGGTGCGACAGTAAGGATCTTTCTATGACATTGAA 237
Qy 241 GATTCCTTGTGATTTAAAGTCCATATTGAAAGCCAAACCTATTTCGTGAGTTGGTG 300
Db 238 GATTCCTTGTGATTTTACAGTTTCATGTGGCGAGCCAAACCTTGTGAGGCGAGTTGATG 297
Qy 301 AAACCTAGAGCGCCACCGATCGCTATCCGTATCCACACCTCAAAATCAAGAGTTGAA 360
Db 298 AAGCTAAAGGATCGCCATCGGATTTGCCATCCAGATCCGCAATCTCAGGACAAAGATTGAA 357
Qy 361 GAAGTGATGACGAGACACACGCTACAAATTTAGTCCGAGCCT---ATTTCCTCCGACCA 417
Db 358 GAAGTGAACATAGGAACATGACCTACAACTTAATAGGAATGACCTCACCTGACCACT 417
Qy 418 GAGGATGACATGGAATTCCTATGCAAGAGACATTCGCAATCAATCAGCTCGAAATGTGGAT 477
Db 418 ACTGATGAGAGGAATTTATTTATGGAAGACATTCGCAACCAATAAGCTTAACAACTTGAG 477
Qy 478 GAAGCTGAGCTTGTGGTTCGATCCCAAGAAAAGGCTGCTTGAATGATCGATACC 537
Db 478 GAAGCTGATCTGTGGGTTTTCTGGACCCAAAAGAGAGTTGCTTGTATCTTATAGATGTC 537
Qy 538 AATGCTAATGATGTCCGCGCAAGTAAATCTGTGTTGTTGGATGGGTGTTTAGGCAAG 597
Db 538 CATGCCAATGAGGACCTCAAAAAGTTGATATGTGTTGCGTATGGGTGTTGGGTAAG 597
Qy 598 ACAGCTCTTTTCGAGGAAGATCTTTTGAAGCGAAGAAGACATTAGGAAGAACTTCCCTTGC 657
Db 598 ACTACTATGCAAGGAAAATTTATGAAGCAAGAGGACATTCGAAAGAAATTTTCTTTC 657
Qy 658 AATGCTTGGATTCAGTGTCAATATCAATTTTCACAGGATTTAGCTACTTAAAGATATGATA 717
Db 658 TGTGCTTGGATTACTGTTTACAGTCTCTTTGTTAGGGTGGAACTACTCAAGGATTTGATG 717

Qy 718 CGCAACTCTTGTGCCAGTTCTCTGATCAACTCTTGTGATGAATTCAGAGGAGGTG 777
Db 718 GTGAACTTTTGGAGAGGAGTACTGAAGAAGCGCTGAGAGAACTCGAAGGAA---G 774
Qy 778 GTGTGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAAAGGTAC 837
Db 775 GTTCACAAGTAGACGACCTCGCCAGCTACCTCAGGACAGAGTTAAAATGAAGGAGGTAC 834
Qy 838 TTTCTGTCTTAGATGATCTATGATTTTACATGATTTGGAATTCGATAAATGAATTCGA 897
Db 835 TTTGTGTGCTTGATTAACGCTGTGGAGTACAGATTCATGGAATGGAATTAATAGTATGCC 894
Qy 898 TTTCTTAAGAACATAAGAGCGGAGCTGAATAGTAATAAACACCTCGGAATGTTGATCTA 957
Db 895 TTTCTTAGAATAACAATAAGGCGCGGTGATAGTAACAACAAGAGATGTTGGCTTA 954
Qy 958 GCGGAGAAGTGTGCCACAGCCTCACTGCTGTACACCTTGTATTTCTTCAGATGAAAGAT 1017
Db 955 ACTAAGGAGTGTACTTCTGAAATTCCTTATCTACAGCTTAAACCCCTAGAAATAAATCTAT 1014
Qy 1018 GCCATTTCTTGTCTGAGAAAACAAATAAATAATCATGAAGACATCGAATCAATAAA 1077
Db 1015 GCAAAAGATTTGCTTCTACGGAAAGCAATAAAGCAATAGGAGATATGGAAGTGATAAA 1074
Qy 1078 AATATGCAAAAGATGCTTGAACGAATTTGTAATAAATGCTGCTCTACCAATTAGCAATA 1137
Db 1075 AAGATGAGTGACATTAATACTAAATAATAAAGAGTGTGGCTATTTACCCTGGCTATA 1134
Qy 1138 CTTAACAATAGAGCTGTGCTTGCACCTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAA 1197
Db 1135 CTCAACAATAGAGCGTGTCTTCCACCAAGAGATAAAGAGATGGGAACTTTTATATAGT 1194
Qy 1198 CAACCTCTCTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTTGGAGAGATGTTGACC 1257
Db 1195 CAGATACTCTCAGAGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAGGATAGTGACC 1254
Qy 1258 CTAGGTTTACAAACACCTACCATCCATCTGAAACCATGCTTTTGTATCTTAAGTATCTTT 1317
Db 1255 CTAAATTACAACCTACTTACCGTCTCACTTAAAGCAATGCTTTTGTATCTTAAGCATATT 1314
Qy 1318 CCTGAGGATTTGAAATFACAAAGGAATGCTCTAGTAGTAGATGGAATAGAGAGGTTT 1377
Db 1315 CCTGAGGATTTGAAATTTAATAGGAACCGTCTGTTAAATAGATGATGATGCGAGAGGTTT 1374
Qy 1378 GTTAGACCAAGGTTGGGATGACGACTAAGATGCTCGGAGAAAGTACTTTTAAATGAGCTA 1437
Db 1375 ATTAAGCTAGGACTAATATGACTATTGAAGATGTTGGGAAAAGTTACTTTTAAAGAACTT 1434
Qy 1438 ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCGACAGCAGGAAAAATTTAAGACTTGT 1497
Db 1435 ATCAACCGTAGCATGATTCAGCCATCAAGAGCGGTTATACGAGGAGATTTTAAAGCTGT 1494
Qy 1498 CGAATCATGATATCATCCGTTGATATCAAGTTCATTCAGTTCGAGACAGGAAAAATTTTGTGA 1557
Db 1495 CGAGTCCACGACATCATGCGTGTATTTACAATTTTGAATTTCTAGAGAGAAAAATTTTACA 1554
Qy 1558 TTATTACAATGGGAGATGGCTCTGATTTAGTTAGTTCAGGAAACACATCCGCCATAGCATTC 1617
Db 1555 CTCTTACCGAGTGGCACTGACTATGATGATCATGGAACACTCGGCAATAGAAATTT 1614
Qy 1618 CATGGGATGATGTCCTTGC---AAAAAGGATTTGATTTGGAGCATTTTTCGATCATTAGCT 1674
Db 1615 CACGGAGTAAGTATTGCTCTGAAACAAGCTTGGACTGGAGCATTTAAGGTCATTAAGT 1674
Qy 1675 ATTTTTCGAGACAGACCAAGAGCTTAGACATGACAGTTTGTTCAGATCAATTTGAGGATG 1734
Db 1675 ATGTTTGTGAGAGGTCGCTAGAACTAGAGCAATTCAGTTCAGTTGTTCTCATCTCAGTTGAGGATG 1734
Qy 1735 TTACGGCTCTTGGATCTTGAAGATGTCACATCTTAACTCACTCAAAAAGTTTCGACCGT 1794
Db 1735 TTACGGCTCTTGGATCTTAAACAGATGCAAAATTTTCTATCACAAAAATGATGTCGACAA 1794
Qy 1795 ATTGCATTTGTTGCCACTTGAATACTTTGAGTATT-----GGATATTCGTCATC 1844

QY	840	TGTTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAAATTTGGATTAATGAAATTTGCATT	899
Db	843	TGTTGTCCTTGATGACCTATGGACCATAGATGATGGAATTTGGATTCATGATATTTGCTTT	902
QY	900	TCCTAAGAACAAATGAAGAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGC	959
Db	903	TCCGAAGATTAAACAACAGAGTAGTCGCATATATATTAACAACGCGAGATGCTGGCTTAGC	962
QY	960	GGAGAAGTGTGCCACAGCCTCACTGGTGTACACACCTTCATTTCTTGGCAGATGAACGATGC	1019
Db	963	TGGAAAGTGTACCTCTGHAATCACTTTATTTACACCTTGACCGTTTACATATAGATGATGC	1022
QY	1020	CATTTTCATTTGCTACTGAGAAAAACAATAAATAATCATGAAGACATGGGAATCAAAATAAAAA	1079
Db	1023	TATACACTTGTACTAGCAAGACAACAATAAAGACTTGAAGACATGGAAAAATGATGAGGA	1082
QY	1080	TATGCAAAAGATGTTGAACGAATGTGTAATAATTAATGTGGTGTCTACCAATTAGCAATACT	1139
Db	1083	CTTGGGCAGCATAGTTACAAAATTTGGTGAAGAAGGTGTGGTTATTTACCGCTGGCTATACT	1142
QY	1140	TACAAATAGAGCTGTGCTTGCACCTTAAACAGGTGTGAGAAATGGGAGAAATTTCTATGAACA	1199
Db	1143	CACAAATAGGAGCAATTTTGCTACTTAAGAAAGATTAATGGAGTGGGAAATTTTACAGAGA	1202
QY	1200	ACTTCTCTTCAGAACTAGAAAATAAACCCCAAGCCTTGAAGCTTTTGAGGAGAAATGGTGACCT	1259
Db	1203	ACTTCTCTTCAGAGCTTGAGAGCAATCCAAAGCCTTAGAAGCCATGAGGAGATGGTGACCT	1262
QY	1260	AGGTTACAAACCACTACCATCCATCTGAAACCAATGCTTTTGTGATCTAAGATATCTTTCC	1319
Db	1263	AAGCTACAATCACTTACCATCTCATCTTTAAACCAATGCTTTCTTTACCTAAGTATTTTCCC	1322
QY	1320	TGAGGATTTTCAAAATACAAAGGAATCGTCTAGTAGGTAGATGAGATAGCAGAGAGGTTTGT	1379
Db	1323	TGAAGATTTTGAATTTCAAGAGGGCGCTGGTAGATAGATGGATAGCAGAGGGTTTGT	1382
QY	1380	TAGACCAAGGTTGGGATGACGACTAAGGATGTGCGGAGAAATTTACTTTAATGAGCTAAT	1439
Db	1383	CAGAGCCACAGATGGGGTGAACATGAGGATTTGGAAATAGTCACTTTATGAGCTTAT	1442
QY	1440	CAACCGAAGTATGATTCACGATCAAGAGTGGGCAACAGCAGGAAATAATTAAGACTGTGCG	1499
Db	1443	CAACAGAAAGTCTGATTCAGCCCTCAAAAAGTTAGTACAGATGGAGTTGTTAAGAGATGCG	1502
QY	1500	AATCCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAATTTTGTATT	1559
Db	1503	AATCCATGATATCATCCGTGATATCATAGTTTCAATTTCTAGAGAGGAAATTTTGTGCT	1562
QY	1560	ATTACCAATGGAGATGGCTCTGATTTAGTTTACAGGAAACAACCTCGCCACATPAGCAATCCA	1619
Db	1563	GTTGACTAGGAGAAGATCACTGTTGTAGCGGAGGAGCATCCGCCATCTAGCAATTCAC	1622
QY	1620	TGGAGTATGCTTGCAAAACAAGGATTTGATTTGAGAGCAATTAATCGATCAATTAGCTATTTT	1679
Db	1623	TGGAGCAAAATGCTCAAAAGATATGCTTGGAGTGGAAACCATCTCGCGCTCAGTAACTTTGTT	1682
QY	1680	TGTTGACAGACCCCAAGAGTCTAGCACATGCAAGTTTGTTCAGATCAATTTGAGGATGTTACG	1739
Db	1683	TGGCGACAGACCTGTGGGGCGAAACACCTGCACTTTGTTTACCACAAATTTAGGATGCTGAG	1742
QY	1740	GGTCTTGATCTTGAAGATGTGAATTTCTTAATCACTCAAAAAGATTTTCGACCCGTATTGC	1799
Db	1743	AGTGTGGAATCTGGAAGATGCAAAATTCAAATTCACACAAATGATATCAGAAATATAGG	1802
QY	1800	ATTGTTGCGCACTTGAAATACCTTGAGTATTTGGATATTTGTCATCCATATATTCACATTCC	1859
Db	1803	GTTGTGCGCCACATGAAATATTTGAAATTTTGAAGAGCCTCAACTATTTATATACACTTCC	1862
QY	1860	CAGATCCATTTGGTAAACTACAGGCGCTACAGACTTTTGAACATGTCAGACCATACATTGC	1919
Db	1863	AAGGTCCATAGGAAAAATTTGCAGTCTTGCAAAATTTTGAACATGAGGAGGCAAAATATCTC	1922

RESULT 11

ADM72252

ID ADM72252 standard; cDNA; 2422 BP.

XX

QY	1920	AGCACTACCAAGTGAGATCAGTAAACTCCAAATGTCTGCATACTCTTCTGTTGATATAAGAGA	1979
Db	1923	AGCACTACCAACTCAGGTGACTAAACTCCAGAAATCTCGTAGCTCCGATCAGCAGAG	1982
QY	1980	GCTTGAATTTTGACAACTTTAGTCTAA---ATCACCCCAATGAAGTGCAATACTAACACAAT	2036
Db	1983	GTCTGGTCTCTGGTTACTTTTAGCATAAATAGATAATCCCAAGGAATGCTTGATGATCACCAT	2042
QY	2037	ATGCTGCTCTAAAGTATTTACACCTTTAGTTAGTTCGGGATTAATCGTGCAAAACAAATTCG	2096
Db	2043	GTGCTTACCGATGTTTCTTAACTTCAATAAAATTCAGTGCACCGTGTGAAGTTAAATTC	2102
QY	2097	TGAATTTCAATGCCACCAAAAGTTTCTGCTCTGAATCATTTCCGTTGTGAAGGTACCCAA	2156
Db	2103	TGAGATATGCAATCATGTTCTACCCGTTGCTGTGATACAAAGGTTGTGAGGTTGCCAAG	2162
QY	2157	AGGAATAGGTAAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACAG	2216
Db	2163	AGGAATTGACAACCTAAAGAGTTTACAGATTTCTAGAAGTCTGGACATCAACAGAACTAG	2222
QY	2217	TAGTAGAGCAATCAAGAGCTGGGGCAGTTAAAGCAAGTTGAGGAAATTTAGCTGTGATAAC	2276
Db	2223	TAGGAAGCGATTGAAGGCTGGGGAGCTPAATTCAGTTAAGAAATTTAAGCGTGACAAAC	2282
QY	2277	AAAAGGCTCGACAAGGAAATAATGTAAAGATCTTTATGAGCCATTTGAGAGGCTCTCTTC	2336
Db	2283	AAAAGGCGCCACAAATAAGAAATATCAGATATTTGTCAGCGATTGGAAGCTCTCTTC	2342
QY	2337	CCTCCAATCTCTATATGATGCTGCTTATTAATCAGATATTTGAAACATTTGAGTGTGCT	2396
Db	2343	TCTGCAATCTCTCGTGTGATGCTGAGGGATTCTCAGATATCTGGAACACTTTGAGTGTGCT	2402
QY	2397	AGATTCTATTTCATCTCTCTCTCCTACTGAGGACACTCGGGTTGAATGGAAGTCTTGA	2456
Db	2403	CAATTCGATTTGCAATGCTCTCTCCATTTCTTGAAGAGACTCAAGTTGAATGATCTCTTC	2462
QY	2457	AGAGATCCCTAACTGGATTTGAGAGCTCACTCACTGAAAGAGTTCAACTTATGGAGTAG	2516
Db	2463	AGATACACCAAACTGGTTTGGGAACCTTAAGCAGCTGGTGAAGATGTGCTTATCCAGATG	2522
QY	2517	TAACTHAAAGGATTAACAACATGCTGATACTTTGGGCACTGCGCCCACTCATGTTCTCT	2576
Db	2523	TGGGCTHAAAGATGGTTAAAACTATGGAGATACTTTGGGGCACTGCCCAACCTTATGGTTCT	2582
QY	2577	TTCTCTTTATCATAAATTTCTTATCTTGGGGAAGCTAGTATTTCAAAAACGGGAGCAATCCC	2636
Db	2583	TCGTCTTTATCGCAACGCATATGCTGACGAGAAATGACATTCAGAGGGGAATTTTCCC	2642
QY	2637	AAATCTTTAGAACACTTGTGATTTTCAATTTGGATCAGCTAAGAGAGATCAGATTTGAGGA	2696
Db	2643	AAATCTCAGGTGTCTTGATATTTTACTTGTCTGAAGCAACTTTAGAGAGATTAAGATTTGAGGA	2702
QY	2697	CGGAGCTCACCCAGTTTGGAAAAGATAGAAATCTCTTGTGTCAGGTTGGNATCAGGGAT	2756
Db	2703	GGGCACCTCCGCCAACGATGGAAAGTATAGAAATTTATGTTGCTGAGGTTGGAAATCAGGGAT	2762
QY	2757	TATTGTTATCATTCACCTTCCAGGCTCAAGGAGATTTCACTTCAATACAAAAGTAAAGT	2816
Db	2763	TATTGTTATCAGACCTTCCAGACTTAAGATTTTTCGTTGAAATATGATGTTAAAGT	2822
QY	2817	GGCTAGGCTTTGGTCACTGAAGGGAGAGTGAACACACACCAATCGCCCCGCTGCTGCG	2876
Db	2823	CGCGAAGCTTTGATGTCTGCAAGAGGAAGTGAATACACACCCCAATCATACTGAATTGCA	2882
QY	2877	AATGGACAGTGACCGAAGGGATCAGACCTTGGGGG	2911
Db	2883	AATGGCAGAGATCGAAGTCAATCATGACCTAGGAG	2917

AC ADM72252;
XX
DT 03-JUN-2004 (first entry)
XX
DE
XX
KW Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance;
KW gene; ss.
XX
OS Oryza minuta.
XX
PN WO2004022715-A2.
XX
PD 18-MAR-2004.
XX
PF 08-SEP-2003; 2003WO-US027913.
XX
PR 09-SEP-2002; 2002US-0409216P.
PR 18-MAR-2003; 2003US-0455713P.
PR 05-SEP-2003; 2003US-00856394.
XX
PA (OHIS) UNIV OHIO STATE.
XX
PI Wang G;
XX
DR WPI; 2004-257576/24.
XX
PT New rice Pi2-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX
PS Example 6; SEQ ID NO 15; 120pp; English.
XX
CC The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS(1-6) genes present in the pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA-21
CC fragment from the Pi2 region, that matched to NBS4.
XX
SQ Sequence 2422 BP; 718 A; 492 C; 561 G; 635 T; 0 U; 16 Other;

Query Match 48.1%; Score 1491.4; DB 12; Length 2422;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1540; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 1479 AGGAAAATTAAAGACTTGTGGAATCCATGATATCATCGTGATATCACAGTTTCAATCTC 1538
Db 1 AGGAAAATTAAAGACTTGTGGAATCCATGATATCATCGTGATATCACAGTTTCAATCTC 60

Qy 1539 GAGACAGAAAATTTTGTATTATTACCAATGGGAGATGGCTCTGATTAGTTTCAGGAAAA 1598
Db 61 GAGACAGAAAATTTTGTATTATTACCAATGGGAGATGGCTCTGATTAGTTTCAGGAAAA 120

Qy 1599 CACTCGCCACATAGCATTCGATGGGAGTATGTCCTGCAAAACAGAGTTGGATTCGAGCAT 1658
Db 121 CACTCGCCACATAGCATTCGATGGGAGTATGTCCTGCAAAACAGAGTTGGATTCGAGCAT 180

Qy 1659 TATTGATCATTTAGTATTTTGGTGACAGACCAGAGTCTAGCACATGCAGTTTGTGCC 1718
Db 181 TATTGATCATTTAGTATTTTGGTGACAGACCAGAGTCTAGCACATGCAGTTTGTGCC 240

Qy 1719 AGATCAATTGAGGATGTTACGGGCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCA 1778
Db 241 AGATCAATTGAGGATGTTACGGGCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCA 300

Qy 1779 AAAAGATTTCCACCGTATTCGATTTGTTGGCATTCGAAATCTTGAATATTCGATATTC 1838
Db 301 AAAAGATTTCCACCGTATTCGATTTGTTGGCATTCGAAATCTTGAATATTCGATATTC 360

Qy 1839 GTCAATCCATATTCACATTCACAGATCCATTTGGTAAACTACAGGCGCTTACAGACTTTGAA 1898
Db 361 GTCAATCCATATTCACATTCACAGATCCATTTGGTAAACTACAGGCGCTTACAAACTTTGAA 420

Qy 1899 CATGCTCAAGCACATACATTTCGAGCACTACCAGTGAGATCAGTAAACTCCAATGCTTGCA 1958
Db 421 CATGCCGAGCACATACATTTCGAGCACTACCAGTGAGATCAGTAAACTCCAATGCTTGCA 480

Qy 1959 TACTCTTCGTTGTATAGAGAGCTTGAATTTGCAAACTTTAGTCTAAATACCCCAATGAA 2018
Db 481 TACTCTTCGTTGTATAGGACAGTTTCAATATGACAACTTTAGTCTAAACCACCAATGAA 540

Qy 2019 GTGCATTAACCAACAATATGCTGCAATTTACATGGCCACCAAAAGTTTCTGGTCTGAATCAT 2078
Db 541 GTGCATTAACCAACAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

Qy 2079 TCGTGCAAAAACAATTCGTAATTTACATGGCCACCAAAAGTTTCTGGTCTGAATCAT 2138
Db 601 TCGTGCAAAAACAATTCGTAATTTGACATGGCCACCAAAAGTTTCTGGTCTGAATCAT 660

Qy 2139 CGGTGTGAAGTACCCAAAGGAATAGTAAAGTTTCGAGACTTACAGGTTCCTAGAGTATGT 2198
Db 661 CGGTGTGAAGTACCCAAAGGAATAGTAAAGTTTCGAGACTTTCAGAGTATGT 720

Qy 2199 AGATATCAGCGGACACAGTAGTAGAGCAATCAAAAGAGCTGGGGCAGTTAAGCAAGTTGAG 2258
Db 721 AGATATCAGCGGACACAGTAGTAGAGCAATCAAAAGAGCTGGGGCAGTTAAGCAAGCTGAG 780

Qy 2259 GAAATTAGCTGTGATACAAAAGGCTCGACAAAAGAAAATGTAAGATACCTTTATCGAGC 2318
Db 781 GAAATTAGCTGTGATACAAAAGGCTCGACAAAAGAAAATGTAAGATACCTTTATCGAGC 840

Qy 2319 CATTGAGAAGCTCTCTTCCCTCCAACTCTCTATATGAATGCTCGCTTATTTATCAGATAT 2378
Db 841 CATTGAGAAGCTCTCTTCCCTCCAACTCTCTCAATGCTGCTGCTGCTGCTGCTGCTGCTG 900

Qy 2379 TGAACAACCTTGAAGTGCCTAGATTTCTATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438
Db 901 TGAACAACCTTGAAGTGCCTAGATTTCTATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960

Qy 2439 GTTGAATGGAAGCTTGAAGAGATGCTTAATGATGAGCAGTCTCACTCACTGAGAA 2498
Db 961 GTTGAATGGAATTTCTTGAGGAGATGCTTAATGATGAGCAGTCTCACTCACTGAGAA 1020

Qy 2499 GTTCAACTTATGAGTAGTAAACTTAAAGAGAGTAAACATGCTGATCTTGGGGCACT 2558
Db 1021 GATCTACTTATGAGGAGCAAACTTAAAGAGAGTAAACATGCTGATCTTGGGGCACT 1080

Qy 2559 GCCCAACCTCATGTTCTCTTTTATCATTAATTTCTTATCTTGGGGAGAGCTAGTATT 2618
Db 1081 GCCCAACCTCATGTTCTCTTTTATCGAATGCTTACCTTGGGGAGAGCTAGTATT 1140

Qy 2619 CAAAACGGGAGCATTCCTCAATCTTAGAACACTTTGATTTTCAATTTGGATCAGCTAAG 2678
Db 1141 CAAAACGGGAGCATTCCTCAATCTTAGAACACTTTGATTTTCAATTTGGATCAGCTAAG 1200

Qy 2679 AGAGATCAGATTTGAGGACGCGAGCTCACCCAGTTGGAAAAGATAGAAATCTCTTGTCTG 2738
Db 1201 AGAGATCAGATTTGAGGACGCGAGCTCACCCCTGTTGGAAAAGATAGAAATAGGGAGTG 1260

Qy 2739 CAGGTTGGAATCAGGGATTTATTTGATCATTTCACTTTCCAAAGCTCAAGGAGATTTCACT 2798
Db 1261 CAGGTTGGAATCTGGGATTACTGATATCATTTCACTTTCCAAAGCTCAAGGAGATTTCCAAT 1320

Qy 2799 TGAATACAAAAGTAAAGTGGCTAGGCTTGGTCACTGAGGAGAGTGAACACACACCC 2858
Db 1321 TAGATACGGAAGTAAAGTGGCTTGGTCACTGAGGAGAGTGAACACACACCC 1380

Qy 2859 AAATCGCCCGCTGCTGCGAATGGACGTGACCGAAGGATCACCACCTTGGGGCTGAAGC 2918
Db 1381 AAATCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440

Qy 2919 CGAAGGATCTTCTATAGAAAGTGAACACAGCAGATCTCTGTTCTGATGCCCAAGGATCAGT 2978
Db 1441 CGAAGGATCTTCTATAGAAAGTGAACACAGCAGATCTCTGTTCTGATGCCCAAGGATCAGT 1500

Qy 2979 CACTGTAGCAGTGGAAGCAACGGATTCCTCTCCGAGCAGGAGGAGAGCTCGCAGTC 3038

Db	1501	CAC	TGTAGCAGTGG	AAGCAACGGATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTC	1560
Qy	3039	GC	AGTGATCACG	TTGACGACGAATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTG	3098
Db	1561	GC	AGTGATCACG	TTGACGACGAATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTG	1620
Qy	3099	A	3099		
Db	1621	A	1621		
RESULT 12					
AD	157169	ID	AD157169	standard; DNA; 2982 BP.	
AC	AD157169;	AC	AD157169;		
XX	XX	XX	XX	XX	XX
XX	XX	XX	XX	XX	XX
DE	22-APR-2004	(first entry)			
XX	Oryza	minuta	Pi9	locus nucleotide binding site (NBS) gene #2.	
XX	nucleotide	binding	site; NBS; Pi9	gene; bacterial blight; rice blast;	
KW	plant	breeding; transgenic	plant; plant; gene; ds.		
XX	XX	XX	XX	XX	XX
OS	Oryza	minuta.			
XX	US2004006788-A1.				
PN	08-JAN-2004.				
XX	27-JAN-2003; 2003US-00352179.				
XX	25-JAN-2002; 2002US-0352106P.				
PR	01-FEB-2002; 2002US-0353304P.				
XX	(WANG/) WANG G.				
PA	(LIUG/) LIU G.				
XX	Wang G, Liu G;				
PI	WFI; 2004-121064/12.				
XX	P-PSDB; AD157170.				
DR	Nucleic	acids encoding	nucleotide binding site (NBS) proteins NBS1, NBS2		
XX	and NBS3, useful for	producing	plants resistant to Magnaporthe grisea		
PT	infection.				
PT	Claim 3; SEQ ID NO 86; 136pp; English.				
XX	The invention	comprises	the amino acid and coding sequences of nucleotide		
XX	binding site (NBS) proteins	from the	Oryza minuta Pi9 locus (bacterial		
CC	blight and rice blast	resistance genes). The	DNA sequences may be used as		
CC	markers for resistance	to infection with	Magnaporthe grisea in plant		
CC	breeding programs. The	present	DNA sequence represents an NBS gene from		
CC	the	Oryza	minuta Pi9 locus.		
XX	Sequence	2982 BP; 921 A; 545 C; 722 G; 794 T; 0 U; 0 Other;			
SQ	Query Match	37.3%; Score 1156.2; DB 12; Length 2982;			
	Best Local Similarity	65.5%; Pred. No. 0;			
	Matches 1917; Conservative	0; Mismatches 918; Indels 90; Gaps 12;			
Qy	1	ATGCGGAGACGGTGTGCTGACGATGGCGAGTGCCTGTGTGGGCGAGTGCCATCAGCAGGCC	60		
Db	1	ATGACTGAGACGGTGGTGAAGCATGGCCATGCTCGCTGGTGGGAGTGCCATCAGAGTGGCT	60		
Qy	61	GCCTCTGCCCGCTGCCAATGAGACGAGCCTCCTGTCTGGCGCTCGAGAAGGACATCTCGTAT	120		
Db	61	TCCTTCTGCTTCACGCCAAGAGATGAGCATGCTGATGTTGTTGCAACGAGATTGTTTC	120		
Qy	121	ATCAAGATGAGCTTAAAAACAATCGAGGCATTCCTTAGAGCTGCTGAAGTTATGAAAAAG	180		

Qy	1261	GGTTACAAACCACTTACCATCCACTCTGAAACCACTGCTTTTGTATCTTAAGTATCTTTCT	1320
Db	1243	AGTTACAATTACTTTGCCATCTCATCTTTAAGCCCTTGTCTGTACCTTTTGCATCTTTCTCT	1302
Qy	1321	GAGGATTTTGAATACAAAGGAACTGCTAGTAGGTAGATGCGATAGCAGAAAGGTTGGTT	1380
Db	1303	GAGGATTTTGTATTTCAAAGGAGGCGCTAGTACATAGATGGATTTGCAGAGGGGTTATT	1362
Qy	1381	AGACCAAGGTTGGGATGACACACTTAAGATGTCCGAGAAAGTTACTTTAATGAGCTAATC	1440
Db	1363	AGAGCTAGGGGTGGAGTGGGAATTGTGGATGTGCCACAAAGTATTTTGATGAGTTGATC	1422
Qy	1441	AACCGAAGTATGATTTCAACGATCAAGAGTGGGCAACAGCAGGAAATTAAGACTTTGCGA	1500
Db	1423	AACCGAAGTATGATTTCAAGCATCTAGAGTGGATATAGAGGAAATATTAAGAGCTGCCGA	1482
Qy	1501	ATCCATCATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAATTTTGTATTA	1560
Db	1483	GTCCATGATATCATGTGCGTGTATCATGATATCAATATCTTAGGGAAGAAATTTTGTATAC	1542
Qy	1561	TTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAACACTCGCCACATAGCATTCAT	1620
Db	1543	TTGATGGGTGATGATGAACTAGTGTAGTGGAGGAAATATTGCCATTTTAGTGCACCAT	1602
Qy	1621	G---GGAGTATGCTCTCAAAACAGGATTTGGATTTGGAGCATTAATTCGATCATTTAGCTATT	1677
Db	1603	GATACTAGCAAGTGTTCAAATATATAGGCATGGATTGGAGCCATGTACGGTCAATTAACCTTG	1662
Qy	1678	TTTGG---TGACAGACCCAGAGCTTAGCACATGTCAGTTTGTCCAGATCAATTTGAGGATG	1734
Db	1663	TTTGGCAATGAGAGACCCAAAGGCTATCTCTTCAATTTTGTTCGCCAATTTGAAGATG	1722
Qy	1735	TTACGGGTCTGGATCTTTGAAGATGTGCACATTTCTTAATCACTCAAAAGATTTTCGACCGT	1794
Db	1723	CTAAGAGTCTGGATCTTCAAGATGTCAAAATTTGGGATGACACAAAAGATATCGGAAA	1782
Qy	1795	ATTGCATTGTTGTGCCACTTTGAAATCTTGAGTATTTGGATATTCGTCAATCCATATATTTCA	1854
Db	1783	ATAGGTTGCTCGCTCACTTGAATAATGTGAATATTCGAGGGCATTCAGTATTTATGCA	1842
Qy	1855	CTTCCAGATCCATTTGTTAACTACAGGGGCTACAGACTTTTGAACATGTCAAGACATAC	1914
Db	1843	CTTCTAGGTGTTAGGAAATTTAAAGACTTTGTGCACCTTTGGACATAAATGACAGTTAC	1902
Qy	1915	ATTGCACACTACCAAGTGGATCAGTAACTAACTCCAAATGCTCGCATCTCTTCCTGTATA	1974
Db	1903	ATTACAGAACTACCACTGAGATTTAGTAATTTGCAGAGTCTATGTATTTCTCCGTTGTAGA	1962
Qy	1975	AGAGAGCTTGAATTTGACAACTTTAGTCTAAATCACCCAAATGAAGTGCATAAATTAACACA	2034
Db	1963	GGAGACCAAACTCGGGGATTTTAATCTAAATGATCCTAAGGNTGTCTAATTTGCTTC	2022
Qy	2035	ATATGCTGCTCTAAAGTATTCACACCTTTTATGTTAGTCGCGATTAATGTCGAAACAAAT	2094
Db	2023	TCATGTTTGCT---CTGCTTATGGCTGCAACCGATTTCTGATGAACGTAATAAAATAAT	2079
Qy	2095	GCTGAATTTACATGGGCCCAAAAGTTTCTGGTC-----TGAAATCAATTCGGGTG	2145
Db	2080	GCTGAGCTACACGTGGGTGTTCAAGTCAATTTGGTCTCCTAATGGTGGTACATATGGTGTG	2139
Qy	2146	AAGGTACCCAAAGGAATAGGTAAAGTTCGGAGACTTTACAGGTTCTAGAGTATGTAGATATC	2205
Db	2140	AGGGTACTAGAGGAATCAAGNATTTGAAAGGCTGCAGGTCTAGAGACAGTGGATATC	2199
Qy	2206	AGGCGGACCAAGTATGAGGCAATCAAAAGAGCTGGGGCAGTTAAGCAAGTTTGAGGAAATTA	2265
Db	2200	AATCGAACCCAGCAGTAAAGTGAAGAGTTGGAGAGCTTATCCAGCTAAGAAACTA	2259
Qy	2266	GCTGTGATTAACAAAGGCTGCACAAAGGAAATATGTAAGTATCTTTATGAGCCATTGAG	2325
Db	2260	AGTGTAGTAAACAAAGGCTCCACCAAGGAAATATGCAAAATCTCTCTGTACAGCCATTGAG	2319

Qy	2326	AGGCTCTCTCCCTCCGATCTCTATATGAATGCTGCGTATTATCAGATATTGAACA	2388
Db	2320	ANGCTAACTCTCCCTCAAAACTCTCTATCTGAATGCTCATGGACCTTGGATCTGGAACA	2379
Qy	2386	CTTGAGTGCCTAGATCTATTTCATCTCTCTCCCTCCCTACTCTGAGGACACTCGCGTTTGAAT	2445
Db	2380	CTTGAATGGCTACATCTATTCTCCATCTCTCTCTCCCTCCCTCTGAGGATCATCAGATTGATC	2436
Qy	2446	GGAAAGTCTTGAAGAGATGCGCTAACTGGATTGAGCAGCTCACTCACTCTGAAGAAGTTCAAC	2505
Db	2437	GGATACATGAAGAGAGATGCCCAACTGGTTTGGGAGCTCAGACAGCTGGTGAAGATTTCAC	2496
Qy	2506	TTATGGAGTAGTAAACTAAAGGAAGGTAAACCAATGCTGATCTTTGGGGCACTGCCCAAC	2565
Db	2497	TTGCAGAATAGCCCAACTAGAGGAGGATAAACCAATGGAGATACTCGGAGAACTGCCTAAT	2556
Qy	2566	CTCATGTTCTCTCTCTTTTATCATATCTTATCTTTCTTTGGGGAAGCTAGTATTCAAAACG	2625
Db	2557	CTCATGCTCTTTTCTTTAGTTGGCAGCGGTCTAA-----	2593
Qy	2626	GGAGCATTCCTCAAAATCTTAGAACACTTTGTGATTTTCAATTTGGATCAGCTAAGAGAGATC	2685
Db	2594	-----TCATTTCGCAATCAGAAGCAACTGAAAGAGGTG	2625
Qy	2686	AGATTGTAGAGACGGCAGCTCACCCAGTTGTGAAAAGATAGAAATCTCTTCTGCTCGAGGTG	2745
Db	2626	AGATTTGAAGAGGGAACCTCACCTCGATGGAAGGATTGATATCAGAGAAATGCAGATTG	2685
Qy	2746	GAATCAGGAGTATTGGTATCATCTACCTTCCAAAGCTCAAGGAGATTTCACTTGAATAC	2805
Db	2686	ACATCAGGAGTATCTGGTATCAAAACCTTCCGAGGCTTAAGGAGATTTCACTTGAATAC	2745
Qy	2806	AAAAGTAAAGTGGCTAGGCTTGGTCTAGCTGAAGGGAGAAAGTGAACACACACCCCAATCGC	2865
Db	2746	AGTGCTAAAGTGGTGGCTAGTCTAGCTAGAGGTTGAAATGGGCACACACCCCAATCGA	2805
Qy	2866	CCCGTGTCTGGAATGACAGTGAACCGAAGGGATCAGACCTGGGG	2910
Db	2806	CCCATGTTGGCCTGTTTGGGGAGCAAGCCGTCATGACCTGGGG	2850
RESULT 13			
ADM72242			
ID	ADM72242 standard; cdna; 4147 BP.		
AC	ADM72242;		
AC	03-JUN-2004 (first entry)		
DT	O. minuta NBS3 polypeptide encoding cdna.		
DE	P12; NBS3; plant protectant; gene therapy; rice; disease resistance;		
KW	gene; ss.		
KW	Oryza minuta..		
OS			
XX	Key		
XX	Location/Qualifiers		
XX	1..1983		
XX	/*tag= a		
XX	/product= "NBS3"		
XX	WO2004022715-A2.		
XX	18-MAR-2004.		
XX	08-SEP-2003; 2003WO-US029113.		
XX	09-SEP-2002; 2002US-0409216P.		
XX	18-MAR-2003; 2003US-0455713P.		
XX	05-SEP-2003; 2003US-00656394.		
XX	(OHIS) UNIV OHIO STATE.		
XX			

AD157180
ID AD157180 standard; DNA; 2351 BP.
AC
AC AD157180;
XX
XX 22-APR-2004 (first entry)
DT
XX
XX
DE Oryza minuta P19 locus-related DNA sequence #2.
XX
XX nucleotide binding site; NBS; P19; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; ds.
XX
XX Oryza minuta.
OS
XX
XX US2004006788-A1.
PN
XX
XX 08-JAN-2004.
XX
XX 27-JAN-2003; 2003US-00352179.
XX
XX 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX
XX (WANG/) WANG G.
PA (LIU/) LIU G.
XX
XX Wang G, Liu G;
PI
XX
XX WPI; 2004-121064/12.
DR
XX
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
XX Disclosure; SEQ ID NO 97; 136pp; English.
PS
XX
XX The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present Oryza minuta DNA sequence was used in the
CC exemplification of the invention.
XX
XX
SQ Sequence 2351 BP; 703 A; 420 C; 559 G; 651 T; 0 U; 18 Other;

Query Match 27.6%; Score 854.2; DB 12; Length 2351;
Best Local Similarity 68.4%; Pred. No. 2.6e-230;
Matches 1263; Conservative 0; Mismatches 563; Indels 21; Gaps 5;

QY 1079 ATATGCAAAAGATGGTTGAACGAATTGTAAATAAATGTGGTCTACCATTTAGCAATAC 1138
DB 5 AATGAAAGAAATATTTGAAAGATCTAAAGAAATGTGGAGTCTACCGTAGCTATAA 64

QY 1139 TTACAATPAGGAGCTGTCTTGCACAACTAAACAGGTGTGCAGAAATGGGAGAAATTTCTATGAAC 1198
DB 65 TCACAAATAGGTGCAGTCTTGTGAGGGAAAGATATAAAAGAGTGGGAAATTTGTATGCTC 124

QY 1199 AACTTCTTCAGAACTAGAAATAAACCAAGCCCTGGAGCTTTTCAGAGAAATGTGTACCC 1258
DB 125 AACTTCCATCAGAACTTTGAAGCAATCCAATCGCTGAACCAATGAAGAAGGTGTGAACCC 184

QY 1259 TAGGTTAACAACCACTACCATCCCATCTGAAACCATCTTTTGTATCTAAGTATCTTTC 1318
DB 185 TTAGTTACAATTAATCTGCCATCTCATCTTAAGCCCTTCTTCTGACTTTGCACTTCTTC 244

QY 1319 CTGAGGATTTTGAATAACAAGGAATCGTCTAGTAGGTAGATGGATGACGAGAGGGTTTG 1378
DB 245 CTGAGGATTTTGAATCAAAAGGAAGCGCTAGTACATAGATGGATGGATTGCAGAGGGTTTA 304

QY 1379 TTAGACCAAGGTTGGGATGACGACTAAGGATGTGGAGAAAGTTACTTTAATGAGCTAA 1438
DB 305 TTAGAGCTAGGGGTGGAGTGGGAATTTGGATGTGGCACAAGAAAGATATTTTGTAGTGA 364

QY 1439 TCAACCGAAGTATGATTCAACGATCAAGAGTGGGCACAGCAGGAGAAAATTAAGACTTGTTC 1498
DB 365 TCAACCGAAGTATGATTCAACGATCTAGAGTGGATATAGAGGGAAAATATTAAAGAGCTGCC 424

QY 1499 GAATCCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTGTAT 1558
DB 425 GAGTCCAATGATATCATCGTGTATCATCAATATCTAGGGAGAAAAATTTTGTAT 484

QY 1559 TATTACCNAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAAAACACCTCGGCACATGATTC 1618
DB 485 ACTTGATGGGTGATGAGAACTAGTGTAGTGGAGGAAAATATTGCGCAATTTAGTGACCC 544

QY 1619 ATGGGAGTAT--GTCCTGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATAGCTA 1675
DB 545 ATGATACTAGCAAGTGTTCAAATATAGCATGGATTGGAGCCATGTACGGTCAATTAACCT 604

QY 1676 TTTTGTG---TGACAGACCCAAAGAGTCTAGCAATGACAGTTTGTCCAGATCAATTTAGGA 1732
DB 605 TGTTTGGCAATGAGAGACCCAAAGGGCTATCTCTTCAATTTGTCTTCCCAATTTGAAGA 664

QY 1733 TGTTCAGGGTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACC 1792
DB 665 TGCTAAGAGTGTGGATCTTCAAGATGTCAAAATTTGGGATGACACAAAAGATATCGAA 724

QY 1793 GTATTGCATTTGTGTGCCACTTTGAAATPACTTTGAGTATTGGATATTCGTCATCCATATATT 1852
DB 725 AATAGGGTTGCTGGTCACTTTGAAATATGTGAATATTGGAGGGCATTTCAAGTATTTATG 784

QY 1853 CACTTCCAGATCCATTTGGTAAACTACAGGCCCTACAGACTTTTGAACATGTCAAGCAAT 1912
DB 785 CACTTCTTAGTGTATAGGAAAAATTTAAAGACTTTGTGCACCTTTGGACATAACTCACAGTT 844

QY 1913 ACATTGCAGCACTACCAAGTGAGATCAGTAACTCCAAATGTCTGCATACTCTTCGTTGTA 1972
DB 845 ACATTACAGAACTACCACACTGAGATAGTAATTTGCAGAGTCTATGTATTTCTCCGTTGTA 904

QY 1973 TAAGAGAGCTTTGAATTTTGACAACTTTTAGTCTAAATCAACCAATGGAAGTGCATATACTAAC 2032
DB 905 GAGGAAGACCAAACTCGGGGGATTTTAATCTTAATGATCTTAAGGATTTGTCTAATTCCT 964

QY 2033 CAATATGCTGCTTAAAGTATTACACTTTTAGTTAGTTCGGGATAATTCGTGCAGAAAACAA 2092
DB 965 TCTCATGTTTTCCTC---CTGCTTATGGCTGCAACCCGATTTCTGATGAACGTAATAAATAA 1021

QY 2093 TTGCTGAATTTTCAATGCGCCACCAAAAGTTTCTGGTC-----TGAATCTTCGCTG 2143
DB 1022 TTGCTGAGCTACACGTGGGTGTTTCAAGTCAATGGTCTCCCTAATGGTGTGATCATATGGTG 1081

QY 2144 TGAAGGTACCCCAAGGAATAGGTAAGTTGCGAGACTTTACAGGTTCTAGAGTATGTAGATA 2203
DB 1082 TGAGGGTACCTAGAGGAATCAAGAAATTTGAAAAGGCTGCAGGTCTAGAGACAGTGGATA 1141

QY 2204 TCAGGGGGAACAGTAGTAGAGCAATCAAGAGCTGGGGCAGTTTAAAGCAAGTTGAGGAAAT 2263
DB 1142 TCAATCGAACACAGCAGTAAAGTCAAGTTGAAGAGTTGGGAGAGCTTATTCAGCTAAGAAAAC 1201

QY 2264 TAGCTGTGATAACAAGGGCTCGACAAAGGAAAAATGTAAGATACTTTTATGSCGCCATTG 2323
DB 1202 TAAAGTGTAGTAACACAGGGGTCCACCAAGGAAAAATGCAAAAATCTCTGTACAGCCATT 1261

QY 2324 AGAAGCTCTCTTCCTCCCAATCTCTATATGAATGCTGCGTTATTTATTCAGATATTGAAA 2383
DB 1262 AGAAGCTAACTTCCCTCANAACCTCTATCTGAATGCTCATGGACCCCTTGGATACTGAA 1321

QY 2384 CACTTGAGTCCCTAGATTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2443
DB 1322 CACTTGAATGGCTACATTTCTATTTTCCCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1378

QY 2444 ATGGAAGTCTTTGAGAGATGCTTAACTGGATTGAGCAGCTCACTCACTCAAGGAAGTTCA 2503
DB 1379 TCGGATACATGAAGAGATGCCCAACTGGTTTGGGAGCTCAGACAGCTGCTGTGAAGATTC 1438

QY 2504 ACTTATGGAGTAGTAAACTAAAGGAAGGTTAAAAACATGCTGTGATACTTTGGGGCACTGCCCA 2563

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
18448.290 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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5: gb_est4:.*
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7: gb_est6:.*
8: gb_gsl1:.*
9: gb_gsl2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1565	50.5	2925	9	CL964072
3	1165.8	37.6	3024	9	CL963354
4	550.8	17.8	662	9	AG210016
5	510.2	16.5	698	9	AG208890
6	441.2	14.2	810	6	CF071622
7	400.6	12.9	703	9	CL832740
8	360	11.6	709	6	CA147958
9	360	11.6	737	9	CL858532
10	359.8	11.6	740	9	CL861885
11	355.8	11.5	875	9	CW518670
12	351	11.3	663	8	AQ578469
13	348.8	11.3	709	9	CL801486
14	342.8	11.1	603	9	CL197270
15	319	10.3	551	9	CL197271
16	314.8	10.2	527	8	AQ510644
17	314.4	10.1	673	8	BZ338669
18	313.8	10.1	708	9	CL582275
19	309	10.0	738	9	AB155403
20	306	9.9	727	9	CL190018
21	305.8	9.9	833	9	CW536681
22	305.4	9.9	650	8	AQ579138
23	285.8	9.2	716	9	CW527324
24	277.8	9.0	846	9	CW503682

25 269.4 8.7 718 2 BE216309
26 263.6 8.5 613 9 AG023674
27 262.2 8.5 696 6 CD862821
28 259.2 8.4 729 9 CL577632
29 255 8.2 618 6 CB652975
30 253.6 8.2 645 8 BZ341503
31 253.4 8.2 775 6 CB652258
32 250.2 8.1 762 8 AZ047631
33 242.4 7.8 435 9 AG208447
34 234.4 7.6 478 9 AG212538
35 233 7.5 583 8 BZ341502
36 231.6 7.5 503 9 AG206783
37 225 7.3 659 8 BZ338670
38 224 7.2 574 9 CL175621
39 223 7.2 1115 7 CK168020
40 221.8 7.2 608 6 CF071576
41 221.4 7.1 1138 7 CK166588
42 221.4 7.1 1158 7 CK166779
43 221 7.1 1115 7 CK167667
44 215 6.9 569 4 BG101746
45 212.8 6.9 635 8 BZ334577

ALIGNMENTS

RESULT 1
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LOCUS CL964074 3159 bp DNA linear GSS 21-SEP-2004
DEFINITION OrlFCC010263 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL964074
VERSION CL964074.1 GI:52382860
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 3159)
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
source
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/mol_type="genomic DNA"
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Query Match 71.3%; Score 2209.2; DB 9; Length 3159;
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Matches 2506; Conservative 0; Mismatches 468; Indels 6; Gaps 1;
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Db 178 ATGCGGAGACGGTGTGAGCATGCCAGGTCGCTGGTGGCAGTCGCATCAGCAAGGCC 237
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Ory 61 GCCTCTCCGCTGCCAATAGACAGCGCTCTCTGCTCGCGCTCGAGAGGACATCTGGTAT 120

[illegible]

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Db	1378	CTTCCTTCGAACTTGAAGCAACCCCAAGCCTTCAGCTTTGAGGAGAATGGTGACCCCTT	1437
Qy	1261	GGTTACAACCACTTACCATCCCATCTGAAACCAATGCTTTTTTGTATCTAAGTATCTTTCCCT	1320
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AUTHORS	1 (bases 1 to 3024) Ma,L., Wang,C., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.									
TITLE	An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis									
JOURNAL	Unpublished (2004)									
COMMENT	Contact: Chen Chen Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559 Fax: 86-10-80488676 Email: chenchen@gemomics.org.cn Rice genomic sequence. Class: exon-trapped.									
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  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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  Miyao,A., Tanaka,K., Murata,K., Sawaki,H., Takeda,S., Abe,K.,
  Shinzuka,Y., Onosaka,K. and Hirochika,H.
  Target Site Specificity of the Tos17 Retrotransposon Shows a
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JOURNAL
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MEDLINE
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PUBMED
  2 (bases 1 to 698)
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AUTHORS
  Miyao,A., Murata,K. and Hirochika,H.
TITLE
  Direct Submission
JOURNAL
  Submitted (16-APR-2002) Akio Miyao, National Institute of
  Agrobiological Sciences, Molecular Genetics; 2-1-2, Kannondai,
  Tsukuba, Ibaraki 305-8602, Japan (E-mail:miyao@affrc.go.jp,
  URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
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4	83.2	2.7	5222	4	US-09-336-946B-3
5	83.2	2.7	5222	4	Sequence 68, Appli
6	83.2	2.7	5696	4	Sequence 57, Appli
7	83.2	2.7	5757	4	US-09-993-170-57
8	83.2	2.7	5757	4	Sequence 60, Appli
9	67.4	2.2	2718	3	US-09-336-946B-1
10	67.4	2.2	2718	3	Sequence 1, Appli
11	67.4	2.2	2718	3	Sequence 4, Appli
12	67.4	2.2	3099	3	US-09-360-186-4
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37 41.6 1.3 136917 4 US-09-949-016-16369 Sequence 16369, A
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43 39.2 1.3 1230230 4 US-09-438-185A-1 Sequence 1, Appli
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ALIGNMENTS

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; APPLICANT: Yano, Masahiro
; APPLICANT: Iwamoto, Masao
; APPLICANT: Katayose, Yuichi
; APPLICANT: Sasaki, Takuji
; APPLICANT: Wang, Zi-Xuan
; APPLICANT: Yamanouchi, Utako
; APPLICANT: Ishimaru, Lisa
; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330.330
; FILING DATE: 11-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 10-181455
; FILING DATE: 12-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/032001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 2:
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; LENGTH: 3925 base pairs
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; MOLECULE TYPE: cDNA to mRNA
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; NAME/KEY: Coding Sequence
; LOCATION: 82...3696
US-09-330-330-2

Query Match	4.2%	Score 129;	DB 3;	Length 3925;
Best Local Similarity	46.3%;	Pred. No. 3.2e-28;		
Matches 549;	Conservative 0;	Mismatches 620;	Indels 18;	Gaps 3;
QY	800	CTGAGTACCTGATAGAGAGCTCAAGGAGNAGAGGTACTTTGGTTGTCTAGATGATCTAT	859	
DB	1472	CTGGCAGTTGAAAGGCTTTTAGAAAGAAAGTTGCTTGATTGTTCTTAGATGATTCT	1531	
QY	860	GGATTTTACATGATTGGAAATTGGATAAATGAAATTGCAATTCCTTAAGAAACAATAAGAAGG	919	
DB	1532	CAGATACCTCAGAAATGGACCGAGNATAAAACCAAGTTATTCCTCCCTGTTGGAAAAGCAA	1591	
QY	920	GCAGTGGAAATAGTAATAACCACTCGGAATGTTGATCTAGCGGAGAGTGTGCCACAGCCT	979	
DB	1592	GCCGAATAATTGTGACTACAAGAAAAGAGAATATTGCCAACCATTGCTCAGGGAAAAAATG	1651	
QY	980	CACTGGTGTACCACTTGATTCTTCTGCAGATGACGATGCCATTCATTTGCTACTCTAGAA	1039	
DB	1652	GAAATGTGCAACACCTTAAAGTCTTAAACATAATGATGCAATGTGCCTCTTGTAGTGAGA	1711	
QY	1040	AAAAAATAAAAAATCATGAAGACATGGAATCAAAATAAAAAATA-----TGCAAAAGATGG	1093	
DB	1712	AGGTAATTGAGGAGCTACATAATTGGATGATCAGACAAATCCAGAGTTGGTTAAAGAAG	1771	
QY	1094	TTGAACGAATTGTAAATAAATGTGGTCTCTACCAATTAGCAATACTTACAATAGGAGCTG	1153	
DB	1772	CAAAAACAATCTTAAAGAAAGTGGCATGGACTGCCCTTGGCAATAGTTGTCTATAGTGGAT	1831	
QY	1154	TGCTTGCAACTAACAAGGTGC-----AGNATGGGAGAAATCTATGAACAACATTCCTT	1207	
DB	1832	TC TTGGCAACCCGACCAAGACCCGAGAGAGTGGAGAAATTTGAACGAGAATATCAATG	1891	
QY	1208	CAGAACTAGAAATAAAACCCAGCCTGGAAGCTTTGAGGAGAAATGGTGACCTAGTTTACA	1267	
DB	1892	CTGAGTTGGAAATGAAATCCAGAGCTTGGAAATGATAAGAACCGTCTTGAANAAGCTATG	1951	
QY	1268	ACCACCTACCATGCCATCTGAACCACTGCTTTTGTATCTAAGTATCTTTCTCTGAGGATT	1327	
DB	1952	ATGCTTTACCATACCATCTCAAGTCATGTGTTTTTATATCTGTCCATTTTCCCTGGAAGAC	2011	
QY	1328	TTGAAATACAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGGTTGTTAGACCAA	1387	
DB	2012	AGATCAATTAGTCGAAGCGGTTTGGTGATCGTTGGGCAGCAGAAGGTTCTCACTCGAG	2071	
QY	1388	AGGTTGGGATGACGACTAAGGATGTCCGAGAAAGTTACTTTAAATGAGCTAATCAACCGAA	1447	
DB	2072	CACATGGGAAATCTGCCAATTGMAATAGCTTAAACGGCTACTTTCATGGAATCAAGAATAGA	2131	
QY	1448	GTATGATTCACGAT-----CAAGATGGGCAAGCAGGAAAAAATTAAGACTTGTGCA	1501	
DB	2132	GCATGATTTTACCATTCAGCAATTCAGGTAGCAGGAGAAATCAATTTGATCTTTCGAAG	2191	
QY	1502	TCCATGATATCATCCGTTGATACACAGTTTCAATCTCGACACAGGAAAAATTTTGTATTTAT	1561	
DB	2192	TCCATGATCTATCGGTGACATGCCCATCTCAAAGTCAACGAGGAAAAAATCTTGTTTTAA	2251	
QY	1562	TACCAATGGGAGATGGCTCTGATTTAGTTTACGAGAAAAACACTCGGCCACATAGCAATTC	1621	
DB	2252	GGGTGGAGGAAGGCTGCAGCGGTACATACATGGTGCAATTCGTGTCATCTTGTCTATAAGTA	2311	
QY	1622	GGAGTATGCTCTGCAAAAACAGGATTTGATTTGGAGCATTATTCGNATCATTAGCTATTTT	1681	
DB	2312	GCACCTGGAAGGAGATAAGAGTGAATTCAGGGGCATAGTGGACCTGCTCCGAATACGAT	2371	
QY	1682	GTGACAGACCAAGAGTCTAGCACATGCAGTTTGTGTCAGATCAATTCAGGATGTTACGGG	1741	
DB	2372	CGTTATCTCTGTTGGGATTTGGNAGCCATTTTGTATTGCAAGATGAGGTTTATAC	2431	
QY	1742	TC TTGGATCTTGAAGATGTGACATCTTTAATCACTCAAAAAGATTTTCGACCGTATTGCAT	1801	
DB	2432	GAGTGTCTGACTTTGAAGGAGCTAGAGGCTCTAGAATAATCATCACTTGATCAGATTGGA	2491	

Qy 1802 TGTGTGCCACTTGAATACCTTGAGTATTGGATATTTCGTCAATCATATATTCATTCCCA 1861

Db 2492 AGCTTATACCTCAAAATTCCTTTCTCTACGAGGATGCTATCGTATTGATCTACTTGCAG 2551

Qy 1862 GATCCATTGTGTAAACTACACGGGCTTCAGAGCTTTTGAACATGTCAAGCACATACATTGCAG 1921

Db 2552 ATTTACTGGGCAACCTTGAGGCACTCCAGATGCTAGACATCAGAGGTACATATGTAAAGG 2611

Qy 1922 CACTTACCAAGTGAGATCAGTAAACTCCAAATGTCTTGCCATACTCTTCGT 1968

Db 2612 CTTTGGCCAAAAACCATCATCAAGCTTCAGAAGCTACAGTACATTCAAT 2658

RESULT 2

US-09-330-330-3

; Sequence 3, Application US/09330330

; Patent No. 6274789

; GENERAL INFORMATION:

; APPLICANT: Yano, Masahiro

; APPLICANT: Iwamoto, Masao

; APPLICANT: Katayose, Yuichi

; APPLICANT: Sasaki, Takuji

; APPLICANT: Wang, Zi-Xuan

; APPLICANT: Yamanouchi, Utako

; APPLICANT: Ishimaru, Lisa

; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/330,330

; FILING DATE: 11-JUN-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 10-181455

; FILING DATE: 12-JUN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Ph.D., J.D., Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 06501/032001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1032 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA

US-09-330-330-3

	Query Match	3.6%	Score 111.4;	DB 3;	Length 10322;
	Best Local Similarity	46.9%;	Pred. No. 1.8e-22;		
	Matches 426;	Conservative 0;	Mismatches 471;	Indels 12;	Gaps 2;
Qy	1072	AATAAAATATGCAAAAGATGGTTGAACGAATGTGTAATTAATGTGGTCTCTACCAATTA	1131		
Db	7027	AATCCAGAGTTGGTTAAAGAAGCAAAACAAATCCTAAAGAAGTCGATGGACTGCCCCCTT	7086		
Qy	1132	GCAATCTTACAATAGGAGCTGTGCTTGCACTAAACAGGTGTC-----AGATGGGAG	1185		
Db	7087	GCAATAGTTGTCATAGTGGATTTCTGGCAAAACCGACCAAAAGACCCAGAAAGAGTGGAGA	7146		


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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-993-170-57

Query Match      2.7%; Score 83.2; DB 4; Length 5222;
Best Local Similarity 46.8%; Pred. No. 5.3e-14;
Matches 308; Conservative 0; Mismatches 338; Indels 12; Gaps 1;

Qy 908 ACAATAAGAGGGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCGGGAAGT 967
Db 3438 ATAATAATAGTTGCGAGTAGAATACTAATAACAAGAAATTGAACCTGTAGCTTTGGCAT 3497
Qy 968 GTGCCACAGCCTCACTGGTGTAACCACTTGATTTCTTCAGATGAACGATGCCATTTTCAT 1027
Db 3498 GCTGTGATATAAATCTCAGAGCACATTAATAAGATTGATCCACTGGGTGATGATGCTCAA 3557
Qy 1028 TGCTACTGAGAAAAACAATAAATAATCATGAGACATGGAAATCAATAAATAATATGCAAA 1087
Db 3558 GTCAATTGTTTTTCAGTGGAGTTGTTGGCCAAAGGAAATGAAATTTCTGGACATCTTACTG 3617
Qy 1088 AGATGGTTGAACGAATTTGTAATAAATGTTGCTCGTCTACCAATTAGCAATCTTACAATAG 1147
Db 3618 AAGTTTCTCATGACATGATAAATAAATGTTGGTCTTGCCTAGCAATACTATACAG 3677
Qy 1148 GAGCTGTGCTTGCACAACTAAACAGGTGTGAGATGGGAGAAATTTCTATGAACAACT----- 1202
Db 3678 CCAGACATTTTAAAGCCAGCTGTTAGATGGAATGCAGCAATGGAATCACAATACAAAAAT 3737
Qy 1203 -----TCCTTCAGAACTAGAAATAAACCCAGCCCTGGAGCTTTGAGGAGAAATGGTGA 1255
Db 3738 CATTGACTACTTCCAATTTGAAGAAAAATCTACTTTGCAGGGGATGAGGCAAGTACTCA 3797
Qy 1256 CCCTAGGTTCACACCACTACCACTCCCATCTGAAACCATGCTTTTGTATCTTAAGTATCT 1315
Db 3798 ACCTATTACATAATCTCTCTCATTTGTTGAAGCATGCTGTTATACCTTAGCATCT 3857
Qy 1316 TTCTGAGGATTTTGAATAACAAGGAATCGTCTAGTAGGATGATGATAGCAAGGAT 1375
Db 3858 ACAAAGAGGACTACATAATTAGGAAGGCCAACTTTGGTGAGGCAATGGATGCTGAAGTT 3917
Qy 1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGC 1435
Db 3918 TCATCAATTCCATAGAAAAATAAGTCTATGGAAGAAAGTTGCAGGGAACATAATTTTGTGAAC 3977
Qy 1436 TAATCAACCGAAGTATGATTCACGATCAAGAGTGGGCACAGCAGGAGAAAAATTAAGACTT 1495
Db 3978 TTGTTGAGGGGCTGCTCCACAGTAGATGTTAACTGCAAAAAATGAGGTATTGTGAT 4037
Qy 1496 GTCGAATCCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTT 1553
Db 4038 GTGTAGTGCCACCATGGTATTAAATTTTCATCAGGTGTAAGTCAATAGAGGAGAAATTT 4095

RESULT 6
US-09-993-170-60
; Sequence 60, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: BB1385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 60
; LENGTH: 5696
; TYPE: DNA
; ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence:Chimeric Gene									
US-09-993-170-60									
FEATURE:									
Query Match									
2.7%; Score 83.2; DB 4; Length 5696;									
Best Local Similarity 46.8%; Pred. No. 5, 7e-14;									
Matches 308; Conservative 0; Mismatches 338; Indels 12; Gaps 1;									
Qy	908	ACAATAAGAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTACGCGAGAAGT	967						
Db	3438	ATAATAATAGTTGCAGTAGAATACTAATAACACAGAAAAATTGAACCTGTAGCTTTGGCAT	3497						
Qy	968	GTGCCACAGCCTCACTGGTGATACACCTTGATTTCTTGCAGATGAACGATGCCATTTTCAT	1027						
Db	3498	GCTGTGATATAACTCAGAGCACATATTATAAGATTGATCCACTGGGTGATGATGCTCAA	3557						
Qy	1028	TGCTACTTGAGAAAAACAAATAAAAAATCATGAAGACATCGGAATCAAAATAAAAAATATGCAA	1087						
Db	3558	GTCAATTTGTTTTCAGTGGAGTGTGTGGCCAAAGAAATGAATTTCTCTGGACATCTTACTG	3617						
Qy	1088	AGATGGTTGAACGAATTTGTAATAAATGTGTGCTCTACCAATTAGCAATACTTCAATATAG	1147						
Db	3618	AAGTTTCTCATGACATGATAAAAAAATGTGTGGCTTGCCACTAGCAATAACTATAACAG	3677						
Qy	1148	GAGCTGTGCTTGCAACTTAACAGAGTGTCAAGATCGGAGAAATTCATTGAACAACT----	1202						
Db	3678	CCAGACATTTTAAAGCCAGCTGTTTAGATGGAATGCAGCAATGGAATCACATACAAAAAT	3737						
Qy	1203	-----TCCTTCAGAACTAGAAATAAACCCAGCCTGGAGCTTCAGAGGAATGGTGA	1255						
Db	3738	CATTGACTACTTCCAAATTGAGAAAAATCTCTTTGCAGGGATGAGGCAAGTACTCA	3797						
Qy	1256	CCCTAGGTTTACAAACCACTACATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCT	1315						
Db	3798	ACCTTATTACAAATACTTCTCTCAATTGTTGAAGCATGTCTGTATACCTTAGCATCT	3857						
Qy	1316	TTCTCTAGGATTTTGAATAACAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGT	1375						
Db	3858	ACAAAGGAGACTACATAATTAGGAAGGCCAACTTGGTGAGGCAATGGATGGCTCAAGGTT	3917						
Qy	1376	TTGTTAGACCAAGGTTGGGATGACGTAGGATGTGCGAGAAGTCTACTTTAATGAGC	1435						
Db	3918	TCATCAATTCCTATAGAAAAATAAGTCATGGGAAGAGTTGACGGGAACCTATTTTGATGAC	3977						
Qy	1436	TAATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCACAGCAGGAAAAAATTAGACTT	1495						
Db	3978	TTGTTGTGAGGGCTGTGTCACACCATGATGTTAACTGCCAAAAATGAGGTATTGTTCAT	4037						
Qy	1496	GTGGAATCCATGATATCATCCGTGATATCACAGTTTCAAATCTCGAGACAGGAAATTT	1553						
Db	4038	GTGTAGTGCACCACTGGTATTTAAATTTTCATCAGGTGTAACTCAATAGAGGGAATTT	4095						

RESULT 7
 US-09-336-946B-1
 : Sequence 1, Application US/09336946B
 : Patent No. 6479731
 : GENERAL INFORMATION:
 : APPLICANT: Valent, Barbara S.
 : APPLICANT: Bryant, Gregory
 : APPLICANT: E. I. du Pont de Nemours and Company
 : TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
 : FILE REFERENCE: BB-1136
 : CURRENT APPLICATION NUMBER: US/09/336, 946B
 : CURRENT FILING DATE: 1999-06-21
 : PRIOR APPLICATION NUMBER: 60/095229
 : PRIOR FILING DATE: 1998-08-04
 : NUMBER OF SEQ ID NOS: 74
 : SOFTWARE: Microsoft Office 97
 : SEQ ID NO 1
 : LENGTH: 5757
 : TYPE: DNA
 : ORGANISM: Oryza sativa

Query Match		2.7%	Score 83.2	DB 4	Length 5757	
Best Local Similarity		46.0%	Pred. No. 5.7e-14			
Matches	308	Conservative	0	Mismatches 338	Indels 12	Gaps 1
Qy	908	ACAATAAGAGGCGATCGAATAGTAATACCACTCGGAATGTTGATCTACGGGAGAAGT	967			
Db	3731	ATAATTAATAGTTGCGAGTAGAATACTAATTAACAACAGAAAAATTGAACCTGTAGCTTTGGCCAT	3790			
Qy	968	GTGCCACAGCCTCACATGGTGCTACACCTTGATTTCTTGACAGATGAACGATGCCATTTTCAT	1027			
Db	3791	GCTGTGATATAACTCAGAGCACATTATTAAAGATTGATCCACTGGGTGATGATGCTCTCAA	3850			
Qy	1028	TGCTACTGAGAAAAACAAATAAAAAATCATGAAGACATGGAATCAAAATAAAAAATATGCAAA	1087			
Db	3951	GTCAAATTGTTTTTCAGTGGAGTTGTTGGCCAAGNAATGAAATTTCTCTGGACATCTTACTG	3910			
Qy	1088	AGATGGTTGAACGAAATTGTAATAAATATGTTGGTCTGCTCAACATTAGCAATCTATTACAATAG	1147			
Db	3911	AAGTTTCTCATGATCATGATAAAAAAATGTGTGGCTTGCCACTAGCAATAAATATTAACAG	3970			
Qy	1148	GAGCTGTGCTTGCACCTAACAGGTGTCAGAAATGGGAGAAATTCATATGAACAACT	1202			
Db	3971	CCAGACATTTTAAAGGCCAGCTCTTGATAGGAATGCAGCAATGGAATCATACAAAAAT	4030			
Qy	1203	-----TCCTTCAGAACTAGAAATAAAACCAAGCCTGGAAGCTTTTGAGGAGAAATGGTGA	1255			
Db	4031	CATTGACTACTTTCCAAATTTGAGAGAAATTCCTACTTTGACGGGATGAGCAAGTACTCA	4090			
Qy	1256	CCCTAGGTTACAACCACTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCT	1315			
Db	4091	ACCTTATTTACAATAATCTTCCTCATTTGTTTGAAGCATGTCTGTTTATACCTTTAGCATCT	4150			
Qy	1316	TTCTGTAGGATTTTGAATAACAAGGAATGCTCTAGTAGTAGATGGATAGCAGAAGGTT	1375			
Db	4151	ACAAAGGAGCTACATAAATTAGGAAGCCCAACTTGGTAGGCCAATGGATGGCTGAAGGTT	4210			
Qy	1376	TTGTTAGACCAAGGTTGGGATGACGACACTAAGGATGTCGAGAGAAAGTTACTTTTAATGAGC	1435			
Db	4211	TCATCAATTCATAGAAAAATAAAGTCATGGAAGAGTTGTCAGGGAACTATTTTGGATGAAC	4270			
Qy	1436	TAATCAACCGAAGTATGATTTCAACCGATCAAGAGTGGGCCACAGCAGGAAAAAATTAAGACTT	1495			
Db	4271	TTGTTGGTAGGGCCCTGGTCCCAACCACTAGATGTTAACTGCCAAAAATAGAGTATTGTCAT	4330			
Qy	1496	GTCCGAATCCATGATATCATCCGTGATATCACAGTTTCCAATCTCGACACAGGAAAAATTT	1553			
Db	4331	GTGTAGTGACCACTAGGTATTAAATTTTCATCAGGTGTAGTCAATAGAGGAGAAATTT	4388			

RESULT 8
US-09-993-170-56
; Sequence 56, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
; APPLICANT: Valant, Barbara
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: B01385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 56
; LENGTH: 5757
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-993-170-56


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Qy 821 TCAAGGAGACAGGTACTTTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATT 880
Db 755 TAAAGAGAAAGAGTACTTAATTTCTTGGATGATATCTGGAGTTGTGAAGTTGGGATG 814
Qy 881 GGATAAATGAAATTTGCTTCTTAAGAACATAAAGAGGGCAGTCGAATAGTAATAACCA 940
Db 815 GCGTGA---GACGATGCTTTCACACTGNAGACATGCGGGAGTCGATATCTGTTGACTA 871
Qy 941 CTCGGAATGTTGATCTAGCGAGAGTGTGCCACAGCCTCACTGGTGTACACCTTGAT 1000
Db 872 CCCGTAATGATGAAGTAGTCTTGTATGCTGTGTAGAGAAATTTTCTTTCGGGATGAGCT 931
Qy 1001 TCTTGCAGATGAACGATGCCATTTTCATTGCTACTGAGAGAAAACAAATAAATAATCATGAG 1060
Db 932 TCATGGATCAAGATGAGAGTTGAGTCTTTTCAAAGTGCAGCATTTTCAAAGTGA----- 986
Qy 1061 ACATGGAATCAAAATAAATAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTGCTC 1120
Db 987 ----AGCATTAACCATATGAGTTCGAGACTGTTGGAAAGCAANTCGCAGATGATGTACG 1042
Qy 1121 GTCTACCATTAGCAATACTTTACAATAGGAGCTGTGCTTGCACACTTAAACAGGTGTAGAAT 1180
Db 1043 GGTACCACCTAATATTGTGCTGTGTCAGGGCTTCTCAAATCTTAAAGGACAATAGAAG 1102
Qy 1181 GGGAGAAATCTATGAACAATCTCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTT 1240
Db 1103 ATTGGAAACTGTTGCTTAAAGATGCAAGTCAATTCGTCACAAAATGATCCTGATGAACGAT 1162
Qy 1241 TGAGGAGAAATGGTGAACCTAGTTTACCAACCACTACCATCCCATCTGAAACCATGCTTTT 1300
Db 1163 GTTCAGTGTCTTGGGTTGAGTTACGATCACTTTGACAAAGCGATCTAAACACATGCTTTC 1222
Qy 1301 TGATCTAAGTATCTTCTCGAGGATTTGAAATACAAAGGAATCGTCTAGTAGGTAGAT 1360
Db 1223 TGCATTTCCGGAATTTTCCAGAACACAGTGTATTCAGTGAAGAAATTTGATGAGATCAT 1282
Qy 1361 GGATAGCAAGAGGTTTGTGA 1381
Db 1283 GGATGGCTGAGGGGTTCTCTGA 1303
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RESULT 11

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US-09-360-186-2
; Sequence 2, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; PRIOR FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
US-09-360-186-2
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Query Match 2.2%; Score 67.4; DB 3; Length 3099;
Best Local Similarity 47.8%; Pred. No. 2.7e-09;
Matches 268; Conservative 0; Mismatches 281; Indels 12; Gaps 2;

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Qy 821 TCAAGGAGACAGGTACTTTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATT 880
Db 847 TAAAGAGAAAGAGTACTTAATTTCTTGGATGATATCTGGAGTTGTGAAGTTGGGATG 906
Qy 881 GGATAAATGAAATTTGCAATTTCTTAAGAACATAAAGAGGGCAGTCGAATAGTAATAACCA 940
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Db 907 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCGGGAGTCGAATATCTGTTGACTA 963
Qy 941 CTCGGAATGTTGATCTAGCGAGAGTGTGCCACAGCCTCACTGGTGTACCACCTTGAT 1000
Db 964 CCCGTAATGATGAAGTAGTCTTGTATGCTGTGTAGAGAAATTTTCTTTCGGGATGAGCT 1023
Qy 1001 TCTTGCAGATGAACGATGCCATTTTCATTGCTACTGAGAGAAAACAAATAAATAATCATGAG 1060
Db 1024 TCATGGATCAAGATGAGAGTTGAGTCTTTTCAAAGTGCAGCATTTTCAAAGTGA----- 1078
Qy 1061 ACATGGAATCAAAATAAATAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTGCTC 1120
Db 1079 ----AGCATTAACCATATGAGTTCGAGACTGTTGGAAAGCAANTCGCAGATGATGTACG 1134
Qy 1121 GTCTACCATTAGCAATACTTTACAATAGGAGCTGTGCTTGCACACTTAAACAGGTGTAGAAT 1180
Db 1135 GGTACCACCTAATATTGTGCTGTGTCAGGGCTTCTCAAATCTTAAAGGACAATAGAAG 1194
Qy 1181 GGGAGAAATCTATGAACAACCTTCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTT 1240
Db 1195 ATTGGAAACTGTTGCTTAAAGATGTCAGTCAATTCGTCACAAAATGATCCTGATGAACGAT 1254
Qy 1241 TGAGGAGAAATGGTGAACCTAGTTTACCAACCACTACCATCCCATCTGAAACCATGCTTTT 1300
Db 1255 GTTCAGCTGTCTTGGGTTGAGTTACGATCACTTTGACAAAGCGATCTAAACACATGCTTTC 1314
Qy 1301 TGATCTAAGTATCTTCTCGAGGATTTGAAATACAAAGGAATCGTCTAGTAGGTAGAT 1360
Db 1315 TGCATTTCCGGAATTTTCCAGAACACAGTGTATTCAGTGAAGAAATTTGATGAGATCAT 1374
Qy 1361 GGATAGCAAGAGGTTTGTGA 1381
Db 1375 GGATGGCTGAGGGGTTCTCTGA 1395
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RESULT 12

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US-09-864-680A-2
; Sequence 2, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B2 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
; OTHER INFORMATION:
US-09-864-680A-2
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Query Match 2.2%; Score 67.4; DB 4; Length 3099;
Best Local Similarity 47.8%; Pred. No. 2.7e-09;
Matches 268; Conservative 0; Mismatches 281; Indels 12; Gaps 2;

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Qy 821 TCAAGGAGACAGGTACTTTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATT 880
Db 847 TAAAGAGAAAGAGTACTTAATTTCTTGGATGATATCTGGAGTTGTGAAGTTGGGATG 906
Qy 881 GGATAAATGAAATTTGCAATTTCTTAAGAACATAAAGAGGGCAGTCGAATAGTAATAACCA 940
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Db 907 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCGAGGGAGTGCAGTAATCTGTTGACTA 963
Qy 941 CTCGGAATGTTGATCTAGCGGAGAGTGTGCCACAGCCTCACTGTGTGTACCACTTGATTT 1000
Db 964 CCGGTAATGATGAAGTAGCTTGTATGCTGTGTGTAGAGAAATTTTCTTTGCGGATGAGCT 1023
Qy 1001 TCTTGACAGATGAACGATGCCATTTTCATTTGCTACTGTGAGAAAAACAATAAATAATCATGAAG 1060
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Qy 1241 TGAGGAGAAATGGTGAACCTAGGTTACAAACCACTACCATCCCATCTGAAACCATGCTTTT 1300
Db 1255 GTTCACGTGTCTTGGGTTGAGTTACGATCACTTGACAAGCGCATCTAAAAACATGTCCTTC 1314
Qy 1301 TGTATCTAAGTATCTTTCCTCAGGATTTTGAATAACAAAGCAATCGTCTAGTAGTAGAT 1360
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RESULT 13

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US-09-360-186-1
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-360-186-1
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Query Match 2.2%; Score 67.4; DB 3; Length 31491;
Best Local Similarity 47.8%; Pred. No. 1.5e-08;
Matches 268; Conservative 0; Mismatches 281; Indels 12; Gaps 2;

Qy 821 TCAAGGAGAGAGGTACTTGTGTTCTAGATGATCTATGGAATTTTACATGATTGGAATT 880
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Qy 881 GGATAATGAATTTGCAATTTCTTAAGAACATAAGAGGGCAGTCGAATAGTAATACCA 940
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Db 2582 ATTGMAAACTGTTTGTCTAAAGATGTCAAGTCTATTCGTCAAAATGATCCTGATGAACGAT 2641
Qy 1241 TGAGGAGAAATGGTGACCTAGGTTTACAACCACTTACCATCCCATCTGAAACCATGCTTTT 1300
Db 2642 GTTCACGTGTCTTGGGTTGAGTTACGATCACTTGACAAGCGATCTAAAAACATGTCCTTC 2701
Qy 1301 TGTATCTAAGTATCTTTCCTCAGGATTTTGAATAACAAAGCAATCGTCTAGTAGTAGAT 1360
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RESULT 14

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US-09-864-680A-1
; Sequence 1, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B2 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-864-680A-1
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Query Match 2.2%; Score 67.4; DB 4; Length 31491;
Best Local Similarity 47.8%; Pred. No. 1.5e-08;
Matches 268; Conservative 0; Mismatches 281; Indels 12; Gaps 2;

Qy 821 TCAAGGAGAGAGGTACTTGTGTTCTAGATGATCTATGGAATTTTACATGATTGGAATT 880
Db 2234 TAAAGAGAAAGAGGTACTTAATTTGTTGGATGATATCTCGAGTTGTGAAGTGGGATG 2293
Qy 881 GGATAATGAATTTGCAATTTCTTAAGAACATAAGAGGGCAGTCGAATAGTAATACCA 940
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Db 2411 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGCATTTTTCAGTGA----- 2465
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Db 2642 GTTCAGTGCTGCTGGTTGAGTTAGCATCACTTGACAAAGGATCTAAACACATGCTTTC 2701
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RESULT 15

US-08-680-327-1
; Sequence 1, Application US/08680327
; Patent No. 5859321
; GENERAL INFORMATION:
; APPLICANT: Staekawicz, Brian S., Oldroyd, Giles Edward,
; APPLICANT: Salmeron, John M., Rommens, Catus
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT
; TITLE OF INVENTION: PATHOGEN RESISTANCE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680.327
; FILING DATE: July 11, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,912
; FILING DATE: September 22, 1994
; CLASSIFICATION: 800
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 5151-45038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5475 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear

US-08-680-327-1
Query Match 1.9%; Score 57.6; DB 2; Length 5475;
Best Local Similarity 45.4%; Pred. No. 4.3e-06;
Matches 207; Conservative 0; Mismatches 249; Indels 0; Gaps 0;
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Qy 1461 ATCAAGAGTGGGCACAGCAGGAAAATTAAGACTTTGAGACTTGTGATCCATGATCATCCGTA 1520
Db 4200 CATGGAGAAGAGACCTAATACCAAGGTGAAAACGTGCCGATTCATGATTTTGTGCAATAA 4259
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Db 4260 ATTCTGCATGGAAGGCGCAACAGAGGATTTTCT 4295

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3099	100.0	3674	18	US-10-656-394A-16
3	2377	96.1	3096	17	US-10-352-179-88
4	2953.2	95.3	99090	18	US-10-656-394A-13
5	2910.2	93.9	3099	18	US-10-656-394A-7
6	2862	92.4	76272	17	US-10-352-179-83
7	2842.2	91.7	3276	17	US-10-352-179-92
8	2501	80.7	4596	18	US-10-437-963-37316
9	2359.8	76.1	2997	18	US-10-656-394A-11
10	1891.6	61.0	2982	18	US-10-437-963-2483
11	1591.8	51.4	3220	17	US-10-352-179-90

12	1571.8	50.7	2940	17	US-10-352-179-84	Sequence 84, Appl
13	1566.6	50.6	2925	18	US-10-437-963-41016	Sequence 41016, A
14	1563	50.4	2982	18	US-10-656-394A-1	Sequence 1, Appl
15	1491.4	48.1	2422	18	US-10-656-394A-15	Sequence 15, Appl
16	1165.8	37.6	3024	18	US-10-437-963-7778	Sequence 7778, Ap
17	1156.2	37.3	2982	17	US-10-352-179-86	Sequence 86, Appl
18	1148	37.0	3492	18	US-10-437-963-49433	Sequence 49433, A
19	1059.2	34.2	2711	18	US-10-437-963-38603	Sequence 38603, A
20	1053.2	34.0	4147	18	US-10-656-394A-5	Sequence 5, Appl
21	949.2	30.6	2265	17	US-10-352-179-96	Sequence 96, Appl
22	854.2	27.6	2351	17	US-10-352-179-97	Sequence 97, Appl
23	555.8	17.9	1355	17	US-10-352-179-94	Sequence 94, Appl
24	541	17.5	2439	18	US-10-437-963-74853	Sequence 74853, A
25	430.8	13.9	2781	18	US-10-437-963-69440	Sequence 69440, A
26	374.6	12.1	1214	18	US-10-656-394A-14	Sequence 14, Appl
27	372.2	12.0	1389	18	US-10-656-394A-9	Sequence 9, Appl
28	215	6.9	569	18	US-10-767-701-21019	Sequence 21019, A
29	197	6.4	4026	18	US-10-437-963-32604	Sequence 32604, A
30	184	5.9	2862	9	US-09-354-453-35	Sequence 35, Appl
31	184	5.9	2862	14	US-10-267-718-35	Sequence 35, Appl
32	183.4	5.9	2931	18	US-10-437-963-70256	Sequence 70256, A
33	177.4	5.7	3012	18	US-10-437-963-78921	Sequence 78921, A
34	177	5.7	2373	18	US-10-437-963-48577	Sequence 48577, A
35	176.8	5.7	2954	9	US-09-354-453-34	Sequence 34, Appl
36	176.8	5.7	2954	14	US-10-267-718-34	Sequence 34, Appl
37	176.8	5.7	6760	9	US-09-354-453-33	Sequence 33, Appl
38	176.8	5.7	6760	14	US-10-267-718-33	Sequence 33, Appl
39	176	5.7	4542	18	US-10-437-963-55316	Sequence 55316, A
40	171	5.5	2883	18	US-10-437-963-75977	Sequence 75977, A
41	167.4	5.4	3165	17	US-10-425-114-31426	Sequence 31426, A
42	167.4	5.4	3430	18	US-10-425-115-34053	Sequence 34053, A
43	166.6	5.4	2886	18	US-10-437-963-51200	Sequence 51200, A
44	164	5.3	2022	18	US-10-437-963-16135	Sequence 16135, A
45	162	5.2	2580	18	US-10-437-963-79337	Sequence 79337, A

ALIGNMENTS

RESULT 1

US-10-656-394A-3

; Sequence 3, Application US/10656394A

; Publication No. US20040210957A1

; GENERAL INFORMATION:

; APPLICANT: Wang et al.

; TITLE OF INVENTION: Cloning and Characterization of the

; FILE OF INVENTION: broad-spectrum resistance gene P12

; FILE REFERENCE: 035719/252052

; CURRENT APPLICATION NUMBER: US/10/656.394A

; CURRENT FILING DATE: 2003-09-05

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 3099

; TYPE: DNA

; ORGANISM: Oryza minuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)....(3099)

US-10-656-394A-3

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Matches 3099;	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;
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DB 1501 ATCCATGATATCATCCGTGATATCACAGTTCCTGAGACAGGAAAAATTTTGTATTA 1560
QY 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAACTCCTGCCACATAGCAATTCAT 1620
DB 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAACTCCTGCCACATAGCAATTCAT 1620
QY 1621 GGGAGTATGTCCTGCAAAAACAGGATTTGGATTTGGAGCAATTTTCGATCATTTAGCTATTTT 1680
DB 1621 GGGAGTATGTCCTGCAAAAACAGGATTTGGATTTGGAGCAATTTTCGATCATTTAGCTATTTT 1680
QY 1681 GGTACAGACCCAAAGAGTCTAGACATGCGATTTGTCCAGATCAATTTGAGGATGTTACGG 1740
DB 1681 GGTACAGACCCAAAGAGTCTAGACATGCGATTTGTCCAGATCAATTTGAGGATGTTACGG 1740
QY 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
DB 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
QY 1801 TTGTTGTCCTTGAATTTAGTATTTGGATTTGGATTTTCGATCATTCATATTTCACTTTCC 1860
DB 1801 TTGTTGTCCTTGAATTTAGTATTTGGATTTGGATTTTCGATCATTCATATTTCACTTTCC 1860
QY 1861 AGATCCATTTGTAATTTACAGGGCTACAGACTTTGAACATGTCAGACACATACATTGCA 1920
DB 1861 AGATCCATTTGTAATTTACAGGGCTACAGACTTTGAACATGTCAGACACATACATTGCA 1920
QY 1921 GCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATCTCTTCGTTGTATTAAGAGAG 1980
DB 1921 GCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATCTCTTCGTTGTATTAAGAGAG 1980
QY 1981 CTTGGAATTTGACAACTTTAGTCTTAATCACCCTAATGAAGTCATTAACACACATATGC 2040
DB 1981 CTTGGAATTTGACAACTTTAGTCTTAATCACCCTAATGAAGTCATTAACACACATATGC 2040
QY 2041 CTGCTAAAGTATTTCACACCTTTAGTTAGTTCGCAATCATTCGTTGTGAAGGATCCCAAGGA 2100
DB 2041 CTGCTAAAGTATTTCACACCTTTAGTTAGTTCGCAATCATTCGTTGTGAAGGATCCCAAGGA 2100
QY 2101 TTTTCACATGGCCACCAAAAGTTTCTGGTCTGGAATCATTCGTTGTGAAGGATCCCAAGGA 2160
DB 2101 TTTTCACATGGCCACCAAAAGTTTCTGGTCTGGAATCATTCGTTGTGAAGGATCCCAAGGA 2160
QY 2161 ATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2220
DB 2161 ATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2220
QY 2221 AGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTTAGCTGTGATTAACAAA 2280
DB 2221 AGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTTAGCTGTGATTAACAAA 2280
QY 2281 GGCTCGCAAAAGGAAAAATGTAAGATCTTTTATGCGCCATTTGAGAGGCTCTCTTCCTC 2340
DB 2281 GGCTCGCAAAAGGAAAAATGTAAGATCTTTTATGCGCCATTTGAGAGGCTCTCTTCCTC

Db 2281 GGCTCGACAAAGGAAAAATGTAAGATACCTTTATGCGCCATTGAGAGCTCTCTCCCTC 2340
Qy 2341 CAATCTCTATATGAATGCTCGGTTATATCAGATATGAAACACATTTGAGTGGCTAGAT 2400
Db 2341 CAATCTCTATATGAATGCTCGGTTATATCAGATATGAAACACATTTGAGTGGCTAGAT 2400
Qy 2401 TCTATTTTCATCTCTCCCTCCCTACTGAGGACACTCGGTTGAAATGGAAGTCTTGAAGAG 2460
Db 2401 TCTATTTTCATCTCTCCCTCCCTACTGAGGACACTCGGTTGAAATGGAAGTCTTGAAGAG 2460
Qy 2461 ATGCTTAATCTGATGAGCAGCTCACTCACTGAGGAAGTTCAACTATGAGTAGTAAA 2520
Db 2461 ATGCTTAATCTGATGAGCAGCTCACTCACTGAGGAAGTTCAACTATGAGTAGTAAA 2520
Qy 2521 CTAAGGAAGTAAAAACATGCTGATCTTGGGCACTGGGCACTGCCCACTCATGTTCTTCT 2580
Db 2521 CTAAGGAAGTAAAAACATGCTGATCTTGGGCACTGGGCACTGCCCACTCATGTTCTTCT 2580
Qy 2581 CTTTATCATATCTTATCTTGGGAGAGCTAGTATTCAAAACGGGAGCATTTCCCAAT 2640
Db 2581 CTTTATCATATCTTATCTTGGGAGAGCTAGTATTCAAAACGGGAGCATTTCCCAAT 2640
Qy 2641 CTTAGAACACTTGTGATTTTCAATTTGATCAGCTTAAGAGAGATCAGATTTGAGGCGG 2700
Db 2641 CTTAGAACACTTGTGATTTTCAATTTGATCAGCTTAAGAGAGATCAGATTTGAGGCGG 2700
Qy 2701 AGCTCACCCAGTTGGAAAGATAGAAATCTTTGCTGACGTTTGGAAATCAGGATTAT 2760
Db 2701 AGCTCACCCAGTTGGAAAGATAGAAATCTTTGCTGACGTTTGGAAATCAGGATTAT 2760
Qy 2761 GGTATCATCTCCTCAAGGCTCAAGGAGATTTTCACTTGAATACAAAGTAAAGTGGCT 2820
Db 2761 GGTATCATCTCCTCAAGGCTCAAGGAGATTTTCACTTGAATACAAAGTAAAGTGGCT 2820
Qy 2821 AGCTTGTGCTGAGTGAAGGAGAGTGAACACACACCCCAATCGCCCGTCTGCGAATG 2880
Db 2821 AGCTTGTGCTGAGTGAAGGAGAGTGAACACACACCCCAATCGCCCGTCTGCGAATG 2880
Qy 2881 GACAGTGACCGAAGGATCAGACCTGGGGCTGAAGCCGAGGATCTTATAGAAGTG 2940
Db 2881 GACAGTGACCGAAGGATCAGACCTGGGGCTGAAGCCGAGGATCTTATAGAAGTG 2940
Qy 2941 CAACAGCAGATCTGTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAACG 3000
Db 2941 CAACAGCAGATCTGTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAACG 3000
Qy 3001 GATCCCTTCCGAGCAGGAGAGAGTCCGAGTCCGAGTGAATCAGCTTGCAGCAG 3060
Db 3001 GATCCCTTCCGAGCAGGAGAGAGTCCGAGTCCGAGTGAATCAGCTTGCAGCAG 3060
Qy 3061 AATGATAGCAGAGATAGGACACAGCTCAAGCTGGCTGA 3099
Db 3061 AATGATAGCAGAGATAGGACACAGCTCAAGCTGGCTGA 3099

RESULT 2

US-10-656-394A-16
; Sequence 16, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; TITLE OF INVENTION: Broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 3674
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-656-394A-16

Query Match 100.0%; Score 3099; DB 18; Length 3674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCGGAGAGCGGTGAGCATCGGAGGTGCGTGGTGGCAGTGCCTCAGCAAGGCC 60
Db 9 ATGCGGAGAGCGGTGAGCATCGGAGGTGCGTGGTGGCAGTGCCTCAGCAAGGCC 68
Qy 61 GCCTCTCGCGTCCCAATGAGACGAGCTCTCTGCTCGGCGTCGAGAGGACATCTGGTAT 120
Db 69 GCCTCTCGCGTCCCAATGAGACGAGCTCTCTGCTCGGCGTCGAGAGGACATCTGGTAT 128
Qy 121 ATCAAGATGAGCTTAAAAAATGAGGAGTCTCTTAGAGTCTGCTGAAAGTTATGAAAAAG 180
Db 129 ATCAAGATGAGCTTAAAAAATGAGGAGTCTCTTAGAGTCTGCTGAAAGTTATGAAAAAG 188
Qy 181 AAAGATGAATCTTAAAGTTTGGGAGAGCAATACGTGACCTGCTGTATGACATGAA 240
Db 189 AAAGATGAATCTTAAAGTTTGGGAGAGCAATACGTGACCTGCTGTATGACATGAA 248
Qy 241 GATTCCCTTGATGAATTTAAAGTCCATATTTGAAAGCCAAACCTATTTCTGCTGGTGTG 300
Db 249 GATTCCCTTGATGAATTTAAAGTCCATATTTGAAAGCCAAACCTATTTCTGCTGGTGTG 308
Qy 301 AAATCTAGAGAGCGCCACCGGATCGCTATCCGTATCCAACTCAATCAAGAGTTGAA 360
Db 309 AAATCTAGAGAGCGCCACCGGATCGCTATCCGTATCCAACTCAATCAAGAGTTGAA 368
Qy 361 GAAGTGAAGTACGAGACACACGCTACAAATTTAGTCCGAGCTATTTCTCGGACACAG 420
Db 369 GAAGTGAAGTACGAGACACACGCTACAAATTTAGTCCGAGCTATTTCTCGGACACAG 428
Qy 421 GATCAGATGGAATCTTATGAGAGAGACATTCGCAATCAATCAGCTCGAAATGTGATGAA 480
Db 429 GATCAGATGGAATCTTATGAGAGAGACATTCGCAATCAATCAGCTCGAAATGTGATGAA 488
Qy 481 GCTGAGCTTGTGGTGTCTGACTTCCAAAGAAAGGCTGCTTGAATGATGATACCAAT 540
Db 489 GCTGAGCTTGTGGTGTCTGACTTCCAAAGAAAGGCTGCTTGAATGATGATACCAAT 548
Qy 541 GCTAATGATGTCGCGGCAAGGTAATCTGTGTTCTGGGATGGGTGTTTAGGCAAGACA 600
Db 549 GCTAATGATGTCGCGGCAAGGTAATCTGTGTTCTGGGATGGGTGTTTAGGCAAGACA 608
Qy 601 GCTCTTTGAGGAGAGATCTTTGAAAGGAGAGACATTTAGGAGAACTTCCCTTGCAT 660
Db 609 GCTCTTTGAGGAGAGATCTTTGAAAGGAGAGACATTTAGGAGAACTTCCCTTGCAT 668
Qy 661 GCTTGGATTACAGTGTCAATCAATTTCAAGGATGAGCTCTTAAAGATATGATAGCG 720
Db 669 GCTTGGATTACAGTGTCAATCAATTTCAAGGATGAGCTCTTAAAGATATGATAGCG 728
Qy 721 CAACTTCTTGGTCCAGTCTCTCGATCAACTCTTGCATGAATTTGCAAGGAGAGTGGTG 780
Db 729 CAACTTCTTGGTCCAGTCTCTCGATCAACTCTTGCATGAATTTGCAAGGAGAGTGGTG 788
Qy 781 GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTACTTT 840
Db 789 GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTACTTT 848
Qy 841 GTTGTCTTAGATGATCTATGGAATTTATCATGTTGGAATTTGGATATAAATGCAATTT 900
Db 849 GTTGTCTTAGATGATCTATGGAATTTATCATGTTGGAATTTGGATATAAATGCAATTT 908
Qy 901 CTTAAGAACATTAAGAGGCGAGTCGAATAGTATTAACCACTCGGAATGTTGATCTAGCG 960
Db 909 CTTAAGAACATTAAGAGGCGAGTCGAATAGTATTAACCACTCGGAATGTTGATCTAGCG 968
Qy 961 GAGAAAGTGCACAGCCTCACTGCTGTACCACTTGAATTTCTTTCGAGATGAACGATGCC 1020
Db 969 GAGAAAGTGCACAGCCTCACTGCTGTACCACTTGAATTTCTTTCGAGATGAACGATGCC 1028

Qy	1021	ATTTCAATGCTACTGAGAAAACAAATTAATAATCATGAGACATGGAAATCAATATAAAAT	1081
Db	1029	ATTTCAATGCTACTGAGAAAACAAATTAATAATCATGAGACATGGAAATCAATATAAAAT	1088
Qy	1081	ATGCAAAAGATGGTTGAGCAAGAAATGTTAAATAAAATGTGGTGGTCTACCATTAGCAATACTT	1140
Db	1089	ATGCAAAAGATGGTTGAGCAAGAAATGTTAAATAAAATGTGGTGGTCTACCATTAGCAATACTT	1148
Qy	1141	ACAATAGGAGCTGTGCTTTGCAACTTAAACACAGGTGTGAGAAATGGGAGAAATTTCTATGAACAA	1200
Db	1149	ACAATAGGAGCTGTGCTTTGCAACTTAAACACAGGTGTGAGAAATGGGAGAAATTTCTATGAACAA	1208
Qy	1201	CTTCCCTTCAGAACTAGAAAAATAAACCCAAAGCTGGAAAGCTTTTGAGAGAAATGGTGACCCCTA	1260
Db	1209	CTTCCCTTCAGAACTAGAAAAATAAACCCAAAGCTGGAAAGCTTTTGAGAGAAATGGTGACCCCTA	1268
Qy	1261	GGTTACAACACCTTACCATCCCATCTCGAAACCAATGCTTTTGTATCTTAAGTATCTTTTCCT	1320
Db	1269	GGTTACAACACCTTACCATCCCATCTCGAAACCAATGCTTTTGTATCTTAAGTATCTTTTCCT	1328
Qy	1321	GAGGATTTTGAAATACAAAGGAATCTGTCTAGTAGGTAGATGGATAGCAGAGAAAGGTTTGT	1380
Db	1329	GAGGATTTTGAAATACAAAGGAATCTGTCTAGTAGGTAGATGGATAGCAGAGAAAGGTTTGT	1388
Qy	1381	AGACCAAGGTTGGGATGACGACTPAAGGATGTGCGAGAAAGTTACTTTAATGAGCTTAATC	1440
Db	1389	AGACCAAGGTTGGGATGACGACTPAAGGATGTGCGAGAAAGTTACTTTAATGAGCTTAATC	1448
Qy	1441	AACCGAAGTATGATTCAACGATCAAGAGTGGGCACAGCAGCAAGAAATTTAAGACTTGTGCA	1500
Db	1449	AACCGAAGTATGATTCAACGATCAAGAGTGGGCACAGCAGCAAGAAATTTAAGACTTGTGCA	1508
Qy	1501	ATCCATCATATCATCCGTGATATCACAGTTTTCAATCTCGAGACAGGAGAAATTTTGTAATTA	1560
Db	1509	ATCCATCATATCATCCGTGATATCACAGTTTTCAATCTCGAGACAGGAGAAATTTTGTAATTA	1568
Qy	1561	TTACCAATGGGAGATGGCTCTGATTTTAGTTTTCAGAAACACTCGCCACATAGCAATTCAT	1620
Db	1569	TTACCAATGGGAGATGGCTCTGATTTTAGTTTTCAGAAACACTCGCCACATAGCAATTCAT	1628
Qy	1621	GGGAGTATGCTTGCAAAAACAGGATTTGGATTTGGAGCATTAATTCATTAATTTAGCTATTTTT	1680
Db	1629	GGGAGTATGCTTGCAAAAACAGGATTTGGATTTGGAGCATTAATTCATTAATTTAGCTATTTTT	1688
Qy	1681	GGTGACAGACCCAAAGGCTTAGCACATGTCAGTTTGTCCAGATCAATTTGAGGATGTTTACGG	1740
Db	1689	GGTGACAGACCCAAAGGCTTAGCACATGTCAGTTTGTCCAGATCAATTTGAGGATGTTTACGG	1748
Qy	1741	GTCTTGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATTGCA	1800
Db	1749	GTCTTGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATTGCA	1808
Qy	1801	TTGTTGTGCCACTTGAAATACTTGAGPATTTGGATATTCGTCATCCATATTAATCACTTCCC	1860
Db	1809	TTGTTGTGCCACTTGAAATACTTGAGPATTTGGATATTCGTCATCCATATTAATCACTTCCC	1868
Qy	1861	AGATCCATTTGGTAAACTACAGGGCCTACAGCTTTGNAACATGTCAAGCACATACATTGCA	1920
Db	1869	AGATCCATTTGGTAAACTACAGGGCCTACAGCTTTGNAACATGTCAAGCACATACATTGCA	1928
Qy	1921	GCACTCAACAGTGAAGTACAGTAAACTCCAATGTCTGCATACTCTTGGTTGTAAGAGAG	1980
Db	1929	GCACTCAACAGTGAAGTACAGTAAACTCCAATGTCTGCATACTCTTGGTTGTAAGAGAG	1988
Qy	1981	CTTGAAATTTGACAACTTTAGTCTTAAATCACCCAAATGAAGTGCATAACTAACCAATATGC	2040
Db	1989	CTTGAAATTTGACAACTTTAGTCTTAAATCACCCAAATGAAGTGCATAACTAACCAATATGC	2048
Qy	2041	CTGCCTAAAGTATTCACACCTTTAGTTAGTCGGGATTAATCGTGCAGAAACAAATTTGCTGAA	2100
Db	2049	CTGCCTAAAGTATTCACACCTTTAGTTAGTCGGGATTAATCGTGCAGAAACAAATTTGCTGAA	2108
Qy	2101	TTTCACTAGTCCCAACAAAGTTTCTGGTCTGAAATCAATTCGGTGTGAAGGTACCCAAAGGA	2160

[illegible]

RESULT 3
US-10-352-179-88
; Sequence 88, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:

APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Plants
FILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
SEQ ID NO 88
LENGTH: 3096
TYPE: DNA
ORGANISM: Oryza minuta
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3096)
OTHER INFORMATION:
US-10-352-179-88

Query Match			
Best Local Similarity 96.1%; Score 2977; DB 17; Length 3096;			
Matches 3013; Conservative 0; Mismatches 60; Indels 0; Gaps 0;			
Qy	1	ATGGCGGAGACGGTCTGAGCATGGCGAGGTGCGTGGTGGCGAGTGCCTCAGCAAGGCC	60
Db	1	ATGGCGGAGACGGTCTGAGCATGGCGAGGTGCGTGGTGGCGAGTGCCTCAGCAAGGCC	60
Qy	61	GCCTCTGCGGTGCCAATGAGACGAGCCTCTGCTCGGCGTGGAGGACATCTGGTAT	120
Db	61	GCCTCTGCGGTGCCAATGAGACGAGCCTCTGCTCGGCGTGGAGGACATCTGGTAT	120
Qy	121	ATCAAGATGAGCTAAACCAATGAGGAGTCTCTTAGAGTGTGCTGGAAGTTATGAAAAAG	180
Db	121	ATCAAGATGAGCTAAACCAATGAGGAGTCTCTTAGAGTGTGCTGGAAGTTATGAAAAAG	180
Qy	181	AAAGATGAATCTTAAAGGTTGGGACAGCAATACGTGACCTGTCTGTATGACATTGAA	240
Db	181	AAAGATGAATCTTAAAGGTTGGGACAGCAATACGTGACCTGTCTGTATGACATTGAA	240
Qy	241	GATTCCTTGTGATGAAATTTAAAGTCCATATGAAAGCCAAACCTATTTTCGTGAGTGGTG	300
Db	241	GATTCCTTGTGATGAAATTTAAAGTCCATATGAAAGCCAAACCTATTTTCGTGAGTGGTG	300
Qy	301	AAACTTAGAGAGCGCACCGGATCGCTATCGGTATCCAAACCTCAAGAGTTGAA	360
Db	301	AAACTTAGAGAGCGCACCGGATCGCTATCGGTATCCAAACCTCAAGAGTTGAA	360
Qy	361	GAAGTAGTAGCAGGAAACACCGCTACAAATTTAGTCGAGCCTATTTCTCCGGCACAGAG	420
Db	361	GAAGTAGTAGCAGGAAACACCGCTACAAATTTAGTCGAGCCTATTTCTCCGGCACAGAG	420
Qy	421	GATGACATGATCTCTATGACAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAA	480
Db	421	GATGACATGATCTCTATGACAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAA	480
Qy	481	GCTGAGCTTGTGGTCTTCTGACTCCAAAGAAAGGCTGTGAAATGATCGATACCAAT	540
Db	481	GCTGAGCTTGTGGTCTTCTGACTCCAAAGAAAGGCTGTGAAATGATCGATACCAAT	540
Qy	541	GCTAATGATGTGCGGCCAAAGTAACTGTGTGTGGATGGTGGTATAGGCAAGACA	600
Db	541	GCTAATGATGTGCGGCCAAAGTAACTGTGTGTGGATGGTGGTATAGGCAAGACA	600
Qy	601	GCTCTTTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAGAACTTCCCTTGCAT	660
Db	601	GCTCTTTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAGAACTTCCCTTGCAT	660
Qy	661	GCTTGGATTTACAGTGTCAAAATCTTTTCAAGGATTTAGTACTTTAAAGATATGATCGC	720
Db	661	GCTTGGATTTACAGTGTCAAAATCTTTTCAAGGATTTAGTACTTTAAAGATATGATCGC	720
Qy	721	CAACTTCTTGGTCCAGTTCTCTGATCAACTCTTGGATGAATTTGCAAGGAGGTGGTG	780

Db	721	CAACTTCTTGGTCCAGTTCTCTGATCAACTCTTTCGAAGATTTGCAAGGAGGTGGTG	780
Qy	781	GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGGTACTTTT	840
Db	781	GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGGTACTTTT	840
Qy	841	GTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATAAATGAAATTTG	900
Db	841	GTTATTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATAAATGAAATTTG	900
Qy	901	CCTAAGAACATTAAGAGGCGAGTGAATTAACCATTAACCATCGGAATTTGATCTAGCG	960
Db	901	CCTAAGAACATTAAGAGGCGAGTGAATTAACCATTAACCATCGGAATTTGATCTAGCG	960
Qy	961	GAGAAAGTGTGCCACAGCCTCACTGCTGTACCACTTGAATTTCTTGCAGATGAACGATGCC	1020
Db	961	GAGAAAGTGTGCCACAGCCTCACTGCTGTACCACTTGAATTTCTTGCAGATGAACGATGCC	1020
Qy	1021	ATTTTCATTTCTGAGAAAAACAAATTAATAATCATGAAGACATGGAATCAAAATAAAT	1080
Db	1021	ATAACATTTGCTACTGAGAAAAACAAATTAATAATCATGAAGACATGGAATCAAAATAAAT	1080
Qy	1081	ATGCAAAAGATGTTGAACGAAATTTGTAATAAATGTTGGTCTGCTACCAATTAGCAATCTT	1140
Db	1081	ATGCAAAAGATGTTGAACGAAATTTGTAATAAATGTTGGTCTGCTACCAATTAGCAATCTT	1140
Qy	1141	ACAATAGAGCTGTGCTTTGCAACTTAAACAGAGTGTGAGAAATGGGAGAAATTTCTATGAACAA	1200
Db	1141	ACAATAGAGCTGTGCTTTGCAACTTAAACAGAGTGTGAGAAATGGGAGAAATTTCTATGAACAA	1200
Qy	1201	CTTCTCTTTCAGAACTAGAAATTAACCCAGCTCGAAAGCTTTGAGGAGAAATGGTGACCTTA	1260
Db	1201	CTTCTCTTTCAGAACTAGAAATTAACCCAGCTCGAAAGCTTTGAGGAGAAATGGTGACCTTA	1260
Qy	1261	GGTTTCAACCCCTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCT	1320
Db	1261	GGTTTCAACCCCTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCT	1320
Qy	1321	GAGGATTTTGAATTAACAAAGGAAATCGTCTAGTAGTAGATGAGTACGAGAAAGGTTTCTGT	1380
Db	1321	GAGGATTTTGAATTAACAAAGGAAATCGTCTAGTAGTAGATGAGTACGAGAAAGGTTTCTGT	1380
Qy	1381	AGACCAAGGTGGGATGACGACTTAAGGATGTCGAGAGAAAGTTACTTTAAATGAGCTAATC	1440
Db	1381	AGACCAAGGTGGGATGACGACTTAAGGATGTCGAGAGAAAGTTACTTTAAATGAGCTAATC	1440
Qy	1441	AACCGAAGTATGATTCACGATCAAGAGTGGGCAAGCAGGAGAAATTTAAGACTTGTGCA	1500
Db	1441	AACCGAAGTATGATTCACGATCAAGAGTGGGCAAGCAGGAGAAATTTAAGACTTGTGCA	1500
Qy	1501	ATCCATGATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTA	1560
Db	1501	ATCCATGATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTA	1560
Qy	1561	TTACCAATGGGAGATGGCTCTGATTTAGTTTTCAGGAAAAACACTCGCCACATAGCATTCAT	1620
Db	1561	TTACCAATGGGAGATGGCTCTGATTTAGTTTTCAGGAAAAACACTCGCCACATAGCATTCAT	1620
Qy	1621	GGGAGTATGCTGCAAAAAAGGATTTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTT	1680
Db	1621	GGGAGTATGCTGCAAAAAAGGATTTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTT	1680
Qy	1681	GGTGACAGACCCAGAGCTTAGCACATGTCAGTTTGTCCAGATCAATTTGAGGATTTTACGG	1740
Db	1681	GGTGACAGACCCAGAGCTTAGCACATGTCAGTTTGTCTAGATCAATTTGAGGATTTTACGG	1740
Qy	1741	GTCTTTGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAAGATTTTCGACCGTATTGCA	1800
Db	1741	GTCTTTGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAAGATTTTCGACCGTATTGCA	1800
Qy	1801	TTGTTGTGCCACTTGAATAATCTTGAATTTGGATTTGCTGATCATATTTCAATTTCTTCCC	1860
Db	1801	TTGTTGTGCCACTTGAATAATCTTGAATTTGGATTTGCTGATCATATTTCAATTTCTTCCC	1860

Db 1801 TTGTTGTGCCACTTGAATACTTGAGTATTTGGATATTCGTCAATCATATATTTCACTTCCC 1860
Qy 1861 AGATCCATTGGTAAACTACAGGGCTCAGAGCTTTGAAACATGTCAAGCACATACATTGCA 1920
Db 1861 AGATCCATTGGTAAACTACAGGGCTCAGAGCTTTGAAACATGTCAAGCACATACATTGCA 1920
Qy 1921 GCATPACCAAGTGAGATCAGTAAACTCCAAATGTTCTGCAATCTCTTCGTTGTTATAGAGAG 1980
Db 1921 GCATPACCAAGTGAGATCAGTAAACTCCAAATGTTCTGCAATCTCTTCGTTGTTAGTAAAG 1980
Qy 1981 CTTGAAATTTGACAACTTTAGTCTAAATCACCACCAATGAAGTGCATAACTAACACATATGC 2040
Db 1981 TTTGTTTATGACAACTTTAGTCTAAACACCAATGAAGTGCATAACTAACACATATATGC 2040
Qy 2041 CTGCTAAAGTATTCACACCTTTAGTCTGCGATATCTGCAAAATCTGCAAAACAAATTTGCTGAA 2100
Db 2041 CTGCTAAAGTATTCACACCTTTAGTCTGCGATATCTGCAAAATCTGCAAAACAAATTTGCTGAA 2100
Qy 2101 TTTCCATGCGCCACCAAAAGTTTCTGCTCTGAATCAITTCGGTGTGAAGGTACCCCAAGGA 2160
Db 2101 TTGCACATGGCCACCAAAAGTTTCTGCTCTGAATCAITTCGGTGTGAAGGTACCCCAAGGA 2160
Qy 2161 ATAGTAAAGTTGCGAGCTTACAGTCTACAGTATGTAGATATCAGCGGACACAGTAGT 2220
Db 2161 ATAGTAAAGTTGCGAGCTTACAGGTTCTAGAGTATGTAGATATCAGCGGACACAGTAGT 2220
Qy 2221 AGAGCAATCAAGAGCTGCGGACGTTAAGCAAGTTTGAGGAAATTAGCTGTGATACAAAA 2280
Db 2221 AGAGCAATCAAGAGCTGCGGACGTTAAGCAAGTTTGAGGAAATTAGCTGTGATACAAAA 2280
Qy 2281 GGCTCGCAAAAGGAAATGTAAGATACCTTATGCGAGCCATTGAGAACTCTCTTCCCTC 2340
Db 2281 GGCTCGCAAAAGGAAATGTAAGATACCTTATGCGAGCCATTGAGAACTCTCTTCCCTC 2340
Qy 2341 CAATCTCTATATGAATGCTGCGTTATATTCAGATATGTAAACATCTGAGTGCCTAGAT 2400
Db 2341 CAATCTCTATGTAATGCTGCGTTATATTCAGATATGTAAACATCTGAGTGCCTAGAT 2400
Qy 2401 TCTATTTTCATCTCTCTCCCTCTAGTGGGACACTCGGTTTGAATGGAAGTCTTTGAAGAG 2460
Db 2401 TCTATTTTCATCTCTCTCCCTCTAGTGGGACACTCGGTTTGAATGGAAGTCTTTGAAGAG 2460
Qy 2461 ATGCTTAACCTGGATGAGCAGCTCACTCACCTGAGAAAGTTCAACTTATGAGGATGATAA 2520
Db 2461 ATGCTTAACCTGGATGAGCAGCTCACTCACCTGAGAAAGTCTACTTATTTAGGAGCAAA 2520
Qy 2521 CTAAGGAGGATAAACATGCTGATCTACTTGGGGCATGCGCCCACTCATGTTCTTCT 2580
Db 2521 CTAAGGAGGATAAACATGCTGATCTACTTGGGGCATTTGCCCACTCATGTTCTTCT 2580
Qy 2581 CTTTATCATATTTCTTATCTTGGGGAGAGCTAGTATTTCAAAACGGGAGCATTTCCCAAT 2640
Db 2581 CTTTATTTGGAATGCTTACCTTTGGGGAGAGCTAGTATTTCAAAACGGGAGCATTTCCCAAT 2640
Qy 2641 CTTAGAACACCTTCGTATTTACGAATTTGGATCAGCTAAGAGAGATGAGATTTGAGATGSC 2700
Db 2641 CTTAGAACACCTTCGTATTTACGAATTTGGATCAGCTAAGAGAGATGAGATTTGAGATGSC 2700
Qy 2701 AGCTCACCCAGTTGGAAGATAGAAATCTCTTCTGCGAGGTTGGAATCAGGATATTT 2760
Db 2701 AGCTCACCCCTGTTGGAAGATAGAAATCTCTTCTGCGAGGTTGGAATCAGGATATTT 2760
Qy 2761 GGTATATTCACCTTCCAAAGCTCAAGGAGATTTTCACTTTGAATACAAAGTAAAGTGCCT 2820
Db 2761 GGTATATTCACCTTCCAAAGCTCAAGGAGATTTTCACTTTGAATACAAAGTAAAGTGCCT 2820
Qy 2821 AGGCTTGGTCAAGCTGGAAGGAGAGTGAACACACCCCAATCGCCCGTCTCGGAATG 2880
Db 2821 AGGCTTGGTCAAGCTGGAAGGAGAGTGAACACACCCCAATCGCCCGTCTCGGAATG 2880
Qy 2881 GACAGTGAACGAGGATACGACCTGCGGGGCTGAAGCCGAGGATCTTCTATAGAAAGTG 2940
Db 2881 GACAGTGAACGAGGATACGACCTGCGGGGCTGAAGCCGAGGATCTTCTATAGAAAGTG 2940

Qy 2941 CAAACAGCAGATCCTGTTCTGTATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAACG 3000
Db 2941 CAAACAGCAGATCCTGTTCTGTATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAACG 3000
Qy 3001 GATCCCCCTTCCGAGCAGGAGGAGAGAGAGTCCGAGTCCGAGGTGATCACGTTGACGACG 3060
Db 3001 GATCCCCCTTCCGAGCAGGAGGAGAGAGAGTCCGAGTCCGAGGTGATCACGTTGACGACG 3060
Qy 3061 AATGATAGCGAAG 3073
Db 3061 AACGATAGGTCAG 3073

RESULT 4

US-10-656-394A-13
; Sequence 13, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 99090
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 23216
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-13

Query Match 95.3%; Score 2953.2; DB 18; Length 99090;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2955; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 116 GGTATATCAAGATGAGCTAAACCAATGAGGCAATTCCTTAGAGCTGCTGAAGTTATGA 175
Db 51390 GGTATATCAAGATGAGCTAAACCAATGAGGCAATTCCTTAGAGCTGCTGAAGTTATGA 51449
Qy 176 AAAGAAAGATGAACTATTAAAGGTTTGGCAGAGCAAAATACGTGCTCGTATGACA 235
Db 51450 AAAGAAAGATGAACTATTAAAGGTTTGGCAGAGCAAAATACGTGCTCGTATGACA 51509
Qy 236 TTGAAGATTCCCTTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCTATTTCGTGAGT 295
Db 51510 TTGAAGATTCCCTTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCTATTTCGTGAGT 51569
Qy 296 TGGTGAAGCTTAGAGAGCGCCACCGGATCGCTATCCGATATCCCAACCTCAAAATCAAGAG 355
Db 51570 TGGTGAAGCTTAGAGAGCGCCACCGGATCGCTATCCGATATCCCAACCTCAAAATCAAGAG 51629
Qy 356 TTGAAGAAAGTGAAGTGAAGGAAACACAGCTACATTTAGTTCGAGCCTATTTCCTCCCGCA 415
Db 51630 TTGAAGAAAGTGAAGTGAAGGAAACACAGCTACATTTAGTTCGAGCCTATTTCCTCCCGCA 51689
Qy 416 CAGAGGATGATCGATGATTCCTATGTCAGAGACATTCGCAATCAATCAAGCTCGAAATGCG 475
Db 51690 CAGAGGATGATCGATGATTCCTATGTCAGAGACATTCGCAATCAATCAAGCTCGAAATGCG 51749
Qy 476 ATGAAGCTGAGCTGTTGGGTTTCTGACTCCAGAAAAGGCTGCTTTGAAATGATCGATA 535
Db 51750 ATGAAGCTGAGCTGTTGGGTTTCTGACTCCAGAAAAGGCTGCTTTGAAATGATCGATA 51809
Qy 536 CCAATGCTAATGATGCTCCCGCCCAAGGTAATCTGTGTTGGATGGGTGGTTTAGCA 595
Db 51810 CCAATGCTAATGATGCTCCCGCCCAAGGTAATCTGTGTTGGATGGGTGGTTTAGCA 51869

Qy	596	AGACAGCTCTTTTCGAGGAAGA	TCTTTGAAAGCGAAGAAGACA	TAATAGGAAGAACTTCCCTT	655
Dd	51870	AGACAGCTCTTTTCGAGGAAGA	TCTTTGAAAGCGAAGAAGACA	TAATAGGAAGAACTTCCCTT	51929
Qy	656	GCAATGCTTGGAATTCAGGTG	TCAAGTGCATAATCTTTCACAG	GATTACAGCTTACTTTAAAGATATGA	715
Dd	51930	GCAATGCTTGGAATTCAGGTG	TCAAGTGCATAATCTTTCACAG	GATTACAGCTTACTTTAAAGATATGA	51989
Qy	716	TAGGCCAACCTTCTTGCTCCAG	TTCTCTGGATCAACTCTTTGCA	TGTAATTTGCAAGGGAAGG	775
Dd	51990	TAGGCCAACCTTCTTGCTCCAG	TTCTCTGGATCAACTCTTTGCA	TGTAATTTGCAAGGGAAGG	52049
Qy	776	TGTTGGTGCAAGTACATCATCT	TTTCTGAGTACTGATAGAGAGC	TCAAGAGGAAGAGGT	835
Dd	52050	TGTTGGTGCAAGTACATCATCT	TTTCTGAGTACTGATAGAGAGC	TCAAGAGGAAGAGGT	52109
Qy	836	ACTTTGTGTCTTAGATGATCAT	TGATGATTTTACATGATTTGGA	ATTTGGAATTTGGAATTTG	895
Dd	52110	ACTTTGTGTCTTAGATGATCAT	TGATGATTTTACATGATTTGGA	ATTTGGAATTTGGAATTTG	52169
Qy	896	CATTTCTTAAGAACAAATAGA	AGGGCAGTCGAATAGTAATA	ACCRACTCGGAATGTTGATC	955
Dd	52170	CATTTCTTAAGAACAAATAGA	AGGGCAGTCGAATAGTAATA	ACCRACTCGGAATGTTGATC	52229
Qy	956	TAGGGAGAAGTGTGCCACAGC	CTCACTGGGTGATCCACTTG	TAATTTCTTGACAGATGAACG	1015
Dd	52230	TAGGGAGAAGTGTGCCACAGC	CTCACTGGGTGATCCACTTG	TAATTTCTTGACAGATGAACG	52289
Qy	1016	ATGCCATTTTCATCTTACTG	AGNAAAACAATAAAAAATCAT	GAACACATCGNAATCAANA	1075
Dd	52290	ATGCCATTTTCATCTTACTG	AGNAAAACAATAAAAAATCAT	GAACACATCGNAATCAANA	52349
Qy	1076	AAAAATATGCAAAAAGATGG	TTGAACGAATTTGTAATAAT	TGCTCGTCTACCATTAGCAA	1135
Dd	52350	AAAAATATGCAAAAAGATGG	TTGAACGAATTTGTAATAAT	TGCTCGTCTACCATTAGCAA	52409
Qy	1136	TACTTAACAATPAGAGCTGTG	CTTGCAACTTAAACAGGTGT	CAGAAATGGGAGAAATCTATG	1195
Dd	52410	TACTTAACAATPAGAGCTGTG	CTTGCAACTTAAACAGGTGT	CAGAAATGGGAGAAATCTATG	52469
Qy	1196	AACAACTTCTTCAGAACTTA	GAATATAACCAAGCCTGGA	AGCTTTGAGGAGNAATGGTGA	1255
Dd	52470	AACAACTTCTTCAGAACTTA	GAATATAACCAAGCCTGGA	AGCTTTGAGGAGNAATGGTGA	52529
Qy	1256	CCCTAGGTTACAAACCACTT	ACCATCCATCTGAAACCA	TGCTTTTTTGTATCTTAAGTATCT	1315
Dd	52530	CCCTAGGTTACAAACCACTT	ACCATCCATCTGAAACCA	TGCTTTTTTGTATCTTAAGTATCT	52589
Qy	1316	TTCTCTGAGGATTTTGAATA	CAAAAGGAATCGTCTAGT	AGGTAGATGGATAGCAGAGGGT	1375
Dd	52590	TTCTCTGAGGATTTTGAATA	CAAAAGGAATCGTCTAGT	AGGTAGATGGATAGCAGAGGGT	52649
Qy	1376	TTGTTAGACCAAGGTTGGAT	GCACACTAAGATGTCGGA	AGAAAGTTACTTTAATGAGC	1435
Dd	52650	TTGTTAGACCAAGGTTGGAT	GCACACTAAGATGTCGGA	AGAAAGTTACTTTAATGAGC	52709
Qy	1436	TAATCAACCGAAGTATGATT	TTCAACGATCAAGAGTGG	GCACACAGCAAAAAATTAAGACTT	1495
Dd	52710	TAATCAACCGAAGTATGATT	TTCAACGATCAAGAGTGG	GCACACAGCAAAAAATTAAGACTT	52769
Qy	1496	GTCCAAATCCAATGATATCAT	CCGTGATATCACAGTTTCA	ATCTCGAGACAGGAAAAATTTTG	1555
Dd	52770	GTCCAAATCCAATGATATCAT	CCGTGATATCACAGTTTCA	ATCTCGAGACAGGAAAAATTTTG	52829
Qy	1556	TATTAATTACCAATGGGAG	ATGGCTGTGATTTAGTTT	CAGGAAAAACA CTGCCACATAGCAT	1615
Dd	52830	TATTAATTACCAATGGGAG	ATGGCTGTGATTTAGTTT	CAGGAAAAACA CTGCCACATAGCAT	52889
Qy	1616	TCCATGGGAGTATGCTCTG	CAAAACAGGATTCGAT	TTGGAGCATTAATCGATCATTAGCTA	1675
Dd	52890	TCCATGGGAGTATGCTCTG	CAAAACAGGATTCGAT	TTGGAGCATTAATCGATCATTAGCTA	52949
Qy	1676	TTTTTTGGTGA CAGACCA	AGAGCTTAGACATCGAC	TTTGTGCCAGATCAATTTGAGGATGT	1735

Db	52950		TTTTGGTGACAGACCAAGAGCTTAGCACATGCGAGTTTGTCCAGATCAATTGAGGATGT	53009
Qy	1736	TACGGGTCTTGGATCTTTGAAGATGTGACATCTCTTAATCACTCAAAAAGATTTTCGACCGGTA	1795	
Db	53010	TA CGGGTCTTGGATCTTTGAAGATGTGACATCTCTTAATCACTCAAAAAGATTTTCGACCGGTA	53069	
Qy	1796	TTGCATTTGTTGGCCACTTTGAAATACTTCGAGTATTGGATATTGCTCATATATTCAC	1855	
Db	53070	TTGCATTTGTTGGCCACTTTGAAATACTTCGAGTATTGGATATTGCTCATATATTCAC	53129	
Qy	1856	TTCCGAGATCCATTGGTAACTTACAGGGCCTACAGACTTTGAACTGTCAAGCACATACA	1915	
Db	53130	TTCCGAGATCCATTGGTAACTTACAGGGCCTACAGACTTTGAACTGTCAAGCACATACA	53189	
Qy	1916	TTGCAGCACTTACCAAGTGAGATCAGTAAACTCCAATGCTCGCATACTCTTCGTTGATAA	1975	
Db	53190	TTGCAGCACTTACCAAGTGAGATCAGTAAACTCCAATGCTCGCATACTCTTCGTTGATAA	53249	
Qy	1976	GAGAGCTTGAATTTGACAACTTTAGTCTAAATCA CCCCATGAAGTGCATACTAAACACAA	2035	
Db	53250	GAGAGCTTGAATTTGACAACTTTAGTCTAAATCA CCCCATGAAGTGCATACTAAACACAA	53309	
Qy	2036	TATGCGCTGCCCTAAAGTATTTCACACCTTTAGTTAGTTCGCGATTAATCGTGCACAAACAAATTG	2095	
Db	53310	TATGCGCTGCCCTAAAGTATTTCACACCTTTAGTTAGTTCGCGATTAATCGTGCACAAACAAATTG	53369	
Qy	2096	CTGAAATTCACATGGGCCACCAAAAGTTCTCGTCTGMAATCATCTTCGCTGTGAAGGTACCCA	2155	
Db	53370	CTGAAATTCACATGGGCCACCAAAAGTTCTCGTCTGMAATCATCTTCGCTGTGAAGGTACCCA	53429	
Qy	2156	AAGGAATAGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCA	2215	
Db	53430	AAGGAATAGTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCA	53489	
Qy	2216	GTAGTAGAGCAATCAAAAGACTGGGGCAGTTAAGCAAGTTGAGGAAAATTAGCTGTGATAA	2275	
Db	53490	GTAGTAGAGCAATCAAAAGACTGGGGCAGTTAAGCAAGTTGAGGAAAATTAGCTGTGATAA	53549	
Qy	2276	CAAAAGGCTCGACAAAGGAAAATGTAAAGATCTTTATGACGCCATTGAGAAAGCTCTCTT	2335	
Db	53550	CAAAAGGCTCGACAAAGGAAAATGTAAAGATCTTTATGACGCCATTGAGAAAGCTCTCTT	53609	
Qy	2336	CCCTCCAAATCTCTATATGAATGTCGCTTATATCAGATATTGAAACACTTGAGTGC	2395	
Db	53610	CCCTCCAAATCTCTATATGAATGTCGCTTATATCAGATATTGAAACACTTGAGTGC	53669	
Qy	2396	TAGATTTATTTCAATCTCTCTCCCTACTGAGGACACTCGGGTTGAATGGAAGTCTTGT	2455	
Db	53670	TAGATTTATTTCAATCTCTCTCCCTACTGAGGACACTCGGGTTGAATGGAAGTCTTGT	53729	
Qy	2456	AAGGATGCTTAACCTGGATTGAGCAGCTCACTCACTGAAGAAGTTCAACTTTATGCGATTA	2515	
Db	53730	AAGGATGCTTAACCTGGATTGAGCAGCTCACTCACTGAAGAAGTTCAACTTTATGCGATTA	53789	
Qy	2516	GTAAATTAAGGAAGGTAAAAACATGCTGATACTTTGGGCACTGCCCAACCTCATGTTCC	2575	
Db	53790	GTAAATTAAGGAAGGTAAAAACATGCTGATACTTTGGGCACTGCCCAACCTCATGTTCC	53849	
Qy	2576	TTTCTCTTTATCAATTTCTTATCTTTGGGGAGAGCTAGTATTCAAAACGGGAGCATTCC	2635	
Db	53850	TTTCTCTTTATCAATTTCTTATCTTTGGGGAGAGCTAGTATTCAAAACGGGAGCATTCC	53909	
Qy	2636	CAAACTTTAGAACACTTTGTGATTTTCAATTTGGATCAGTAAAGAGATCAGATTTGAGG	2695	
Db	53910	CAAACTTTAGAACACTTTGTGATTTTCAATTTGGATCAGTAAAGAGATCAGATTTGAGG	53969	
Qy	2696	ACGGCAGCTCACCCAGTTGGAAAAGATAGAAATCTCTTGTGTCAGGTTGGAATCAGGGA	2755	
Db	53970	ACGGCAGCTCACCCAGTTGGAAAAGATAGAAATCTCTTGTGTCAGGTTGGAATCAGGGA	54029	
Qy	2756	TTATTGGTATCATTTCACTTCCAGGCTCAAGGAGATTTCACTTGAATCAAAAGTAAAG	2815	

Db 54030 TTATTGGTATCAATTACCTTCAAAGGCTCAAAGGAGATTTCATTGAAATACAAAAAGTAAAG 54089
Qy 2816 TGGCTAGGCTTGGTCAGCTGAAGGAGAAAGTGAACACACACCAATCGCCCGGTGTCG 2875
Db 54090 TGGCTAGGCTTGGTCAGCTGAAGGAGAAAGTGAACACACACCAATCGCCCGGTGTCG 54149
Qy 2876 GAATGGACAGTGAACGAAGGATCAAGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAG 2935
Db 54150 GAATGGACAGTGAACGAAGGATCAAGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAG 54209
Qy 2936 AAGTGCACACAGCAGATCTCTTCTGATGCCAAGGATCACTCACTGACAGTGGAG 2995
Db 54210 AAGTGCACACAGCAGATCTCTTCTGATGCCAAGGATCACTCACTGACAGTGGAG 54269
Qy 2996 CAACGGATCCCTTCCCGAGCAGGAGGAGAGAGCTCGCAGTCCGAGGTGATCAAGTTGA 3055
Db 54270 CAACGGATCCCTTCCCGAGCAGGAGGAGAGAGCTCGCAGTCCGAGGTGATCAAGTTGA 54329
Qy 3056 CGACGAATGATAGCGAAG 3073
Db 54330 CGACGAATGATAGTCCAG 54347

RESULT 5

US-10-656-394A-7

; Sequence 7, Application US/10656394A

; Publication No. US20040210957A1

; GENERAL INFORMATION:

; APPLICANT: Wang et al.

; TITLE OF INVENTION: Cloning and Characterization of the

; FILE OF INVENTION: broad-spectrum resistance gene P12

; FILE REFERENCE: 035718/252062

; CURRENT APPLICATION NUMBER: US/10/656.394A

; CURRENT FILING DATE: 2003-09-05

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 3099

; TYPE: DNA

; ORGANISM: Oryza minuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(3099)

; US-10-656-394A-7

Query Match 93.9%; Score 2910.2; DB 18; Length 3099;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
Qy 1 ATGGCGGAGACGGTGTGAGCATGGCGAGGTGCGTGGTGGGCGAGTGGCCATCAGCAAGGCC 60
Db 1 ATGGCGGAGACGGTGTGAGCATGGCGAGGTGCGTGGTGGGCGAGTGGCCATCAGCAAGGCC 60
Qy 61 GCCTTCGCCGTGCCAATGAGACGAGCCTCTGCTCGGCGGTGCGAAGAGGACATCTGGTAT 120
Db 61 GCCTTCGCCGTGCCAATGAGACGAGCCTCTGCTCGGCGGTGCGAAGAGGACATCTGGTAT 120
Qy 121 ATCAAGATGAGCTTAAACCAATCAATCAGGCATCTCTTAGAGTGTCTGAAGTTATGAAAAG 180
Db 121 ATCAAGATGAGCTTAAACCAATCAATCAGGCATCTCTTAGAGTGTCTGAAGTTATGAAAAG 180
Qy 181 AAAGATGAACTATTAAAGGTTTGGGCGAGGCAAAATAGCTGACCTGTCTGATGACATTGAA 240
Db 181 AAAGATGAACTATTAAAGGTTTGGGCGAGGCAAAATAGCTGACCTGTCTGATGACATTGAA 240
Qy 241 GATTCCCTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCCATTTTCGTCAGTTGGTG 300
Db 241 GATTCCCTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCCATTTTCGTCAGTTGGTG 300
Qy 301 AAACCTTAGAGGCGCCACCGGATCGCTATCGGTATCCACACCTCAATCAAGAGTTGAA 360
Db 301 AAACCTTAGAGGCGCCACCGGATCGCTATCGGTATCCACACCTCAATCAAGAGTTGAA 360

Qy 361 GAAGTGAGTAGCAGGAACACACGCTACAAATTTAGTCGAGCCTATTTCTCTCGGCACAGAG 420
Db 361 GAAGTGAGTAGCAGGAACACACGCTACAAATTTAGTCGAGCCTATTTCTCTCGGCACAGAG 420
Qy 421 GATGACATGATTCCTATGACGAAGACATTTGCGCAATCAATCAGCTCGAAATGTGATGAA 480
Db 421 ATTGACATGATTCCTATGACGAAGACATTTGCGTAATCAGTCAGCTCGCAATGTGATGAG 480
Qy 481 GCTCAGCTTGTGGTGGTTCCTGACTCCAAAGAAAGGCTGCTTGAATAATGATCGATACCAAT 540
Db 481 GCTCAGCTTGTGGTGGTTCCTGACTCCAAAGAAAGGCTGCTTGAATAATGATCGATACCAAT 540
Qy 541 GCTAATGATGCTCGGCAAGGTAATCTGTGTTGTTGGGATGGTGGTTTAGGCAAGACA 600
Db 541 GCTAATGATGCTCGGCAAGGTAATCTGTGTTGTTGGGATGGTGGTTTAGGCAAGACA 600
Qy 601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 660
Db 601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 660
Qy 661 GCTTGGATTACAGTGTCCAAATCAATTTACAGGATTCAGCTTCTTAAAGATATGATACGC 720
Db 661 GCTTGGATTACAGTGTCCAAATCAATTTACAGGATTCAGCTTCTTAAAGATATGATACGC 720
Qy 721 CAACCTCTTGGTCCAGTTCCTCTGGATCAACTCTTGGATCAATTTGCAAGAAATTTGCAAGGGAAGTGGTG 780
Db 721 CAACCTCTTGGTCCAGTTCCTCTGGATCAACTCTTGGATCAATTTGCAAGGGAAGTGGTG 780
Qy 781 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGAGTACTTT 840
Db 781 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGAGTACTTT 840
Qy 841 GTTGTCTTACATGATCATGATTTTACATGATTTTGAATTTGGATAAATGAAATGCAATTT 900
Db 841 GTTGTCTTACATGATCATGATTTTACATGATTTTGAATTTGGATAAATGAAATGCAATTT 900
Qy 901 CCTAAGAACCAATTAAGAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCG 960
Db 901 CCTAAGAACCAATTAAGAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCG 960
Qy 961 GAGAAAGTGCCACAGCCTCACTGGTGTACACCTTGATTTCTTGCAGATGAACGATGCC 1020
Db 961 GAGAAAGTGCCACAGCCTCACTGGTGTACACCTTGATTTCTTGCAGATGAACGATGCC 1020
Qy 1021 ATTTTCATTGCTACTTGAGAAAACAAATAAAATCATGAACACATGGAATCAAAATAAAAAT 1080
Db 1021 ATTAACATTGCTACTTGAGAAAACAAATAAAATCATGAACACATGGAATCAAAATAAAAAT 1080
Qy 1081 ATGCAAAAGATGGTTGAACGAAATTTGTAATAAATGTCGTCTTACCAATTAGCAATACTT 1140
Db 1081 ATGCAAAAGATGGTTGAACGAAATTTGTAATAAATGTCGTCTTACCAATTAGCAATACTT 1140
Qy 1141 ACAATAGGAGCTGTGTTGCAACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACAA 1200
Db 1141 ACAATAGGAGCTGTGTTGCAACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACAC 1200
Qy 1201 CTTTCCTTCAGAACTAGAAATAAACCCAGCCTCGAGCTTTTGGAGGAATGGTGACCCCTA 1260
Db 1201 CTTTCCTTCAGAACTAGAAATAAACCCAGCCTCGAGCTTTTGGAGGAATGGTGACCCCTA 1260
Qy 1261 GGTACAACACCACTTACCATCCCATCTGAAACCAATGCTTTTGTATCTAAGATATCTTTCCT 1320
Db 1261 GGTACAACCACTTACCATCCCATCTGAAACCAATGCTTTTGTATCTAAGATATCTTTCCT 1320
Qy 1321 GAGATTTTGAATAACAAAGGAATCGCTAGTAGGTAGATGGATAGCAGAGGGTTGTT 1380
Db 1321 GAGATTTTGAATAACAAAGGAATCGCTAGTAGGTAGATGGATAGCAGAGGGTTGTT 1380
Qy 1381 AGACCAAGGTTGGGATGACGACTAAGGATGTCCGAGAAAGTTACTTTTAAATGAGCTAATC 1440
Db 1381 AGACCAAGGTTGGGATGACGACTAAGGATGTCCGAGAAAGTTACTTTTAAATGAGCTAATC 1440
Qy 1441 AACCGAAGTATGATTTCAACGATCAAGAGTGGGCAACAGAGGAAAAATTAAGACTTGTGCA 1500

Db		39322	TTGAAGATTCCGCTTGATGAATTTAAAGTCCATATTTGAAAGGCCAAACCCCTATTTTCGTCAGT	39381		40402	TTCTCTGAGGATTTTGAATCAAAAAGGAATCGTCTAGTAGGTAGATGCGATGACGAGAGGGT	40461
Qy		296	TGGTGAACATTTAGAGAGCGCCACCGGATCGGTATCCGATATCCACAACCTCAAAATCAAGAG	355		1376	TTGTTAGACCAAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTTACTTTTATATGAC	1435
Db		39382	TGGTGAACATTTAGAGAGCGCCACCGGATCGGTATCCGATATCCACAACCTCAAAATCAAGAG	39441		40462	TTGTTAGACCAAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTTACTTTTATATGAC	40521
Qy		356	TTGAAGAAGTAGTAGCAGGAACAACACGCTACAATTTAGTCGAGCCTATTTTCTCCCGGCA	415		1436	TAATCAACCGGAAGTATGATTCACGATCAAGAGTGGGCACAGCAGGAAAAAATTAAGACTT	1495
Db		39442	TTGAAGAAGTAGTAGCAGGAACAACACGCTACAATTTAGTCGAGCCTATTTTCTCCCGCA	39501		40522	TAATCAACCGGAAGTATGATTCACGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTT	40581
Qy		416	CAGAGGATGACATGGATTCCTATGACAGAAGACATTCGCAATCAATCAGCTCGAATATGG	475		1496	GTGGAATCCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTG	1555
Db		39502	CAGAGGATGACATGGATTCCTATGACAGAAGACATTCGCAATCAATCAGCTCGAATATGG	39561		40582	GTGGAATCCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTG	40641
Qy		476	ATGAAGCTGAGCTTGTGGGTTTTCTGACTCCAGAAAGGCTGCTGAAATGATCGATA	535		1556	TATTATTACCAATCGGAGATGGCTCTGATTTTGTAGTTTCAGGAAAAACACTCGCCACATAGCAT	1615
Db		39562	ATGAAGCTGAGCTTGTGGGTTTTCTGACTCCAGAAAGGCTGCTGAAATGATCGATA	39621		40642	TATTATTACCAATCGGAGATGGCTCTGATTTTGTAGTTTCAGGAAAAACACTCGCCACATAGCAT	40701
Qy		536	CCAATGCTAAATGATGGTCCGGCCAAAGGTAATCTGTGTTTGGGATGGGTGGTTTAGGCA	595		1616	TCCAATGGGAGTATGTCTCTGCAAAAACAGGATTTGGAGTTCGAGCATTTATTTCGATCATTTAGCTA	1675
Db		39622	CCAATGCTAAATGATGGTCCGGCCAAAGGTAATCTGTGTTTGGGATGGGTGGTTTAGGCA	39681		40702	TCCAATGGGAGTATGTCTCTGCAAAAACAGGATTTGGAGTTCGAGCATTTATTTCGATCATTTAGCTA	40761
Qy		596	AGACAGCTCTTTTCGAGGAAGATCTTTTGAAGCGAAGAGACATTTAGGAAGAACTTCCCTT	655		1676	TTTTTGTGTGACAGACCCCAAGAGCTTAGACACATGACAGTTTGTTCAGATCAATTTGAGGATGT	1735
Db		39682	AGACAGCTCTTTTCGAGGAAGATCTTTTGAAGCGAAGAGACATTTAGGAAGAACTTCCCTT	39741		40762	TTTTTGTGTGACAGACCCCAAGAGCTTAGACACATGACAGTTTGTCTAGATCAATTTGAGGATGT	40821
Qy		656	GCAATGCTTGGATTACAGTGTACAAATCATTTTCACNGGATTCAGTACTTAAAGATATGA	715		1736	TACGGGCTTTGGATCTTTGAAAGATGTGACATTTCTTAATCCTCAAAAAGATTTTCGACCGTA	1795
Db		39742	GCAATGCTTGGATTACAGTGTACAAATCATTTTCACNGGATTCAGTACTTAAAGATATGA	39801		40822	TACGGGCTTTGGATCTTTGAAAGATGTGACATTTCTTAATCCTCAAAAAGATTTTCGACCGTA	40881
Qy		716	TACGCCAACTCTTTGGTCCCAAGTCTCTCGGATCAACTCTTCGATGAATTCGCAAGGAGG	775		1796	TTGCATTTGTTGTGCACTTTGAAATPACTTTGAGTATTTGGATATTTTCGTATCCATATATTTCAC	1855
Db		39802	TACGCCAACTCTTTGGGCCCCAGTTCTCTGGATCAACTCTTCGATCAACTCTTCGCAAGATTCGAGGAGG	39861		40882	TTGCATTTGTTGTGCCACTTGAATPACTTTGAGTATTTGGATATTTTCGTATCCATATATTTCAC	40941
Qy		776	TGTTGGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGT	835		1856	TTCCAGATCCATTTGGTAAACTACAGGGCCCTACAGACTTTTGAACAATGTCAAGACATACACA	1915
Db		39862	TGTTGGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGT	39921		40942	TTCCAGATCCATTTGGTAAACTACAGGGCCCTACAGACTTTTGAACAATGTCAAGACATACACA	41001
Qy		836	ACTTTGTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGAAATG	895		1916	TTGCAGACACTACCAAGTGAGATCAGTAAACTCCCAATGTCTGCATACCTCTTCGTGTGATAA	1975
Db		39922	ACTTTGTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGAAATG	39981		41002	TTGCAGACACTACCAAGTGAGATCAGTAAACTCCCAATGTCTGCATACCTCTTCGTGTGATA	41061
Qy		896	CATTTCTTAAGAACAAATAAGAAAGGCGAGTCGAATAGTAATAACCACTCGGAATGTGCATC	955		1976	GAGAGCTTGAATTTGACCAACTTTTAGTCTAAATCAACCAAGTGAAGTGCATTAACACAA	2035
Db		39982	CATTTCTTAAGAACAAATAAGAAAGGCGAGTCGAATAGTAATAACCACTCGGAATGTGCATC	40041		41062	GAAAGTTTGTATTGACCAACTTTTAGTCTTAACCAACCAAGTGAAGTGCATTAACACAA	41121
Qy		956	TAGCGGAAGTGTGCCACAGCCCTCACTGGTGTACCACTTGATTTCTTGAGATGAACG	1015		2036	TATGCTTCCTTAAAGTATTCACACTTTTAGTTCGCGATATTCGTGCGAAAAACAATTTG	2095
Db		40042	TAGCGGAAGTGTGCCACAGCCCTCACTGGTGTACCACTTGATTTCTTGAGATGAACG	40101		41122	TATGCTTCCTTAAAGTATTCACACTTTTAGTTCGCGATATTCGTGCGAAAAACAATTTG	41181
Qy		1016	ATGCCATTTCAATCTGACTAGAAATAACAATAAATCATGAAGACATGGAATCAATA	1075		2096	CTGAAATTTACATGGCCCAACCAAGATTTCTGGTCTGAATCAATTCGGTGTGAAGGTACCCA	2155
Db		40102	ATGCCATTAACATTTCTACTGAGAAAAAACAATAAATAATCATGAAGACATGGAATCAATA	40161		41182	CTGAAATTTGACATGGCCCAACCAAGATTTGCTGGTCTGAATCAATTCGGTGTGAAGGTACCCA	41241
Qy		1076	AAATATGCAAAAGATGTTGAAAGGATTTGAAATAAATGTTGTTCCCTACCATTAGCAA	1135		2156	AAGGAATPAGTAAAGTTCGCGAGACTTACAGGTTCTTAGAGTATGTAGATATCAGGCGGACCA	2215
Db		40162	AAATATGCAAAAGATGTTGAAAGGATTTGAAATAAATGTTGTTCCCTACCATTAGCAA	40221		41242	AAGGAATPAGTAAAGTTCGCGAGACTTACAGGTTCTTAGAGTATGTAGATATCAGGCGGACCA	41301
Qy		1136	TACTTACAATAGGAGCTGTGCTTCCAACTAACAGGTTGTCAAGATGGGAGAAATTTCTATG	1195		2216	GTAGTAGAGCAATCAAAAGAGCTGGGCGAGTTTAAGCAAGTTGAGGAAATTTAGCTGTGATAA	2275
Db		40222	TACTTACAATAGGAGCTGTGCTTCCAACTAACAGGTTGTCAAGATGGGAGAAATTTCTATG	40281		41302	GTAGTAGAGCAATCAAAAGAGCTGGGCGACTTAAGCAAGTTGAGGAAATTTAGCTGTGATAA	41361
Qy		1196	AACAACTTCTTTCAGAACTAGAAATAAACCCAGCTGGAGCTTTGAGGAGATGTGA	1255		2276	CAAAAGCTCGAACAAGGAAATGTAAGATACATTTATCAGAGTATTTAGGAAAGCTCTCTT	2335
Db		40282	AACAACTTCTTTCAGAACTAGAAATAAACCCAGCTGGAGCTTTGAGGAGATGTGA	40341		41362	CAAAAGCTCGAACAAGGAAATGTAAGATACATTTATCAGAGTATTTAGGAAAGCTCTCTT	41421
Qy		1256	CCCTAGGTTTCAACACCTACCATCCCATCTGAAACCATGCTTTTGTGATCTAAGTATCT	1315		2336	CCCTCCAATCTCTATATGAATGCTCGGTTATTATCAGATATTTGAAACACTTCAGGTGCC	2395
Db		40342	CCCTAGGTTTCAACACCTACCATCCCATCTGAAACCATGCTTTTGTGATCTAAGTATCT	40401		41422	CCCTCCAATCTCTATGTAAGTGTGCTGGTTATTATCAGATATTTGAAACACTTCAGGTGCC	41481
Qy		1316	TTCTCTGAGGATTTTGAATACAAAGGAATCGTCTAGTAGGTAGATGACGAGAGGGT	1375		2396	TAGATTTCTATTTCATCTCTCTCCCTACTGAGGACACATCGCGGTTGAAATGGAAGTCTTG	2455
Db						41482	TAGATTTCTATTCTCTCTCTCCCTACTGAGGACACATCGGGTTGAAATGGAAGTCTTG	41541

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Qy 2456 AAGAGATGCCCTAACTGGATTGAGCAGCTCACTACCTGGAAGAGTTCACTTATGGAGTA 2515
Db 41542 AAGAGATGCCCTAACTGGATTGAGCAGCTCACTACCTGGAAGAGATCTACTTATGGAGGA 41601
Qy 2516 GTAACTAAAGGAAGGTAAACATGCTGATCTTGGGCACTGCCAACCTCATGTTCC 2575
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Qy 2576 TTCTCTTTATCATATAATCTTTATCTTGGGGAGAGCTAGTATTCAAAACGGGAGCATTC 2635
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Db 41962 GAATGGACAGTGACCGAAGGATCACGACCTGGGGGCTGAAGCCGAGGATCTTCTATAG 42021
Qy 2936 AAGTGCAAAACAGCAGATCCTGCTGATGCCCAAGGATCACTGACAGTGGGAAG 2995
Db 42022 AAGTGCAAAACAGCAGATCCTGCTGATGCCCAAGGATCACTGACAGTGGGAAG 42081
Qy 2996 CAACGGATCCCTTTCCGAGCAGAGGAGAGAGCTGCGAGTGCAGGTGATCAGTTGA 3055
Db 42082 CAACGGATCCCTTTCCGAGCAGAGGAGAGAGCTGCGAGTGCAGGTGATCAGTTGA 42141
Qy 3056 CGACGAATGATAGCGNAG 3073
Db 42142 CGACGAATGATAGGTGAG 42159
RESULT 7
US-10-352-179-92
; Sequence 92, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3276)
; OTHER INFORMATION:
US-10-352-179-92
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Query Match 91.7%; Score 2842.2; DB 17; Length 3276;
Best Local Similarity 97.0%; Pred. No. 0;

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Matches 2895; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
Qy 117 GTATATCAAAAGATGAGCTAAACAAATTCAGGCAATCTCTTAGAGCTGCTGAAGTTATGAA 176
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Qy 177 AAAGAAAGATGAACTATTAAAGTTTGGGAGAGCAAAATAGTCACTGCTGATGATGACAT 236
Db 354 AAAGAAAGATGAACTATTAAAGTTTGGGAGAGCAAAATAGTCACTGCTGATGATGACAT 413
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Db 474 GGTGAAACTTAGAGAGCGCCACCGGATCGGTATCCGTATCCCAACCTCAAAATCAAGAGT 533
Qy 357 TGAAGAAAGTGAAGTACAGGAAACACACGCTACAAATTTAGTCGAGCTTATTCCTCGGCAC 416
Db 534 TGAAGAAAGTGAAGTACAGGAAACACACGCTACAAATTTAGTCGAGCTTATTCCTCGGCAC 593
Qy 417 AGAGATGACATGATGATTCCTATGCAAGAGACATTCGCAATCAATCAGCTCGAAATGTGGA 476
Db 594 AGAGATGACATGATGATTCCTATGCAAGAGACATTCGCAATCAATCAGCTCGAAATGTGGA 653
Qy 477 TGAAGCTGAGCTTGTGCGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATATGATGATGAC 536
Db 654 TGAAGCTGAGCTTGTGCGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATATGATGATGAC 713
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Qy 597 GACAGCTCTTTTCGAGGAAGATCTTTTGAAGCGAAGAGACATTAAGGAAGACTTCCCTTG 656
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Qy 717 ACGCAACTTCTTGGTCCGAGTTCTCTGGATCAACTCTTGGATGAATTCGAAGGAGAGGT 776
Db 894 ACGCAACTTCTTGGTCCGAGTTCTCTGGATCAACTCTTGGATGAATTCGAAGGAGAGGT 953
Qy 777 GGTGTCGAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTA 836
Db 954 GGTGTCGAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTA 1013
Qy 837 CTTTGTGTTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGAATTTGGAATTTGC 896
Db 1014 CTTTGTGTTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGAATTTGGAATTTGC 1073
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Qy 1137 ACTTACAATAGGAGCTGCTTGCACCTAAACAGGTGTGAGAAATGGGAGAAATTTCTATGA 1196
Db 1314 ACTTACAATAGGAGCTGCTTGCACCTAAACAGGTGTGAGAAATGGGAGAAATTTCTATGA 1373
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Db 1222 AGTATGATTCAAGGATCAAGAGTGGGCATAGCAGGAAAATAAAGATTGTGCAATTCAAT 1281
Qy 1507 GATATCATCCGTTGATATCACAGTTTCAATCTCGACACAGGAAAAATTTTGTATATTACCA 1566
Db 1282 GATATCATCCGTTGATATCACAGTTTCAATCTCGACACAGGAAAAATTTTGTATATTACCA 1341
Qy 1567 ATGGGAGATGGCTCTGATTTAGTTTACAGGAACAACCTCGCCACATAGCATTCATCGGAGT 1626
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Qy 1747 GATCTTGAAGATGTCACATTTCTTAATCACTCAAAAAGATTTTCGACGGTATTCGATTGTTG 1806
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Db 1702 CCAAGTGAGATCAGTAACACTCAATGTCTGCATCTCTCTGTTGTATAGAGAGCTTGT 1761
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Qy 2047 AAAGTATTACACCTTTAGTTAGTTCGCGATATCGTGCATAAATAAATTTGCTGAAATTCAC 2106
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Qy 2107 ATGGCCACCAAAAGTTTCTGTTCTGAATCAATTCGGTGTGAAGGTACCAAAAGGAATAGT 2166
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Qy 2167 AAGTTCCGAGACTTACAGTCTTACAGTATGTAGATATCAGCGCAGCAGTAGTAGCA 2226
Db 1942 AAGTTCCGAGACTTACAGTCTTACAGTATGTAGATATCAGCGCAGCAGTAGTAGCA 2001
Qy 2227 ATCAAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTAGCTGTGATAACAAAAGCTCG 2286
Db 2002 ATCAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTAGCTGTGATAACAAAAGCTCG 2061
Qy 2287 ACAAAAGGAAAAATGTAAGATCTTTATGAGCAGCATTTGAGAGAGCTCTTCCCTCCAAATCT 2346
Db 2062 ACAAAAGGAAAAATGTAAGATCTTTTGTGAGCAGCATTTGAGAGAGCTCTTCCCTCCAAAT 2121
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Qy 2407 TCATCTCTCTCCCTACTAGGAGACACTCGGTTGAAATGGAAGTCTTGAAGAGATGCT 2466
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Qy 2467 AACTGGAATGAGCAGCTCACTCACTGAAAGATTTCAACTTATGAGGATGTAACATAAG 2526
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Qy 2527 GAGGTAACATGCTGATCTACTTGGGCACTGCCCCAACCTCATGTTCTTCTCTTTAT 2586
Db 2302 GAGGTAACATGCTGATCTACTTGGGCACTTGGCCCAACCTCATGTTCTTCTCTTTAT 2361

Qy 2587 CATAAATTTCTTATCTTTGGGAGAGAGCTAGTATTTCAAAAACGGGAGCATTTCCCAAATCTTAGA 2646
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Qy 2707 CCCAGTTGGAAAAGATAGAAATCTCTTGTCTGACAGTTTGGAAATCAGGAGTATTTGCTATC 2766
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Qy 2767 ATTCACTTCCAAAGCTCAAGGAGATTTCACTTTGAATACAAAAGTAAAGTGGCTAGGCTT 2826
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Qy 2827 GGTCAAGCTGAAGGAGAGATGAACACACACCAATTCGCCGCTGCTGCGAATGACAGT 2886
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Qy 2887 GACCAAGGAGATCAGACCTGGGGGCTGAAGCCGAAAGATCTTCTATAGAAAGTCAAAACA 2946
Db 2662 GACCGAAGTATCAGACCTTGTGTGACGCGGAGGATCCCTGTTGAAAGTGAAGCA 2721
Qy 2947 GCAGATCTGTTCTGTGATGCCCAAGGA 2973
Db 2722 ACGGATCCCTCCAGAGCAGGAGGA 2748

RESULT 10
US-10-437-963-2483
; Sequence 2483, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 2483
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102251C.1
US-10-437-963-2483

Query Match 61.0%; Score 1891.6; DB 18; Length 2982;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 2358; Conservative 0; Mismatches 439; Indels 183; Gaps 2;
Qy 1 ATGGCGGAGACGGTGTGAGCATGGCGAGGTCTGTTGGGCGAGTGCATCAGCAAGGCC 60
Db 178 ATGGCGGAGACGGTGTGAGCATGGCGAGGTCTGTTGGGCGAGTGCATCAGCAAGGCC 237
Qy 61 GCCTCTCCGCTGCCAATGAGACGAGCTCTCTGCTGGCGCTCGAAGAGCATCTGGTAT 120
Db 238 ACCTCTGGCGGGCCCATGAGCGAGCTCTCTACTCGCGCTCGAAGAGCATCTGGTAT 297
Qy 121 ATCAAGATGAGCTAAACCAATCAGGCATTTCTTAGAGCTGCTGAAGTATGAAAAG 180
Db 298 ATCAAGATGAGCTGAAAACCAATGCAAGCGTTCTTACGAGCTGCTGAAGTATGAAAG 357

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Qy 2395 CTAGATCTATTCAATCTCTCCCTCACTAGGACACACTGGGGTGAATGGAAGTCTT 2454
Db 2401 CTAGATCTATTCTATCTCTCTCTGTTACTAAGACACTCAAGTGTGTATGGAGTCTT 2460
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Qy 2635 CCAATCTTAGAACACTTTGTGATTTTCAATTTGGATCAGCTAAGAGATCAGATTTGAG 2694
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RESULT 11
US-10-352-179-90
; Sequence 90, Application US/10352179
; Publication No: US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 3220
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-90

Query Match 51.4%; Score 1591.8; DB 17; Length 3220;
Best Local Similarity 73.2%; Pred. No. 0;
Matches 2179; Conservative 0; Mismatches 752; Indels 46; Gaps 9;
Qy 1 ATGCGGAGACGGTGTGAGCATGGCAGGTCGCTGGTGGGAGTGCATCAGCAAGGCC 60
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Db 121 ATCAAGATGAGCTACAAACGATACAAAGCATTTTGTGCTGCCGAAG---CATCAAAG 177
Qy 181 AAAGATGAATATTAAGGTTTGGGACAGAGCAATACGTGACCTGTGCTATGACATTTGAA 240
Db 178 AAAAGCATACTATTGGAAGGTTTGGGTGCAGCAAGTAAGGGATCTTTCCTATGACATTGAA 237
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Db 478 GAAGCTGATCTTGTGGGTTTTCTGGACCCAAAGAGAGTTGCTTTGATCTTATAGATGTC 537
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Db 538 CATGCCAATGACGACCTACAAAAGTTGTATGTGTGTCGGTATGGGTGGTTTGGGTAAAG 597
Qy 598 ACAGCTCTTTCGAGAGAGATCTTTGAAAGCGAAGACATTTAGGAAAGAACTTCCTTCGTC 657
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Qy 778 GTGTTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAGGAGAGAGGTAC 837
Db 775 GTTCCACAAGTAGACGACCTCGCCAGCTACCTCAGGACAGAGTTAATGAAAGGAGGTAC 834
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Db 1015 GCAAAAGAGTTGCTTCTACGGAAGCAATTAAGCAATAGGAGATATGGAAGTATGATA 1074
Qy 1078 AATAATGCAAAAGAGTGGTTGAAACGAATTTGAAATTAATTAATTTGCTCTACCTACCA 1137
Db 1075 AAGATGAGTGACATTATAACTAAATAATTAAGAGAGTGTGGCTATTTACCGCTGGCTATA 1134
Qy 1138 CTTACAAATAGAGCTGTGCTTGTGCAACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAA 1197

Db 1135 CTCACATAGAGGGGCTGCTTCCACCACAAAGAGATAGAGAGTGGGAACTTTTATATAGT 1194
Qy 1198 CAACCTTCCTTCAGAACTAGAAATAAACCCAGCCCTGGAGCTTTGAGGAGAAATGCTGACC 1257
Db 1195 CAGATACCTTCAGAGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAAAGTATGACC 1254
Qy 1258 CTAGGTTACAAACCACTACCAATCCCATCTGAAACCAACGCTTTTGTATCTAAGTATCTTT 1317
Db 1255 CTAAGTTACAACCTACTTACCGCTCATCTTAAGCAATGCTTTTGTATCTAAGCATATTT 1314
Qy 1318 CCTGAGGATTTGAAATAACAAGGATCGTCTAGTAGTAGATGATGAGAGGAGGTTT 1377
Db 1315 CCTGAGGATTTGAAATTAATAGGAACCGCTGCTGTAATAGATGATGCGAGAGGGGTTT 1374
Qy 1378 GTTAGACAAAGGTTGGGATCAGCACTAAGGATGTCGGAGAAAGTTACTTTAATAGAGCTA 1437
Db 1375 ATTAAGCTAGGACTAATATGACTATTGGAAGATTTGGGAAAGTTACTTTAAGAACTT 1434
Qy 1438 ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCAAGAGGAAATAATTAAGACTTGT 1497
Db 1435 ATCAACCGTAGCATGATTCAGCCATCAAGAGCGGTATACGAGGAGATTTTAAAGAGCTGT 1494
Qy 1498 CGAATCCATGATATCATCCGCTGATATCACAGTTTCAATCTCGACACAGGAAAAATTTGTA 1557
Db 1495 CGAGTCCACGACATCATGCGTGATATTACAAATTTTCAATTTCTAGAGAGAAAAATTTCA 1554
Qy 1558 TTATTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAAACTTCGGCACATAGCATTC 1617
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Qy 1618 CATGGGAGTATGCTCTGC- - -AAAACAGGAATGGATTTGGAGCATTTATTCGATCATTTAGCT 1674
Db 1615 CACGGGAGTAAATTTGCTCTGAAACCAAGCTTGAGCTGGAGCAATTAATAGCGTCAATTA 1674
Qy 1675 ATTTTGGTGAAGAGCTGAGCTAGCAATGAGCTTTGTCAGATCAATTAAGAGATG 1734
Db 1675 ATGTTGGTGAAGAGCTCGGTAGAACTAGAGCAATTCAGTTTGTTCATCTCAGTTGAGGATG 1734
Qy 1735 TTACGGGCTTTGGATCTTGAAGATGTGACATCTTAACTCACTCAAAAAGATTTTCGACCGT 1794
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Qy 1795 ATTGCATTTGTTGCCACTTGAATTAATCTTGAGTATT-----GGATATTGCTCATC 1844
Db 1795 ATAGTGCTCTTGTGCCACTTGAATTAATCTATGATTAAGATACAGATACCGTTCAACCAT 1854
Qy 1845 CATATATTCTCTCCAGATCCATTTGTAATCACTACAGGCGCTACAGACTTTGAACATGTC 1904
Db 1855 TATTTATTCACTTCCCAATCCATAGCTAGACTGCTGATGCTGAGACATTTGGACTTTGGG 1914
Qy 1905 AAGCACATACATTCGACACTPACCAAGTGAGATCAGTAAACTCCAATGCTGCTGCTACTCT 1964
Db 1915 TCAGAGGTACATTTCAACACTGCGCACTCAGATTAAT- - -AATTCGGAGCTTCCGTAAGCT 1973
Qy 1965 TCGTTGTATAGAGAGCTTGAATTTGACAACTTTAGTCTAAATCACCAATGAAGTGCAT 2024
Db 1974 TCGATGCATGAAGAAATATTTTCTCTCTCTT-----AACACATATTT 2018
Qy 2025 AACTAACATATATGCTGCTGCTTAAAGTATTACACACTTTAGTAGTCGGGATTAATCGTGC 2084
Db 2019 AACTAACATATATGCTGCTGCTTAAAGTATTACACACTTTTGTAGTAGTACCTCGGATCGTTC 2078
Qy 2085 AAAACAAATGCTGCAATTTACATGCGCCACCAAGATTTCTGGTCTGCAATCATTCGGTGT 2144
Db 2079 TGAACCAATTTGCAATTTGCAATGCGCCACCAAGGCTTCCGTTCAAAATCAAAATGTTGT 2138
Qy 2145 GAAGGTACCCAAAGGAATAGT- - -AAGTTGCGAGACTTACAGGTTCTAGAGTATGTAG 2200
Db 2139 CAAGGTACCAAAAGGAATATGTAATAAAAAAATCGACTTACAAATATTTGAGGTAGTGG 2198
Qy 2201 ATATCAGCGGACAGTAGTAGAGCAATCAAGAGCTTGGGGCAGTTAAGCAAGTTGAGGA 2260
Db 2199 ATATTAGAAGGACTAGCAGTAGAGCAATCAAGAGTTGGGGCAGTTAAGCAAGCTGAGGA 2258

Qy 2261 AATTAGCTGTGATTAACAAAGGCTCGACAAAGGAAAAATGTAAGATACTTTATGACGCA 2320
Db 2259 AATTATGTGTGGTAAACAAAGGATCCACAAAGGAAAAATGTGAGATACTCTTATACAGCTA 2318
Qy 2321 TTGAGAAGCTCTCTTCCCTCCAAATCTCTATATGAATGCTGCGGTTATATACAGATATTG 2380
Db 2319 TCCAGAAGCTCTGTTTCTTCCATCTCTCCATGTGAATGCTGTGGGATTTTCAGGTATTG 2378
Qy 2381 AAACACATGTAGTGCCTAGATTTCTATTTTATCTCTCTCTCCCTACTGAGGACACTCGGCT 2440
Db 2379 GAACACATTCAGTGTATGATTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438
Qy 2441 TGAATGGAAGTCTTGAAGAGATGCTTAACCTGGAATGAGCAGCTCACTCACCTGAAGAAGT 2500
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Qy 2501 TCAACTTATGAGGATGATTAACCTAAAGGAAGTAAAAATCATGCTGATACTTTGGGGCAGTGC 2560
Db 2499 TCAACTTATGAGGAGCAAACTAAAGGAAGTAAAAATCATGCTGATCTTTGCTGCGGCTTGC 2558
Qy 2561 CCAACCTCATGTTCTCTCTTTTATCATTAATTTCTTCTTGGGGAAGCTAGTATTCA 2620
Db 2559 CCAACCTCATGTTCTCTTTTATCTTCAATGCTTACCATGGGGAAGCTAGTATTCA 2618
Qy 2621 AAACGGGAGCATTCCTCCAAATCTTAGAACACATTTGTGATTTTCAATTTGGATCAGCTAAGAG 2680
Db 2619 AAATGGGAGCATTCCTCCAAATCTTAGAACATTTTCGATTTACAAATTTGGAGCAGCTAAGAG 2678
Qy 2681 AGATCAGATTTGAGGACGGCAGCTCACCCAGTTGGAAAAAGATAGAAATCTCTTTGCTGCA 2740
Db 2679 AGATTAGATTTGAGGACGGCAGCTCAATCTTTGTTGAAAAAGATAGAAATATTCAG- - -G 2734
Qy 2741 GGTGGGAATCAGGATTTATTTGGTATCATTCACCTTCCAGGCTCAAGGATTTCACTTG 2800
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Qy 2801 AATCAAAAGTAAAGTGGCTAGGCTTGGTCACTGAGTGAAGGGAAGTGAACACACACCAA 2860
Db 2795 GATACGGAAGTAAAGTGGCTAGGCTTGGTCACTGAGGGAAGTGGCACACACCAA 2854
Qy 2861 ATGCCCCGCTGCTGCAATGGAAGTGAAGTGAAGGGAATCAGACCTGGGGGCTGAAGCG 2920
Db 2855 ATCAACCCGCTGCTGCAATGAGGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2914
Qy 2921 AAGGATCTTCTATAGAGTGCACACACAGATCTCTGT 2957
Db 2915 AAGGATCTTCTATAGAGTGCACACACAGATCTCTGT 2951

RESULT 12

US-10-352-179-84
; Sequence 84, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2940)
; OTHER INFORMATION:

US-10-352-179-84

Query Match 50.7%; Score 1571.8; DB 17; Length 2940;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 2098; Conservative 0; Mismatches 812; Indels 9; Gaps 3;

Qy	1	ATGGCGGAGCGGTCTGAGCATGCGGAGTGGCTGGTGGGCGAGTGCATCAGCAAGGCC	60
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Qy	61	GCCTCTGCGCGTGCCTAATGACAGCAGCCTCTGCTCGGCGTGCAGAGGAGCATCTGGTAT	120
Db			
Qy	61	GCCTCGCGCGCGGACGAGGCCACCTCTGCTCGGCGTCCAGAGGAGATCTGGTAC	120
Db			
Qy	121	ATCAAGATGAGCTAAACAAATCAGCAGCTTCCTTAGAGCTGCTGTAAGTTATGAAAAG	180
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Qy	121	ATCAAGGACGAGCTGAAAACCTATTTCAGGCAATCTTAAGAGCTGCTGAAGTAACAAAG	180
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Qy	181	AAAGATGAACTATTAAAGGTTTGGGCGAGAGCAATACGTGACCTGCTGATGACATTTGAA	240
Db			
Qy	181	AAAGATGAACTTTGCTAAAGGTTATGGGCGAGAGCAAGTACGAGATCTGTCATATAACATTTGA	240
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Qy	241	GATTCCCTTGATGAATTTAAAGTCCATATTGAAAGCCAAACCTATTTCGTGAGTGGTG	300
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Qy	241	GATTGCTAGACGAATTCAGGTTTCATGTTGAGAGCCAAAGCTTGGCAAGCAACTAATG	300
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Qy	301	AAACTTAGAGAGCGCCACCGGATCGCTATCCGTTATCCACCAACCTCAAATCAAGAGTTGAA	360
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Qy	361	GAAGTGAAGTACGAGAACACAGCTACAGCTTAAATCAAGCTCATTTCCCTCTATTAACACA	420
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Qy	418	GAGGATGACATGGAATTCCTATGACAGAGACATTCGCAATCAATCAGCTCGAATGTCGAT	477
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Qy	421	GAGGATGAGAGGGAATTCCTACTAGAGATGCTCGCAATCATGATGAGTACCACTGAC	480
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Qy	478	GAAGCTGAGCTTGTGGGTTTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATACC	537
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Qy	481	GAGTCAGAACTTGTGGGCTTTGCCAAGACTAAAGATGAGTTGCTTTAACTGATAGATGC	540
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Qy	541	AATACTAATGACGCTCCAGCTTAAAGTGTATGTGTGTTGGAATGGGTGGATTAGGCAAG	600
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Qy	598	ACAGCTCTTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAGACATTCCTCTGC	657
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Qy	601	ACTACCTTTGCAAGGAGGCGATATGAAACCAAGGAACACAT---GAAGAACTTCTCGTGT	657
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Qy	658	AATCTTTGGATTACAGTGTCACAATCAATTTCAAGGATTTAGCTACTTAAAGATATGATA	717
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Qy	778	GTGGTGAAGTACATCATCTTCTGAGTACCTGATAGAGGCTCAAGGAGAGAGGTAC	837
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Qy	898	TTTCTTAAGAACAAATAAGAGGCGAGTGAATAGTAATAACCACTCGGAAATGTTTGAATCTA	957
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Qy	958	GCGGAGAAAGTGGCAACAGCCTCACTGGTGTACCACTTGTATTTCTTCTGAGATGAACGAT	1017
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Qy	958	GCTGGAAGGTGTACCTCTGAAATCACTTATTTTACCACCTTGAACCGGTTACATATAGATGAT	1017
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Qy	1018	GCCATTTTCATTGCTCTGAGAGAAAACAAATATAAATCATGAGACATGGAATCAAAATAAA	1077
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Qy	1138	CTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTAGAAATGGGAGAAATTTCTATGAA	1197
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Qy	1138	CTCAATAGGAGCACTTCTTGCTTACTAAGAGATAAATGGAATGGGAAAATTTTACAGA	1197
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Qy	1258	CTAGTTTACAACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTT	1317
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Qy	1258	CTAAGCTACAATCACTTACCATCTCATCTTAAACCATGCTTTTCTTTACCTAAGTATTTTC	1317
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Qy	1318	CCTGAGGATTTTGAATACAAAGGAATCGTCTAGTAGTAGATGATGATGATGATGATGATGATG	1377
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Qy	1318	CCTGAAGATTTTGAATTTCAAAGAGGGGCTGCTGATAGATAGATAGATAGATAGATAGATAG	1377
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Qy	1378	GTGAGGCCACAGATGGGTGAAACATTTAGGATGTTGGAATAGTCACTTTAATGAGCTT	1437
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Qy	1558	CTGTTGACTAGGGAAGAAGTCACTGTTGTAGCGGAGGAGAGCATCCGCCACTAGCATTT	1617
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Qy	1618	CATGGGAGTATGCTCTGCAAAAACAGGATTTGGATTTGGAGGACATTTTCAATTTAGCTATT	1677
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Qy	1678	TTTGGTCACAGACCAAGAGTCTAGACATGTCAGTGTGTCAGATCAATTTAGGAGATGTTA	1737
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Qy	1738	CGGTCTTTGGATCTTGAAGATGTGACATTTCTAATCACTCAAAAAGATTTTCGACCGTATT	1797
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Qy	1738	AGAGTGTGGATCTCGGAAGATGCAAAATTCAAATTTCAACAAAATGATATCAGGAATATA	1797
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Qy	1798	GCATTTGTTGCCACTTGAATACTTCAGTATTTGGATATTCGTTCATCCATATATTCACCT	1857
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Qy	1858	CCAGATCCATTTGTTAAACTACAGGGCTACAGACTTTGAAACATGTCAAGCACATACAT	1917
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Qy	1918	GCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATCTCTTCTGTTGTATAGA	1977
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Qy	1978	GAGTCTGAATTTGACAACTTTTAGTCTAA---ATCACCCAATGAAGTGATTAACACACA	2034
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Qy	2035	ATATGCTGCTTAAAGTATTTCAACCTTTAGTGTAGTCGCGATATTCGTGCAAAACAAAT	2094
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Qy	2038	ATGTGCTTACCGATGGTTTTCTCAACTTCAATAAAATTTCAAGTGTGAGGATTAAT	2097
Db			


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Qy 2095 GCTGAATTTTCATGCGCCACCAAAAGTTTCTGGTCTGAATCATTCGGTGTGAAGGTACCC 2154
Db 2098 CCTGAGATATGATGTCATGTTCTACCCGTTGGTCTGATACAAAGGGTGTGAGGGTGCCA 2157
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Db 2158 AGAGGAATGACAAACCTAAAGAGTTACAGATTCTAGAAAGTCGTGGACATCAACAGAACT 2217
Qy 2215 AGTAGTAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGTTTGAGAAATTAAGCTGTGATA 2274
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Qy 2515 AGTAACTAAAGGAAGGTAAAGACATGCTGATACCTTGGGGACCTGCCCACTCATGTTTC 2574
Db 2518 TGTGTGCTACAAAGATGGTAAACTATGAGATACCTTGGGGCACTGCCCACTTATGGTT 2577
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Qy 2695 GAGGAGCTCAACCCAGTTGGAAGAAAGATAGAAATCTCTGCTCAGGTTGGAATCAGGG 2754
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Qy 2755 ATATTGCTATCACTTCAAGCTCAAGGCTCAAGGAGATTTCACTTTGAATACAAAGTAAA 2814
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Qy 2875 CGAATGACAGTGACCGAAGGAGTACAGACCTGGGGCT 2913
Db 2878 CAAATGCGAGGATCGAAGTCAATCATGACCTAGGAGT 2916
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RESULT 13
US-10-437-963-41016
; Sequence 41016, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41016
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1
US-10-437-963-41016

Query Match      50.6%; Score 1566.6; DB 18; Length 2925;
Best Local Similarity 71.8%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 814; Indels 9; Gaps 3;

Qy 3 GGGCGAGACGGTGTGAGCATGGCGAGTGCCTGGTGGGAGTCCCATCAGCAAGGCGC 62
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Db 66 CTCGCGCGCCGCGAGGCGCCCTCTGCTCGGCATCCAGAAAGGAGATCTGGTACAT 125
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Db 126 CAAGGACGAGCTGAAAACTATTTCAGGCATTTCTTAAGAGCTGCTGAAGGTAAACAAAGAA 185
Qy 183 AGATGAATTAAGGCTTTGGGCGAGGCAAAATACGTGACCTGCTGATGACATTTGAAGA 242
Db 186 AGATGACTTGTAAAGTATGGGCGAGGCAAGTACGAGATCTGTCATATATCAATTTGAAGA 245
Qy 243 TTCCCTTGATGAATTTAAAGTCCATATTGAAAGCAAAACCTATTTCGTCAGTTGGTGAA 302
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Qy 303 ACTTAGAGAGCGCACCGGATTCGCTATCCGATCCACAACCTCAAAATCAAGAGTTGAAGA 362
Db 306 GCTTGGTGAAGCGCATCGAATTTGCTGACAGATTCGCAACTTAAATAACAAGATTGAAGA 365
Qy 363 AGTGAGTAGCAGGACACACGCTTACATTTTAGTCGAGCCTATTTCCTC---CGCACAGA 419
Db 366 AGTGAGCAACAGGAATACACGCTACAGCTTAATCAAGCCCACTTCTCTATTAACACAGA 425
Qy 420 GGATGACATGGATTTCTTATGCAAGACATTCGCAATCAATCAGCTCGAATGTGGATGA 479
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Qy 480 AGCTGAGCTTTGTTGGGTTTCTGATCCAAAGAAAGGCTGCTTGAATATGATACCAA 539
Db 486 GTCAGAACTTTGTGGGCTTTGCCAAGACTTAAAGATGAGTTGCTTAAACTAGATGTCAA 545
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Db 723 GCAACTTCTGGGTGCTGATTTTCAATTAGACAAACTCTTGAAAGAAATTTAGTGAGAAAGTGTCT 782
Qy 780 GGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGACTTCT 839
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Db 843 TGTTCTCTTGATGACCTATGGACCATAGATGTCATGGAATTGGATTTCATGATATTGCTTT 902
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Qy 1140 TACAATAGAGCTGTGCTTGCACACTAAACACAGTGTCAAGTGGGAGAAATCTATGAACA 1199
Db 1143 CACAATAGAGGCATCTTGTCTACTTAAGAAGATAATGGAGTGGGAAATTTTACAGAGA 1202
Qy 1200 ACTTCTCTTTCAGAACTAGAAAATAAACCAGCTCGAAGCTTGTAGGAGAAATGGTGACCT 1259
Db 1203 ACTTCTCTTTCAGAGCTTGAAGCAATCCAGCTTAGAAGCCATGAGGAGATGGTGACCT 1262
Qy 1260 AGGTTAACACCACTTACCATCCATCTGAAACCAATGCTTTTGTATCTAAGTATCTTTCC 1319
Db 1263 AAGCTACAATCACTTACCATCTCATCTTAAACCATGCTTTCTTAACTTAACTTATTTCC 1322
Qy 1320 TGAGGATTTTCAATACAAAGGATCTGTCTAGTAGGTAGATGATAGGAGAGGTTTGT 1379
Db 1323 TGAAGATTTTGAATTTCAAGAGGGCGCTCGTAGATAGATGGAATGAGAGGTTTGT 1382
Qy 1380 TAGACCAAGGTTGGGATGACGACTAAGCATGTGCGAGAAAGTTACTTTAATGAGCTAAT 1439
Db 1383 CAGAGCCACAGATGGGGTGAACATTGAGGATGTTGGAAATAGTCACTTTAATGAGCTTAT 1442
Qy 1440 CAACGGAAGTATGATTCACCAATCAAGATGGGCAACAGAGGAAATTAAGACTTTGCG 1499
Db 1443 CAACAGAAGTCTGATTACAGCCCTCAAAAGTTAGTACAGATGGAGTTGTTAAGAGATGCG 1502
Qy 1500 AATCCATGATATCATCCGTGATATACAGTTTCAATCTCGAGACAGGAAATTTTGTAT 1559
Db 1503 AATCCATGATATCATCGCTGATATCATAGTTTCAATTTCTAGAGAGGAAATTTTGTCT 1562
Qy 1560 ATTACCAATGGAGATGGCTCTGATTTAGTTTCAAGGAAACATCGCCACATAGCATCCA 1619
Db 1563 GTTGACTAGGAGAAAGATCACTGTTGTAGCGGAGAGAGCATCCGCCATCTAGCAATTTCA 1622
Qy 1620 TGGAGTATGTCCTGCAAAACAGGATTTGGATTGGAGCAATTTATCGATCAATTAGCTATTTT 1679
Db 1623 TGGAGCAAAATGCTCAAGATATGCTTGGAGTGGAAACCATCTGCGCTCAGTAACTTTGT 1682
Qy 1680 TGGTGAACAGCCCAAGAGCTTAGCACATGCGAGTTGTCCAGATCAATTTGAGGATGTTACG 1739
Db 1683 TGGGACAGAGCTGTGGGGCGAAACCTCTGCACTTTGTTTACCACAAATTTAGGATGCTGAG 1742
Qy 1740 GGTCTTGATCTTGAAGATGTGACATCTTAATCACTCAAAAGATTTTCGACCGTATGTC 1799
Db 1743 AGTGTGGATCTGGAAGATGCAAAATTTCAATTTACACAAATGATATCAGGAATATAGG 1802
Qy 1800 ATTGTGTGCCACTTGAATATCTTGATTTGGATTTTCTCATCCATATATTTCACTTCC 1859
Db 1803 GTTGTGGCCACATGAATATTTGAATTTTGAAGAGCCTCACTATTTATACACTTCC 1862
Qy 1860 CAGATCCATTTGGTAACTTACAGGGCTTACAGACTTTGAAACATGTCAAGCAATACATTCG 1919
Db 1863 AAGTCCATAGGAAATTTGCAAGTGTGCAAAATTTTGAACATGAGGAGGCAAAATATCTC 1922
Qy 1920 AGCACTACAGTGTGATCAGTAACTTCAATGTCTGATCTTCTGTTGTATAGAGA 1979
Db 1923 AGCACTAACTAGGTGTAACTCCAAATCTCGTAGCTCCGATCGATCGAGGAG 1982

Qy 1980 CTTTGAATTTGACAACTTTAGTCTAA---ATCACCCAAATGAAGTGCATAACTTAACACAAAT 2036
Db 1983 GTCTGGTCTCTGGTTACTTTAGCATAAATAGATAAATCCCAAGGAATGCTTTGATGATCACCAT 2042
Qy 2037 ATGCTGCTTAAAGTATTACACCTTTTAGTTCGCGATTAATCGTGCNAACAAATATGC 2096
Db 2043 GTGCTTACCGATGGTTTCTTAACTTCAATAAATTTAGTGACCGCTGTGAAGTTAATTC 2102
Qy 2097 TGAATTTTCAATGCGCCACCAAAAGTTTCTGGTCTGAATCATTTGCGGTGTGAAGGTACCCAA 2156
Db 2103 TGAGATATGCGATGTCATGTTCTTACCCGTTGCTCTGATACAAAGGCTGTGAGGTCGCCAAG 2162
Qy 2157 AGGAATAGTTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGCGACAG 2216
Db 2163 AGGAATTTGACAACTTAAAGAGTTTACAGATTTCTAGAGTCTGGAACATCAACAGAACTAG 2222
Qy 2217 TAGTAGAGCAATCAAGAGCTGGGCGACTTAAGCAAGTTGAGGAAATTTAGCTGTGATTAAC 2276
Db 2223 TAGGAAGCGGATTTGAAGAGCTGGGGGAGCTAATTCAGTTAAGAAATTTAAGGCTGACAAAC 2282
Qy 2277 AAAAGGCTCGACAAAGGAAATTTAGATATCTTTATGACGCCATTTGAGAACTCTCTTTC 2336
Db 2283 AAAAGGCGCCACAAATGAAGATATCAGATATTTTGTGACGGATTTGAGAGCTCTCTTTC 2342
Qy 2337 CCTCAATCTCTCTATATGAATGCTGCGTTATTTATCAGATATTTGAAACAATTGAGTGCCT 2396
Db 2343 TCTGCAATCTCTCGCTGTGATGCTGAGGAGTTCTCAGATACTGGAACACTTTAGTGGCT 2402
Qy 2397 AGATTTCTATTTCACT 2456
Db 2403 CAATTCGATTTGCAATGCT 2462
Qy 2457 AGAGATGCTTAACTGGGATTTGAGCAGCTCACTCACCTGAAGAAAGTTTCAACTTTATGAGTAG 2516
Db 2463 AGATACACCAAACTGGTTTGGGAACCTTTAGCAGCTGTGGAAGATGCTTTATCCAGATG 2522
Qy 2517 TAAACTAAGGAAGGTAAAAACATGCTGATATCTTGGGGCACTGCCCCAACCTCATGTTCT 2576
Db 2523 TGGGCTAAAGATGTTAAACCTATGGAGATATCTTGGGGCACTGCCCCAACCTTATGTTCT 2582
Qy 2577 TTCTCTTTATCATATTTCTTTATCTTGGGGAAGCTAGTATTTCAAAACGGGAGCAATCCC 2636
Db 2583 TCGTCTTTATCGCAACGCATATGCTGACGAGAAATGACATTTCAAGAGGGGAACATCCC 2642
Qy 2637 AAATCTTAGAACACTTGTGATTTTCAATTTTGGATCAGCTAAGAGAGATCAGATTTGAGGA 2696
Db 2643 AAATCTCAGGTCTTGTATTTTACTTGTCTGAAGCACTTAGAGAGATGAATTTGAGGA 2702
Qy 2697 CGGAGCTTCACTCCAGTTTGGAAAAAGATAGAAATCTTTGCTGACAGTTTGGAAATCAGGAT 2756
Db 2703 GGGCACCTCGCAACGATGGAAAGTATAGAAATTTATGTTTGCAGTTTGGAAATCAGGAT 2762
Qy 2757 TATTGGTATCATTTCACTTCCAGGCTCAAGGAGATTTCACTTGNATACAAAGTAAAGT 2816
Db 2763 TATTGGTATCAAGCACTTCCAAAGCTTAAAGTATTTTTCGTTTGAATATGATGTTAAAGT 2822
Qy 2817 GGCTAGGCTTGGTCAAGCTGGAAGGAGAGTGAACACACACCAATGCCCGCTGCTCG 2876
Db 2823 CGGAGAGCTTGTGCTGCAAGAGAGTGAATACACACCCCAATCATCTGAATTCGA 2882
Qy 2877 AATGACAGTGAACCGAAGGATTCAGACCTTGGGGCT 2913
Db 2883 AATGGCAGAGATCGAAGTCAATCATGACCTAGGAGGT 2919

RESULT 14

US-10-656-394A-1

; Sequence 1, Application US/10656394A

; Publication No. US20040210957A1

; GENERAL INFORMATION:

; APPLICANT: Wang et al.

; TITLE OF INVENTION: Cloning and Characterization of the

; TITLE OF INVENTION: broad-spectrum resistance gene P12

; FILE REFERENCE: 035718/252062

; CURRENT APPLICATION NUMBER: US/10/656.394A

; CURRENT FILING DATE: 2003-09-05

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2982

; TYPE: DNA

; ORGANISM: Oryza minuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2982)

us-10-656-394A-1

Query Match 50.4%; Score 1563; DB 18; Length 2982;

Best Local Similarity 71.7%; Pred. No. 0;

Matches 2091; Conservative 0; Mismatches 815; Indels 9; Gaps 3;

Qy	3	GGCGGAGACGGTCTGAGCATGGCGAGTCTGGTGGCGAGTGCCTATCAGCAAGGCGCG	62
Db	6	GGCGGAGACGGTCTGAGCATGGCGAGTCTGGTGGCGAGTGCCTATCAGCAAGGCGCG	65
Qy	63	CTCTGCGCGTCCGAATGAGAGAGCGCTCTGCTCGGCGTGCAGAAAGACATCTGGTATAT	122
Db	66	CTCGCGCGCGCGGACGAGGCCACCTCTGCTCGGCATCCAGAAAGGAGATCTGGTACAT	125
Qy	123	CAAAAGATGAGCTAAACAACTGAGGAGTTCCTTAGAGCTGCTCAAGTTATGAAAAGAA	182
Db	126	CAAGGAGAGCTGAAACTATTTCAGGCAATCTTAAAGAGCTGCTGAAGTAAACAAAGAA	185
Qy	183	AGATGAACCTATTAAAGGTTTGGGCGAGCAAAATACGTGACCTCTGCTATGACATTTGA	242
Db	186	AGATGACTTGTAAAGGTTTGGGCGAGCAAGTACGAGATCTGTCATATAACATTTGA	245
Qy	243	TTCCCTTGATGAATTTAAAGTCCATATGAAAGCCAAACCTATTTCTGATGTTGGTGAA	302
Db	246	TTGCCTAGACGAATTCAGAGTTTCATGTTGAGGCGCAAGCTTGGCAAGCAACTAAATGA	305
Qy	303	ACTTAGAGAGCGCACCGGATCGTATCCGATATCCAACTCAAACTCAAGTCAAGTTGA	362
Db	306	GCTTGGTGAAGCGCCATCGAATTTGCTGACAGATTCGCAACTTAAATCAAGAAATTTGA	365
Qy	363	AGTGAGTAGCAGGAAACACAGCTACAATTTAGTCGAGCTATTTCCTC---CGGCACAGA	419
Db	366	AGTGAGCAA CAGGAATACACGCTACAGCTTAATCAAGCCCAATTCCTCTATAACCAAGA	425
Qy	420	GGATGACATGGATTCCTATGACAGAGACATTCGCAATCAATCAGCTCGAAATGGAATGA	479
Db	426	GGATGAGAGGGAATTCCTACCTAGAAAGATGCTCGCAATCGATCAGGTAGCAACACTGACGA	485
Qy	480	AGCTGAGCTTTGGGTTTCTGACTCCAGAAAGGCTGCTTGAATGATCGATACCA	539
Db	486	GTCAAGAACTTTGGGGCTTTGCCAAGCTAAAGATGAGTTGCTTAAACTGATAGATGCA	545
Qy	540	TGCTTAATGATGTCGCGCAGGTAATCTGTGTTGGTGGATGGTGGTTTAGGCAAGAC	599
Db	546	TACTAATGACGGTCCAGCTAAAGTATGATGTGTTGGTATGGGTGGATTTAGGCAAGAC	605
Qy	600	AGCTCTTTTCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTCGAA	659
Db	606	TACCCTTGCAAGGAAGCATATGAAACCAAGGAACACAT---GAAGAACTTCTCGTGTG	662
Qy	660	TGCTTGATACAGTGTCAACATCATTTTCACAGATTTGAGTACTTAAAGATATGATACG	719
Db	663	TGCTTGATACAGTGTGTCTGATCATTTTGAAGGAAAGAAATCTGAAACAAATGATCAG	722
Qy	720	CCAACTTCTTGGTCCCGAGTCTCTGGATCAACTCTTCGATGAATTTGCAAGGAGGTTGGT	779
Db	723	GCAACTTCTGGGTGCTGATTCATTTAGCAAACTCTTGAAGAAATTTAGTGAGAAAGTTGCT	782
Qy	780	GGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAAGCTCAAGGAGAGGATCTT	839

Db	783	CGTCAAGTCCAGCATCTCGCTGATCACTTGGTTGAAGGGCTAAAGGAGAAAAAGTACTT	842
Qy	840	TGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATAAATGGAATTTGCATT	899
Db	843	TGTTGTTCTTGTATGACCTATGGACCATAGATGCAATGGATTTGGAATTCATGATATTTGCTTT	902
Qy	900	TCCTAAGAACAAATAAGAGGCGAGTTCGAATAGTAAATAAACCACTCGGAATTTGATCTAGC	959
Db	903	TCCGAGATTAAACAAACAGAGGTAGTCGCATAAATAAACAACGCGAGATGCTGGCTTAGC	962
Qy	960	GGAGAAGTGTGCCACAGCCTCAGCTGTTGACCATCTGATTTCTTGCAGATGAAGATGC	1019
Db	963	TGGAAGGTGACCTCTGAATCACTTATTACCACTTTGAACCGTTACATATAGATAGTC	1022
Qy	1020	CATTTCAATGCTACTGAGAAAAACAAATAAAATCATGAACATGGAATCAAAATAAAAA	1079
Db	1023	TATACACTTGTCTCTAGCAAGACAAACATAGACTTTGAAGACATGGAATAATGATGAGGA	1082
Qy	1080	TATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTGGTCTGTACCATTTAGCAATACT	1139
Db	1083	CTTGGCGAGCATAGTTACAAAAATTTGGTGAAGAGTGTGTTATTTACCGCTGGCTATACT	1142
Qy	1140	TACATAGGAGCTGTGTTGCACTAAACAGGTGTCAAGATGGAGAAATTTCTATGAACA	1199
Db	1143	CACAAATAGGAGGCAATCTTGTCTACTAAGAAATATGGAGTGGGGAATAATTTACAGAGA	1202
Qy	1200	ACTTCTTCAGAACTAGAAATAAACCAAGCTCGAAAGCTTTGAGGAGAAATGGTGACCT	1259
Db	1203	ACTTCTTCAGAGCTTGAGAGCAATCCAGCCTTAGAAGCCATGAGGAGATTTGGTGACCT	1262
Qy	1260	AGGTTACAACACCTACCTCCATCTGTAACCAATGCTTTTGTATCTAAGATCTTTTCC	1319
Db	1263	AAGCTACAATCACTTACCATCTCATCTTAAACCATGCTTCTTTTACCTAAGTATTTTCCC	1322
Qy	1320	TGAGGATTTTGAATAAAGGAATCTGTATAGTGTAGATGATGATGAGAGAGGTTTGT	1379
Db	1323	TGAAGATTTTGAATTTCAAGAGGGCGCTGGTAGATAGATGGAATGAGAGGTTTGT	1382
Qy	1380	TAGACCAAGAGTTGGGATGACGCTAAGGATGTCGGAGAAAGTTACTTTAATGAGCTAAT	1439
Db	1383	CAGAGCCACAGATGGGTTGAACATTTGAGGATTTTGGAAATAGTCACTTTAATGAGCTTAT	1442
Qy	1440	CAACCGAAGTATGATTCACCGATCAAGAGTGGGCGACAGCAGGAAAAAATTAAGACTTTGCG	1499
Db	1443	CAACAGAGTCTGATTCAGCCCTCAAAAGTTAGTACAGATGGAGTTGTTAAGAGATGTCG	1502
Qy	1500	AATCCATGATATCATCGTGATATCAAGTTTCACTCTCGAGACAGGAAAAATTTTGTATT	1559
Db	1503	AATCCATGATATCATCGTGATATCATAGTTTCAATTTCTAGAGAGGAAAAATTTTGTGCT	1562
Qy	1560	ATTACCAATCGGAGATGGCTCTGATTTAGTTTCAGAAAAACACTGCCACATAGCATTTCCA	1619
Db	1563	GTGACTAGGAGAGATCACTGTTGTAGCGGAGGAGAGATCCGCCATCTAGCAATTTCA	1622
Qy	1620	TGGAGTATGCTCTGCAAAAACAGGATTTGGATTTGGAGCAITTAATTCGATCATTTAGCTATTTT	1679
Db	1623	TGGAGCAATGCTCAAGATATGCTTTGGAGTGGAACCACTCTGCGCTCAGTAACTTTGTT	1682
Qy	1680	TGGTGACAGACCCAGAGTCTAGCAATGCAAGTTTGTCTCAGATCAATTTAGGAGATGTTACG	1739
Db	1683	TGGCGACAGACCTGTGGGGGCAACACCTGCACCTTTGTTTCCACCAAAATTTAGGATGCTGAG	1742
Qy	1740	GGTCTTGGATCTTGAAGATGTCATCTTAAATCACTCAAAAGATTTCCGACCTTATGTC	1799
Db	1743	AGTGTGGATCTGGAAGATGCAAAATTCAAATTCACAAATAATGATTCAGAAATATAGG	1802
Qy	1800	ATTGTTGTGCACTTGAATACTTTGATTTTGGATTTTGGATATTCGTCATCCATATATTCACCTTC	1859
Db	1803	GTTGTTGCGCCACATGAATAATTTGAATTTTGAAGAGCTCAACTATTTATACACTTCC	1862
Qy	1860	CAGATCAATTTGGTAAACTACAGGCGCTTACAGACTTTGAAACATGTCAAGACATACATTCG	1919
Db	1863	AAGTCCATAGGAAAAATTCAGTGTGCTTGCATAATTTTGAACATGAGGGAGGCAATATCTC	1922

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Qy 1920 AGCACTACCAAGTGAGATCAGTAACCTCAATGCTCGCATACTCTTGGTTGTATAAGAGA 1979
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1923 AGCACTAACAACTGAGGTGACTAAACTCCGAATCTCGTAGCCTCCGATCGACGAGAG 1982
Qy 1980 GCTTGAATTTGCACAACTTTAGTCTAA--ATCACCCCAATGAAGTGCATACTACACAAAT 2036
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1983 GTCTGGTTCCTGGTTACTTTTACATATAGATAAATCCCAAGGAATGCTTGATGATCACCAT 2042
Qy 2037 ATGCTGCTTAAAGTATTACACACCTTTAGTTAGTCGGGATAATCGTGCMAAACAAATTCG 2096
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2043 GTGCTTACCGATGGTTTCTTAACTTCAATAAATTCAGTGCACGCTGGAAGTTAAATTC 2102
Qy 2097 TGAATTTACATGGCCACCAAAAGTTTCTGTGCTGAATCATTCGGTGTGAAGGTACCCAA 2156
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2103 TGAGATATGCATGTCTGTTCTTACCCGTTGCTGTGATACAAAGGCTGTGAGGGTGCCAA 2162
Qy 2157 AGGAATAGGTAAAGTTCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGCGGACCG 2216
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2163 AGGAATTGACAACTAAAGAGTTTACAGATTCTAGAAGTCGTGACATCAACAGAACTAG 2222
Qy 2217 TAGTAGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTAGCTGTGATAAC 2276
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2223 TAGGAAGCGGATGAGAGCTGGGGAGCTAAATTCAGTTAAGAAATTTAGCGTGCACAC 2282
Qy 2277 AAAAGGCTCGCAAAAGGAAAAATGTAAAGATCTTTATGACGCCATTGAGAAAGCTCTCTTC 2336
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2283 AAAAGGCGCCACAAATAAGAAAGTATCAGATATTTGTGCAGCGATTGAGAAAGCTCTCTTC 2342
Qy 2337 CCTCAATCTCTATATGANTGCTGCGTTATATCAGATATTGAACACATTGAGTGCCT 2396
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2343 TCTGCAATCTCTCCGTGTGGATGTGAGGGATTTCTCAGATACCTGGAACACTTGTAGTGGCT 2402
Qy 2397 AGATTCTATTTCATCTCTCTCCCTACTCAGGACACTCGGGTTGAATGGAAGCTTTGA 2456
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2403 CAATTCGATTCGATGCTCTCTCTCATCTTGAAGAGACTGAATGGAATGGAATCTCTTC 2462
Qy 2457 AGAGATGCTTAATCGGATTGAGCAGCTCACTCAGTGAAGAGTTTCAACTTATGGAGTAG 2516
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2463 AGATACACCAAACTGGTTTGGGAACCTTAAGCAGCTGGTGAAGATGTGCTTTATCCAGATG 2522
Qy 2517 TAAACTAAGGAAGGTAAACATGCTGATACTTGGGGCACTGGCCCAACCTCATGTTCT 2576
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2523 TGGGCTTAAAGATGGTAAACCTATGGAGATACTTGGGGCACTGGCCCAACCTTATGGTTCT 2582
Qy 2577 TTCTCTTTATCAATAATCTTATCTTGGGGGAAGCTAGTATTCAAAAGCGGAGCAATCCC 2636
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2583 TCGTCTTTATCGCAACGGATATGCTGACGAGAAATGACATTCAGAGGGGNACTTTCCC 2642
Qy 2637 AAATCTTAGAACACTTGTGATTTTCAATTTTGGATCAGCTAAGAGAGATCAGATTTGAGGA 2696
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2643 AAATCTCAGGTGCTTGTGATTTTACTTGTCTGAAGCACTTAGAGAGATAAGATTTGAGGA 2702
Qy 2697 CGGAGCTCACCCAGTTGGAAAGATAGAAATCTTGTGCTGAGGTTGGAATCAGGGAT 2756
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2703 GGGCACCCTCGCAACGATGGAAGTATAGAAATTTATGGTTGCAAGTTGGAATCAGGGAT 2762
Qy 2757 TATTGGTATCATTCACCTTCCAGGCTCAAGGAGATTTCACTTCAATACAAAGTAAAGT 2816
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2763 TATTGGTATCAAGCACCTTCCAGACTTTAAGATTTATTTTCGTTGAATATGATGATGAAGT 2822
Qy 2817 GGCTAGGCTTGGTCAAGTGAAGGGAGAGTGAACACACACACCCCAATCGCCCGTGCAG 2876
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2823 CGCGNAGCTTGATGTGCTGCAAGAGAGAGTGAATACACACCCCAATCATACTGAATTGCA 2882
Qy 2877 AATGACAGTGAACGAGGGATTCAGACCTGGGG 2911
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2883 AATGCGAGAGGATCGAAGTCAATCATGACCTAGGAG 2917
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RESULT 15

US-10-656-394A-15

; Sequence 15, Application US/10656394A

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; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2422
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2014, 2043, 2099, 2114, 2154, 2172, 2178, 2199, 2205, 2226,
; LOCATION: 2268, 2299, 2333, 2337, 2339, 2356
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-15
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Query Match 48.1%; Score 1491.4; DB 18; Length 2422;

Best Local Similarity 95.0%; Pred. No. 0;

Matches 1540; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

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Dy 1 AGGAAAAATTAAGACTTTGTCCGAATTCATGATATCATCCGTGATATCAGATTTCAATCTC 60
Qy 1539 GAGACAGAAAAATTTTGTATATTATTAACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAA 1598
Dy 61 GAGACAGAAAAATTTTGTATATTATTAACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAA 120
Qy 1599 CACTCGCCACATAGACTTCATATGGGAGTATGTCTCTGCAAAACAGGATTTGGAGCAT 1658
Dy 121 CACTCGCCACATAGACTTCATATGGGAGTATGTCTCTGCAAAACAGGATTTGGAGCAT 180
Qy 1659 TATTTCGATCAATTAGCTATTTTGGTGAACAGACCCCAAGAGTCTAGCACATGCAGTTTGTCC 1718
Dy 181 TATTTCGATCAATTAGCTATTTTGGTGAACAGACCCCAAGAGTCTAGCACATGCAGTTTGTCC 240
Qy 1719 AGATCAATTGAGGATGTTCAGGCTCTTGGATCTTTGAAGATGTGACATTTTAATCACTCA 1778
Dy 241 AGATCAATTGAGGATGTTCAGGCTCTTGGATCTTTGAAGATGTGACATTTTAATCACTCA 300
Qy 1779 AAAAGATTTTCACCGTATTCGATTTGTGTCACCTTGAAATACCTTGAGTATTTGGATATTC 1838
Dy 301 AAAAGATTTTCACCGTATTCGATTTGTGTCACCTTTGAATACCTTGAGTATTTGGATATTC 360
Qy 1839 GTCATCCATATATTCACTTCCCAGATCCATTTGGTAAACTACAGGGCCCTACAGACTTTGAA 1898
Dy 361 GTCATCCATATATTCACTTCCCAGATCCATTTGGTAAACTACAGGGCCCTACAGACTTTGAA 420
Qy 1899 CATGTCAAGCACATACATTTGCAGCACTACCAAGTGAGATCAGTAAATCTCCAATGCTGCA 1958
Dy 421 CATGCCGAGCACATACATTTGCAGCACTACCAAGTGAGATCAGTAAATCTCCAATGCTGCA 480
Qy 1959 TACTCTTGGTTGTATAGAGAGCTTGAATTTTGACAACTTTAGTCTTAATCAACCCCAATGAA 2018
Dy 481 TACTCTTGGTTGTATAGAGAGCTTGAATTTTGACAACTTTAGTCTTAATCAACCCCAATGAA 540
Qy 2019 GTGCATAAATAACACAAATATGCTGCTTAAAGTATTTCACACCTTTAGTTCGCGATAA 2078
Dy 541 GTGCATAAATAACACAAATATGCTGCTTAAAGTATTTCACACCTTTAGTTCGCGATGA 600
Qy 2079 TCGTGCAAAAACAAATTCGCTGAAATTTTCATGGCCACCAAAAGATTTCTGGTCTGAATCAT 2138
Dy 601 TCGTGCAAAAACAAATTCGCTGAAATTTTCATGGCCACCAAAAGATTTCTGGTCTGAATCAT 660
Qy 2139 CGGTGTGAAGGTACCCAAAGGATAGCTTAAGTTGCGGAGACTTACAGGTCTAGAGTAGT 2198
Dy 661 CGGTGTGAAGGTACCCAAAGGATAGCTTAAGTTGCGGAGACTTACAGGTCTAGAGTAGT 720
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:34:07 ; Search time 109.873 Seconds
(without alignments)
3632.700 Million cell updates/sec

Title: US-10-656-394A-4

Perfect score: 5255

Sequence: 1 MAFVLMSARSLVGSIAISKA.....SQVITLTNDSEIGTAQAG 1032

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	4997	95.1	1031	8	ADI57172
3	4966.5	94.5	1091	8	ADI57176
4	4906	93.4	1032	8	ADM72245
5	4140	78.8	998	8	ADM72249
6	3064	58.3	993	8	ADM72239
7	3055.5	58.1	979	8	ADI57168
8	2595	49.4	993	8	ADI57170
9	2427	46.2	1054	8	ADI57174
10	2134.5	40.6	660	8	ADM72243
11	1389	26.4	451	8	ADI57178
12	1191	22.7	1251	3	AAI93135
13	1100	20.9	1205	3	AAI94934
14	1100	20.9	1205	8	ADM72280
15	1041.5	19.8	953	3	AAI58854
16	919.5	17.5	901	2	AAW80251
17	919.5	17.5	901	2	AAI01965
18	919.5	17.5	901	3	AAI81925
19	918.5	17.5	901	2	AAI01966
20	918.5	17.5	901	3	AAI81926
21	908.5	17.3	961	4	ABB06869
22	908	17.3	949	4	ABB06876
23	907.5	17.3	961	4	ABB06871
24	903	17.2	967	4	ABB06878
25	902.5	17.2	961	4	ABB06870

26	899.5	17.1	958	4	ABB06875	Abb06875	Mia1 prot
27	874.5	16.6	943	4	ABB06877	Abb06877	Rghlbed p
28	868.5	16.5	956	4	ABB06874	Abb06874	Mia6 prot
29	853.5	16.2	939	4	ABB06879	Abb06879	Rghle/f p
30	824.5	15.7	945	4	ABB06873	Abb06873	Barley M1
31	824.5	15.7	2827	7	ADC08012	Adc08012	Rice prot
32	816	15.5	922	4	ABB06872	Abb06872	Barley M1
33	739.5	14.1	1471	8	ADI45353	Adi45353	Rice isop
34	715	13.6	937	4	AAU02144	Aau02144	Rx 28, mo
35	710.5	13.5	937	4	AAU02149	Aau02149	Rx 32, mo
36	710	13.5	937	2	AAV52152	Aay52152	Potato re
37	707	13.5	937	4	AAU02143	Aau02143	Rx 25, mo
38	707	13.5	938	3	AAI45004	Aay45004	Protein e
39	706	13.4	937	4	AAU02145	Aau02145	Rx 72, mo
40	704	13.4	937	4	AAU02146	Aau02146	Rx 39, mo
41	703.5	13.4	912	3	AAI44818	Aay44818	Potato Gp
42	700	13.3	937	4	AAU02148	Aau02148	Rx 7, mod
43	698.5	13.3	1003	8	ADK98521	Adk98521	S Bulboca
44	696	13.2	937	4	AAU02147	Aau02147	Rx 193, m
45	695.5	13.2	861	6	AAE30349	Aae30349	Tomato Tm

ALIGNMENTS

RESULT 1
ADM72241
ID ADM72241 standard; protein; 1032 AA.

XX
AC ADM72241;

XX
DT 03-JUN-2004 (first entry)

XX
DE O. minuta NBS2 polypeptide.

XX
KW P12; NBS2; plant protectant; gene therapy; rice; disease resistance.

XX
OS Oryza minuta.

XX
PN WO2004022715-A2.

XX
PD 18-MAR-2004.

XX
PF 08-SEP-2003; 2003WO-US027913.

XX
PR 09-SEP-2002; 2002US-0409216P.

XX
PR 18-MAR-2003; 2003US-0455713P.

XX
PR 05-SEP-2003; 2003US-00656394.

XX
(OHIS) UNIV OHIO STATE.

XX
Wang G;

XX
WPI; 2004-257576/24.

XX
N-PSDB; ADM72240.

XX
PT New rice P12-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.

XX
PS Claim 1; SEQ ID NO 4; 120pp; English.

XX
CC The invention relates to novel broad-spectrum resistance gene P12 and the NBS(1-6) genes present in the P12 gene cluster region. The rice P12-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS2 polypeptide.

XX
SQ Sequence 1032 AA;

Query Match 100.0%; Score 5255; DB 8; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MAETVLSMARSLVGSATSKAASAAANETSLLGVGEKDIWIYKDELKTMOAFLRAAEVMMK 60
DB 1 MAETVLSMARSLVGSATSKAASAAANETSLLGVGEKDIWIYKDELKTMOAFLRAAEVMMK 60
QY 61 KBELLKVAEQIRDLSYDIEDSLDEFKVIHIESOTLPQLVKLRERHRIAIRIHNLSRVE 120
DB 61 KBELLKVAEQIRDLSYDIEDSLDEFKVIHIESOTLPQLVKLRERHRIAIRIHNLSRVE 120
QY 121 EVSSRNTRYNLVEPISSGTEDDDMSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDTN 180
DB 121 EVSSRNTRYNLVEPISSGTEDDDMSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDTN 180
QY 181 ANDGPAKVICVVGMGGLGKTALSRKIFESSEDIRKNFPCNAWITVSQSFHRIELKDMIR 240
DB 181 ANDGPAKVICVVGMGGLGKTALSRKIFESSEDIRKNFPCNAWITVSQSFHRIELKDMIR 240
QY 241 QLLGPSSLDQLLHELQGVVQVHLSYLIIEELKEKRYFVLDLWLHDMWNWINEIAF 300
DB 241 QLLGPSSLDQLLHELQGVVQVHLSYLIIEELKEKRYFVLDLWLHDMWNWINEIAF 300
QY 301 PKNNKXGSRIVITTRNVDLAECATASLVYHLDLFLQNDALISLLLRKTNKHEDMESNKN 360
DB 301 PKNNKXGSRIVITTRNVDLAECATASLVYHLDLFLQNDALISLLLRKTNKHEDMESNKN 360
QY 361 MQMWERIVNKCGRPLPLAIIITIGAVLATKOVSEWEKFEYEQLPSELEINPSLEALRRMVT 420
DB 361 MQMWERIVNKCGRPLPLAIIITIGAVLATKOVSEWEKFEYEQLPSELEINPSLEALRRMVT 420
QY 421 GYNHLPKPCFLYLSIFPEDFEIQNRNLVGRWIAEGFVRPKVGMTTKDVGSYFNELI 480
DB 421 GYNHLPKPCFLYLSIFPEDFEIQNRNLVGRWIAEGFVRPKVGMTTKDVGSYFNELI 480
QY 481 NRSWIQSRVGTAGIKTCRIHDIIRDTIVTSISROENFVLLPMGDGSDLVQENTRIAPH 540
DB 481 NRSWIQSRVGTAGIKTCRIHDIIRDTIVTSISROENFVLLPMGDGSDLVQENTRIAPH 540
QY 541 GMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDTITOKDFDRIA 600
DB 541 GMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDTITOKDFDRIA 600
QY 601 LLCHLKYSIGYSSISYSLPRSIGKLGQGLQTLNMSSTYIAALPSEISKQLHLRCIRE 660
DB 601 LLCHLKYSIGYSSISYSLPRSIGKLGQGLQTLNMSSTYIAALPSEISKQLHLRCIRE 660
QY 661 LEFDNPSLNHPMKCITNTIICLPKVFTPLVSRDRRAKQIAEFHMATKSFWSSEFGVKVPKG 720
DB 661 LEFDNPSLNHPMKCITNTIICLPKVFTPLVSRDRRAKQIAEFHMATKSFWSSEFGVKVPKG 720
QY 721 IGKLRDLQVLEYVDIRTSRAIKELQGLSKRLKLAIVITKGSTKECKILYAAIEKLSSL 780
DB 721 IGKLRDLQVLEYVDIRTSRAIKELQGLSKRLKLAIVITKGSTKECKILYAAIEKLSSL 780
QY 781 QSLYMAAALSDIETLECLDSISPPPLRLTLGLNGSLEEMPNNWIEQLTHLKKFNLWSSK 840
DB 781 QSLYMAAALSDIETLECLDSISPPPLRLTLGLNGSLEEMPNNWIEQLTHLKKFNLWSSK 840
QY 841 LKEGKNMLILGALPNLMFLSLYHNSYLGEKLVKFTGAPPNLRITLVFNLDQLREIRPEDG 900
DB 841 LKEGKNMLILGALPNLMFLSLYHNSYLGEKLVKFTGAPPNLRITLVFNLDQLREIRPEDG 900
QY 901 SSPQLEKIEISCCRLESIGIITHLPRLKEISLEYKSKVARLGQKGEVNTNRPVLRM 960
DB 901 SSPQLEKIEISCCRLESIGIITHLPRLKEISLEYKSKVARLGQKGEVNTNRPVLRM 960
QY 961 DSDRRHDLGAEGSSIEVQTADPVPDAQSVTVAVEATDPLPEQEGSSSQSVITLT 1020
DB 961 DSDRRHDLGAEGSSIEVQTADPVPDAQSVTVAVEATDPLPEQEGSSSQSVITLT 1020
QY 1021 NDSEETGTAQAG 1032
DB 1021 NDSEETGTAQAG 1032
```

```
RESULT 2
ADIS7172
ID ADIS7172 standard; protein; 1031 AA.
XX
XX ADIS7172;
DT 22-APR-2004 (first entry)
XX
DE Oryza minuta P19 locus nucleotide binding site (NBS) protein #3.
XX
XX nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant.
XX
XX Oryza minuta.
XX
XX US2004006788-A1.
XX
XX 08-JAN-2004.
XX
XX 27-JAN-2003; 2003US-00352179.
XX
XX 25-JAN-2002; 2002US-0352106P.
XX
XX 01-FEB-2002; 2002US-0353304P.
XX
XX (WANG/) WANG G.
XX
XX (LIU/) LIU G.
XX
XX Wang G, Liu G;
XX
XX WPI; 2004-121064/12.
XX
XX N-PSDB; ADIS7171.
XX
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX and NBS3, useful for producing plants resistant to Magnaporthe grisea
XX infection.
XX
XX Claim 1; SEQ ID NO 89; 136pp; English.
XX
XX The invention comprises the amino acid and coding sequences of nucleotide
XX binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
XX blight and rice blast resistance genes). The DNA sequences may be used as
XX markers for resistance to infection with Magnaporthe grisea in plant
XX breeding programs. The present amino acid sequence represents an NBS
XX protein encoded by a gene from the Oryza minuta P19 locus.
XX
XX Sequence 1031 AA;
XX
XX Query Match 95.1%; Score 4997; DB 8; Length 1031;
XX Best Local Similarity 96.4%; Pred. No. 0;
XX Matches 985; Conservative 12; Mismatches 25; Indels 0; Gaps 0;
QY 1 MAETVLSMARSLVGSATSKAASAAANETSLLGVGEKDIWIYKDELKTMOAFLRAAEVMMK 60
DB 1 MAETVLSMARSLVGSATSKAASAAANETSLLGVGEKDIWIYKDELKTMOAFLRAAEVMMK 60
QY 61 KBELLKVAEQIRDLSYDIEDSLDEFKVIHIESOTLPQLVKLRERHRIAIRIHNLSRVE 120
DB 61 KBELLKVAEQIRDLSYDIEDSLDEFKVIHIESOTLPQLVKLRERHRIAIRIHNLSRVE 120
QY 121 EVSSRNTRYNLVEPISSGTEDDDMSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDTN 180
DB 121 EVSSRNTRYNLVEPISSGTEDDDMSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDTN 180
QY 181 ANDGPAKVICVVGMGGLGKTALSRKIFESSEDIRKNFPCNAWITVSQSFHRIELKDMIR 240
DB 181 ANDGPAKVICVVGMGGLGKTALSRKIFESSEDIRKNFPCNAWITVSQSFHRIELKDMIR 240
QY 241 QLLGPSSLDQLLHELQGVVQVHLSYLIIEELKEKRYFVLDLWLHDMWNWINEIAF 300
DB 241 QLLGPSSLDQLLHELQGVVQVHLSYLIIEELKEKRYFVLDLWLHDMWNWINEIAF 300
QY 301 PKNNKXGSRIVITTRNVDLAECATASLVYHLDLFLQNDALISLLLRKTNKHEDMESNKN 360
```

Db 301 PKNKKGSRIVITTRNVDAEACATASLVYHLDPLQMDAIATLLLRKTKNKHEDNESKN 360
Qy 361 MOKMYERIVNKGCRPLAILITIGAVLATKQVSEWEKPYEQLPSELEINPSLEALRRMTL 420
Db 361 MOKMYERIVNKGCRPLAILITIGAVLATKQVSEWEKPYEQLPSELEINPSLEALRRMTL 420
Qy 421 GYNHLPKPCFLYLSIPPEDEFEIQRNLRVGRWIAEGFVRPKVGMVTKDVGESYFNELI 480
Db 421 GYNHLPKPCFLYLSIPPEDEFEIQRNLRVGRWIAEGFVRPKVGMVTKDVGESYFNELI 480
Qy 481 NRSMTQSRVGTAGIKTCRIHDIIRDTIVTSIROENFVLLPMWGDGSLVQENTHIAFH 540
Db 481 NRSMTQSRVGTAGIKTCRIHDIIRDTIVTSIROENFVLLPMWGDGSLVQENTHIAFH 540
Qy 541 GSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQRLRMLRVLDLEDVTLTKQDFDRIA 600
Db 541 GSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQRLRMLRVLDLEDVTLTKQDFDRIA 600
Qy 601 LLCHLKYSIGYSSSIYSLPRSIGKLGLOQLTNMSTVYIAPLPSISKQLCHLTLRCIRE 660
Db 601 LLCHLKYSIGYSSSIYSLPRSIGKLGLOQLTNMSTVYIAPLPSISKQLCHLTLRCIRE 660
Qy 661 LEFDNPSLNHPMKCITNTICLPKFTPLVSRDNRKQIAEFHMAKTSFWSSESFGVKVPKG 720
Db 661 LEFDNPSLNHPMKCITNTICLPKFTPLVSRDNRKQIAEFHMAKTSFWSSESFGVKVPKG 720
Qy 721 IGLKRLDQVLEVDIRRTSSRAIKELGOLSKRLAVITKGTKECKILYAAIEKLSL 780
Db 721 IGLKRLDQVLEVDIRRTSSRAIKELGOLSKRLAVITKGTKECKILYAAIEKLSL 780
Qy 781 QSLYNAALLSDIETLECLDSISSPPPLRLTLGLNGSLEMPNWTIEQLTHLKFNLMWSK 840
Db 781 QSLYNAALLSDIETLECLDSISSPPPLRLTLGLNGSLEMPNWTIEQLTHLKFNLMWSK 840
Qy 841 LKEGKMILGALPNLMFLSYHNSYLGEKLVFTGAPNLTIVIFNLQDLRETRFEDG 900
Db 841 LKEGKMILGALPNLMFLSYHNSYLGEKLVFTGAPNLTIVIFNLQDLRETRFEDG 900
Qy 901 SSPLEKIEISCCRLSEGIIGIHLPRKEISLEYKSVARIGOLKGEVNTHPNRPVLRM 960
Db 901 SSPLEKIEISCCRLSEGIIGIHLPRKEISLEYKSVARIGOLKGEVNTHPNRPVLRM 960
Qy 961 DSDRRDHLGAEAGSSIEVQTADVPDQAGSVTVVAEATDPLPQEGESSQSQVITLTT 1020
Db 961 DSDRRDHLGAEAGSSIEVQTADVPDQAGSVTVVAEATDPLPQEGESSQSQVITLTT 1020
Qy 1021 ND 1022
Db 1021 ND 1022

RESULT 3
ADIS7176

ID ADIS7176 standard; protein; 1091 AA.
XX AC ADIS7176;
XX DT 22-APR-2004 (first entry)
XX DE Oryza minuta P19 locus nucleotide binding site (NBS) protein #5.
XX KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
XX KW plant breeding; transgenic plant; plant.
XX OS Oryza minuta.
XX PN US2004006788-A1.
XX PD 08-JAN-2004.
XX PF 27-JAN-2003; 2003US-00352179.
XX

PR 25-JAN-2002; 2002US-0352106P.
XX 01-FEB-2002; 2002US-0353304P.
PA (WANG/) WANG G.
XX (LIUG/) LIU G.
PI Wang G, Liu G;
XX WPI; 2004-121064/12.
DR N-PSDB; ADIS7175.
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX Claim 1; SEQ ID NO 93; 136pp; English.
XX The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present amino acid sequence represents an NBS
CC protein encoded by a gene from the Oryza minuta P19 locus.
XX Sequence 1091 AA;
SQ
Query Match 94.5%; Score 4966.5; DB 8; Length 1091;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 986; Conservative 20; Mismatches 26; Indels 59; Gaps 1;
Qy 1 MAETVLSMARSLVGSATSKAASAAANETSLLLGVEKDIW----- 39
Db 1 MAETVLSMARSLVGSATSKAASAAANETSLLLGVEKDIWIKDELKIMQAFPLRAAEVMMKK 60
Qy 40 -----YIKDELKTMQAFPLRAAEVMMKK 61
Db 61 KDELKVMAEQIRDLLYDIEDSLDEFKVHVESQTLFRQYIKDELKTMQAFPLRAAEVMMKK 120
Qy 62 DELKVMAEQIRDLSDIEDSLDEFKPVHIESQTLFROLVKLRERHRIAIRHNLSRVEE 121
Db 121 DELKVMAEQIRDLSDIEDSLDEFKPVHIESQTLFROLVKLRERHRIAIRHNLSRVEE 180
Qy 122 VSSRTRYNLVPEISSGTEDDMSYAEIDRQNSARNVDEAEVLGSDSKLLEMDTNA 181
Db 181 VSSRTRYNLVPEISSGTEDDMSYAEIDRQNSARNVDEAEVLGSDSKLLEMDTNA 240
Qy 182 NDGPAKVICVVGMLGKLTALSRKIPFSEEDIRKNFPCNAWITVQSFRHTELLKDMIRQ 241
Db 241 NDGPAKVICVVGMLGKLTALSRKIPFSEEDIRKNFPCNAWITVQSFRHTELLKDMIRQ 300
Qy 242 LIGPSSLDQLLAHELOGKVVQVHHLSEYLIIEELKEKRYFVVLDDLIWLDHNNWINEIAPP 301
Db 301 LIGPSSLDQLLAHELOGKVVQVHHLSEYLIIEELKEKRYFVVLDDLIWLDHNNWINEIAPP 360
Qy 302 KNNKKGSRIVITTRNVDAEACATASLVYHLDPLQMDAIATLLLRKTKNKHEDNESKN 361
Db 361 KNNKKGSRIVITTRNVDAEACATASLVYHLDPLQMDAIATLLLRKTKNKHEDNESKN 420
Qy 362 QOMYERIVNKGCRPLAILITIGAVLATKQVSEWEKPYEQLPSELEINPSLEALRRMTL 421
Db 421 QOMYERIVNKGCRPLAILITIGAVLATKQVSEWEKPYEQLPSELEINPSLEALRRMTL 480
Qy 422 YNHLPSHLKPCFLYLSIPPEDEFEIQRNLRVGRWIAEGFVRPKVGMVTKDVGESYFNELI 481
Db 481 YNHLPSHLKPCFLYLSIPPEDEFEIQRNLRVGRWIAEGFVRPKVGMVTKDVGESYFNELI 540
Qy 482 RSMIQRSRVGTAGIKTCRIHDIIRDTIVTSIROENFVLLPMWGDGSLVQENTHIAFH 541
Db 541 RSMIQRSRVGTAGIKTCRIHDIIRDTIVTSIROENFVLLPMWGDGSLVQENTHIAFH 600
Qy 542 SMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQRLRMLRVLDLEDVTLTKQDFDRIA 601
Db 601 SMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQRLRMLRVLDLEDVTLTKQDFDRIA 660

Qy	961	DSRRDHDLGAEAGSSIEVQTADPVPDPAQGSVTVVAEATDPLPEQGESSQSQVITLTT	1020
Db	961	YSRRYRHDLGAEAGSSIEVQTADPVPDPAQGSVTVVAEATDPLPEQGESSQSQVITLTT	1020
Qy	1021	NDSEEIGTAQAG 1032	
Db	1021	NDSEEIGTAQAG 1032	
RESULT 5			
ADMT2249	ID	ADM72249 standard; protein; 998 AA.	
XX	AC	ADM72249;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	O. minuta NBS6 polypeptide.	
XX	KW	Pi2; NBS6; plant protectant; gene therapy; rice; disease resistance.	
XX	OS	Oryza minuta.	
XX	PN	WO2004022715-A2.	
XX	PD	18-MAR-2004.	
XX	PF	08-SEP-2003; 2003WO-US027913.	
XX	PR	09-SEP-2002; 2002US-0409216P.	
XX	PR	18-MAR-2003; 2003US-0455713P.	
XX	PR	05-SEP-2003; 2003US-00656394.	
XX	PA	(OHIS) UNIV OHIO STATE.	
PI	Wang G;		
XX	WPI;	2004-257576/24.	
XX	N-PSDB;	ADM72248.	
PT	New rice Pi2-like disease resistance nucleic acid molecule that confers		
PT	disease resistance in plants, useful for creating or enhancing disease		
PT	resistance in plants.		
XX			
PS	Claim 1; SEQ ID NO 12; 120pp; English.		
XX			
CC	The invention relates to novel broad-spectrum resistance gene Pi2 and the		
CC	NBS (1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like		
CC	disease resistance nucleic acid molecules are useful for enhancing		
CC	disease resistance in plants. The present sequence represents a rice NBS6		
CC	polypeptide.		
XX			
SQ	Sequence 998 AA;		
Query Match 78.8%; Score 4140; DB 8; Length 998;			
Best Local Similarity 82.5%; Pred. No. 0;			
Matches 837; Conservative 23; Mismatches 58; Indels 96; Gaps 4;			
Qy	1	MAETVLSMARSLVGSASIKSAASAAANTSLLLGVEKDIWIYIKDELKTWQAPLRAAEVYMKK	60
Db	1	MAETVLSMARSLVGSASIKSAASAAADETSLLLGVEKDIWY-----	40
Qy	61	KDELLKVAEQIRDLSDIEDSLDEPKVHIESQTLPRQLVKLRERHRIAIRIHNLSERVE	120
Db	41	-----LFRGV-----	46
Qy	121	EVSSRTRYNLVPEISSGTED--DMDSYAEDIRNQSRNVDEAEVLGVFSDSKKRLLEMD	178
Db	47	---GRSNGGPPVGVNAGSQSLAIDSYAEDIRNQSRNVDEAEVLGVFSDSKKRLLEMD	103
Qy	179	TNANDGPAKVICVVMGGLKGTALSRKIPSEEDIRKFPNCNAWITVQSFRHIELKDM	238

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PF 08-SEP-2003; 2003WO-US027913.
XX
XX
XX 09-SEP-2002; 2002US-0409216P.
XX
XX 18-MAR-2003; 2003US-0455713P.
XX
XX 05-SEP-2003; 2003US-00656394.
XX
XX (OHIS ) UNIV OHIO STATE.
XX
XX Wang G;
XX
XX WPI; 2004-257576/24.
XX
XX N-PSDB; ADM72238.
XX
XX New rice pi2-like disease resistance nucleic acid molecule that confers
XX disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.
XX
XX Disclosure; SEQ ID NO 2; 120pp; English.
XX
XX The invention relates to novel broad-spectrum resistance gene pi2 and the
XX NBS(1-6) genes present in the pi2 gene cluster region. The rice pi2-like
XX disease resistance nucleic acid molecules are useful for enhancing
XX disease resistance in plants. The present sequence represents a rice NBS1
XX polypeptide.
XX
XX Sequence 993 AA;
XX
XX
XX Query Match 58.3%; Score 3064; DB 8; Length 993;
XX Best Local Similarity 61.9%; Pred. No. 7.1e-242;
XX Matches 613; Conservative 146; Mismatches 222; Indels 10; Gaps 4;
XX
XX 2 AETVLSMARSIVGSAISKAASAAANETSLIGVEKDIWIYKDELKTQAFRAAEVMMKK 61
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 3 AETVVSMAVIGSAGVGAASAAADEATLLGIGKEIWIYKDELKTQAFRAAEVYKK 62
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 62 DELKVAEQIRDLSDIEDSLDFKVIHIESQTLFRQLVQLRERHRIAIRIHNLSRVEE 121
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 63 DDLKVAEQVRDLSYNIEDCLDFKVIHVESQSLAKQLMKLGERHRIAVQIRNLSRIEE 122
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 122 VSSRNTRYLVEPISS-GTEDDMSYABDIRNQARNVDEAEIVGSDSKKILEMIDTN 180
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 123 VSNENTRYSLIKPISSITTEDERDSYLEDAENRSGSNTDESELVGFAKTDELKGLIDVN 182
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 181 ANDGPAKVICVVGMLGKTKTALSRIPESEDIRKNPCNAWITVSQSFHRIELKDMIR 240
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 183 TNDGPAKVICVVGMLGKTKTLAKAVENKEHM-XNFSCCAWITVSQSFDRKEILKQIR 241
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 241 QLLGFPSSLDQLLHLELQGVVQVHLSYLLIEELKERYFVVLDDLMILHDMWNINEIAF 300
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 242 QLLGADSLDLKLEFSEKLLVQVQHLADHVLVEGLKERYFVVLDDLMILHDMWNIDIAF 301
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 301 PKNKKSRIVITTRNVDLAEKATASIVYHLDPLQWDAISILLRKNKHEDMESKN 360
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 302 PKINNRGSRITITTRDAGLAGRCTSESILYHLEPLHIDDAIHLLAKTNIRLEDMDDED 361
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 361 MQKVERTVNCGRPLPAILITIGVLAATKQVSEWEKPYEQLPSELEINPSLEALRRMVTL 420
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 362 LGSIVTKLVKRCGYPLAILIIGGILATKMEWGKFYRELPSLENSPSEANRRMVTL 421
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 421 GYNHPLSHLPCFLYLSIFPEDFEIQNRNLVGRWIAEGFVRPKVGMTTKQVGSYFNELI 480
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 422 SYNHPLSHLPCFLYLSIFPEDFEIQGRVLVDRWIAEGFVRATDGVNIEDVGNSHFNELI 481
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 481 NRSIMQSRVCTAGKIKTCRTHIDITVTSISQENFVLLPMGDSGLVOENTRHIAFH 540
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 482 NRSIIQPSKVTDGVVRCRTHIDIRDIIVSISREENFVLLTREKITVVAEESIRHLAFH 541
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 541 GSKMCKTGLDWSITRSLAIFGDRPKSLAHAVCPQOLRMLRLDLEDVTFLLTKQDFORIA 600
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 542 GSKSKICLEWHARSVTLFGDRPVGRTPALCSQFMLRLVLDLEDKAFKQTDINRIG 601
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 601 LLCHLKYSIGYSSISYLSIPRSIGKLOGLQTLNMSSTYIAALPSEISKLOCLHTLCIRE 660
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX RESULT 7
XX ID ADI57168 standard; protein; 979 AA.
XX
XX AC ADI57168;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #1.
XX
XX KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
XX plant breeding; transgenic plant; plant.
XX
XX OS Oryza minuta.
XX
XX PN US2004006788-A1.
XX
XX PD 08-JAN-2004.
XX
XX PF 27-JAN-2003; 2003US-00352179.
XX
XX PR 25-JAN-2002; 2002US-0352106P.
XX
XX PR 01-FEB-2002; 2002US-0353304P.
XX
XX (WANG/) WANG G.
XX (LIUG/) LIU G.
XX
XX PI Wang G, Liu G;
XX
XX XX WPI; 2004-121064/12..
XX
XX DR N-PSDB; ADI57167.
XX
XX PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX and NBS3, useful for producing plants resistant to Magnaporthe grisea
XX infection.
XX
XX PS Claim 1; SEQ ID NO 85; 136pp; English.
XX
XX CC The invention comprises the amino acid and coding sequences of nucleotide
XX binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
XX blight and rice blast resistance genes). The DNA sequences may be used as
XX markers for resistance to infection with Magnaporthe grisea in plant
XX breeding programs. The present amino acid sequence represents an NBS
XX protein encoded by a gene from the Oryza minuta Pi9 locus.
XX
XX Sequence 979 AA;
```

Query Match		58.1%; Score 3055.5; DB 8; Length 979;
Best Local Similarity		62.8%; Pred. No. 3.5e-241;
Matches		610; Conservative 143; Mismatches 216; Indels 3; Gaps 3;
Qy	1 MAETVLSMARSLVGSATSKAASAAANETSLLGVEKDIWIYKDELTKMQAFLRAAEVYMK 60	
Db	1 MAETVLSMARSLVGSATSKAASAAANETSLLGVEKDIWIYKDELTKMQAFLRAAEVYMK 60	
Qy	61 KDELKVAEQIRDSYDIEDSLDEFKVIHIESQTLFRQLVKLRHRHRIAIRHNLKSRVE 120	
Db	61 KDELKVAEQIRDSYDIEDSLDEFKVIHIESQTLFRQLVKLRHRHRIAIRHNLKSRVE 120	
Qy	121 EVSSRNRYNLVPEISS-GTDEDDMSYAEADIRNQSARNVDAELVGFSDSKRLLEMDT 179	
Db	121 EVSSRNRYNLVPEISS-GTDEDDMSYAEADIRNQSARNVDAELVGFSDSKRLLEMDT 179	
Qy	180 NNDGPAKVICVGMGGIGKTLARKIPESEEDIRKPPCNNAWITVSQSFHRIELDKMI 239	
Db	180 NNDGPAKVICVGMGGIGKTLARKIPESEEDIRKPPCNNAWITVSQSFHRIELDKMI 239	
Qy	240 RQLGPSLDDLHQLHQLVQVHHHSEYLIIEELKEKRYFVVLDDMLWLDMMWINEIA 299	
Db	240 RQLGPSLDDLHQLHQLVQVHHHSEYLIIEELKEKRYFVVLDDMLWLDMMWINEIA 299	
Qy	300 PPKNNKGSRIIVITRNVDLAEKCATASLVYHLDFLQNDALISLLLRKTNKNHEDMESNK 359	
Db	300 PPKNNKGSRIIVITRNVDLAEKCATASLVYHLDFLQNDALISLLLRKTNKNHEDMESNK 359	
Qy	360 NMQKQVERIYNKCGRLPLAILTIGAVLATKQVSEWEKPYEQLPSELEINPSLEALRMVT 419	
Db	360 NMQKQVERIYNKCGRLPLAILTIGAVLATKQVSEWEKPYEQLPSELEINPSLEALRMVT 419	
Qy	420 LGYNHLSHLKPCFLYLSIPPEDEFEIORNLVGRWIAEGFVRPKVGMTTKDVGVSFYNEL 479	
Db	420 LGYNHLSHLKPCFLYLSIPPEDEFEIORNLVGRWIAEGFVRPKVGMTTKDVGVSFYNEL 479	
Qy	480 INRSMIQRSGVTAGKIKTCRIHDIIRDITVTSIRQENFVLLPMDGSDLVQENTRIAP 539	
Db	480 INRSMIQRSGVTAGKIKTCRIHDIIRDITVTSIRQENFVLLPMDGSDLVQENTRIAP 539	
Qy	540 HGSMSCTGTDWSIIRSLAIFGDRPKSLAHAVCPDQLRMRLVLEDDVPLITOKDPRI 599	
Db	540 HGSMSCTGTDWSIIRSLAIFGDRPKSLAHAVCPDQLRMRLVLEDDVPLITOKDPRI 599	
Qy	600 ALLCHLYSLTIGYSSSIYSPRSIGKQLQGLQTLNMSYIAALPSEISKLOCLHLRCIR 659	
Db	600 ALLCHLYSLTIGYSSSIYSPRSIGKQLQGLQTLNMSYIAALPSEISKLOCLHLRCIR 659	
Qy	660 ELEFPNFS-LNHPMKCTINTICLPKVTPLVSRDNRNRAQIAEPHMAKFSWSESGYKVP 718	
Db	660 ELEFPNFS-LNHPMKCTINTICLPKVTPLVSRDNRNRAQIAEPHMAKFSWSESGYKVP 718	
Qy	719 KGICKLRDLQVLEVDYDRTSSRAIKELGQLSKRLKLAIVTKGSKCKILYAAIEKLS 778	
Db	719 KGICKLRDLQVLEVDYDRTSSRAIKELGQLSKRLKLAIVTKGSKCKILYAAIEKLS 778	
Qy	779 SIQSLYNAALLSDIETLECLDSTSSPPPLRTTGLNGSLEEMPNWIEQLTHLKKFLWS 838	
Db	779 SIQSLYNAALLSDIETLECLDSTSSPPPLRTTGLNGSLEEMPNWIEQLTHLKKFLWS 838	
Qy	839 SKLKEGKNMLTLGALPNLMFLSYHNSYLGKLVFKTGAPFNRLTLVFNLDQLREIRFE 898	
Db	839 SKLKEGKNMLTLGALPNLMFLSYHNSYLGKLVFKTGAPFNRLTLVFNLDQLREIRFE 898	
Qy	899 DGSFPQLEKIEISCRLESIGIIGHLPRLKIEISLEYKVARGLQKGEVNTHPNRPVL 958	
Db	899 DGSFPQLEKIEISCRLESIGIIGHLPRLKIEISLEYKVARGLQKGEVNTHPNRPVL 958	
Qy	959 RMDSDRDHDLG 970	
Db	959 RMDSDRDHDLG 970	
Qy	960 QMAEDRSHDLG 971	
Db	960 QMAEDRSHDLG 971	
RESULT 8		
ADI57170		
ID	ADI57170 standard; protein; 993 AA.	
XX	AC ADI57170;	
XX	AC ADI57170;	
DT	22-APR-2004 (first entry)	
XX	XX	
DE	Oryza minuta P19 locus nucleotide binding site (NBS) protein #2.	
XX	XX	
KW	nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;	
KW	plant breeding; transgenic plant; plant.	
XX	Oryza minuta.	
OS	OS	
XX	XX	
FN	US2004006788-A1.	
XX	XX	
PD	08-JAN-2004.	
XX	XX	
PF	27-JAN-2003; 2003US-00352179.	
XX	XX	
PR	25-JAN-2002; 2002US-0352106P.	
PR	01-FEB-2002; 2002US-0353304P.	
XX	XX	
PA	(WANG/) WANG G.	
PA	(LIU/) LIU G.	
PI	Wang G, Liu G;	
XX	XX	
DR	WPI; 2004-121064/12.	
DR	N-PSDB; ADI57169.	
XX	XX	
PT	Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2	
PT	and NBS3, useful for producing plants resistant to Magnaporthe grisea	
XX	infection.	
PS	Claim 1; SEQ ID NO 87; 136pp; English.	
XX	XX	
CC	The invention comprises the amino acid and coding sequences of nucleotide	
CC	binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial	
CC	blight and rice blast resistance genes). The DNA sequences may be used as	
CC	markers for resistance to infection with Magnaporthe grisea in plant	
CC	breeding programs. The present amino acid sequence represents an NBS	
CC	protein encoded by a gene from the Oryza minuta P19 locus.	
SQ	Sequence 993 AA;	
Query Match		49.4%; Score 2595; DB 8; Length 993;
Best Local Similarity		55.3%; Pred. No. 2.3e-203;
Matches		539; Conservative 164; Mismatches 242; Indels 30; Gaps 12;
Qy	1 MAETVLSMARSLVGSATSKAASAAANETSLLGVEKDIWIYKDELTKMQAFLRAAEVYMK 60	
Db	1 MTETVSMAMSLVGSATSKAASAAANETSLLGVEKDIWIYKDELTKMQAFLRAAEVYMK 60	
Qy	61 KDELKVAEQIRDSYDIEDSLDEFKVIHIESQTLFRQLVKLRHRHRIAIRHNLKSRVE 120	
Db	61 KDELKVAEQIRDSYDIEDSLDEFKVIHIESQTLFRQLVKLRHRHRIAIRHNLKSRVE 120	
Qy	121 EVSSRNRYNLVPEISSGTDEDDMSYAEADIRNQSARNVDAELVGFSDSKRLLEMDT 180	
Db	121 EVSSRNRYNLVPEISSGTDEDDMSYAEADIRNQSARNVDAELVGFSDSKRLLEMDT 180	
Qy	181 ANDGPAKVICVGMGGIGKTLARKIPESEEDIRKPPCNNAWITVSQSFHRIELDKMI 240	
Db	181 EN-ABEQTIWIVGEGGLGKTLAKKYVES-SDVSSKFPCCAWITVSRPNVKKLLKNMK 238	
Qy	241 QLLGPSLDDLHQLHQLVQVHHHSEYLIIEELKEKRYFVVLDDMLWLDMMWINEIA 300	
Db	239 QLLGPSLDDLHQLHQLVQVHHHSEYLIIEELKEKRYFVVLDDMLWLDMMWINEIA 297	
Qy	301 PPKNNKGSRIIVITRNVDLAEKCATASLVYHLDFLQNDALISLLLRKTNKNHEDMESNK 360	

Db 298 -GNMEGSRVVVTRNNKLAGSST-SPVYCLKLEKEDATKLLLRKTKRSLHDIKXQ- 354
Qy 361 MQKQVVERIVNKGRLPLAIIITIGAVLATQKQVSEWEKFEYQLPSELEINPSLEARRMTL 420
Db 355 MKEIFEIKLKCGLPLAIIITIGAVLEGGKOTKEWEILYAQLPSELESNPIAEPKMKVVTL 414
Qy 421 GYNHLPKPCFLYLSIFPEDFEIQRNRLVGRVIAEGFVRPKVGMTTKOVGESYFVELI 480
Db 415 SYNTLPKPCFLYLSIFPEDFDIQRLVHRVIAEGFIRARGGVIVDVQKIFDELI 474
Qy 481 NRSMIQSRVGTAGKIKTCRIHDIIRDITVSISROENFVLLPMGDGSDLVQENTRHIAFH 540
Db 475 NRSMIQSRVDIEGNIKSCRVDIMRDVMISISREENFVYLMGDDGTSVVEENIRHLVHH 534
Qy 541 GSMCKT-GLDWSIIRSLAIPG-DRPKSLAHAVCPDQLRMURVLDELDVTLITQKDFDR 598
Db 535 DTSKCSNIGMDWSHVSRLTGFNERPKGLSPFCFPQLKMLRVLDLQDVKFGMTQKDIG 594
Qy 599 IALLCHLKYLISIGYSSSTYSIPRSGIKLQGLQTLNMSSTYIAALPSEISKLCQCLHTRCI 658
Db 595 IGLRHUKYVNIHGSHSYALPRICIGKUKOLCTIDITDSYITELPTELSKQSLCILRCR 654
Qy 659 RELEFDNFSLNHPMKCTNTTICLPKFTPLVSRDRNRAKQIAEFHMTKSPMSE---SFGV 715
Db 655 GRPNSGDFNLNDPKDCLIAFSCPLPMAATDS-DERNKIIAELHVGCSSQWSPNGGTGV 713
Qy 716 KVPKIGIKRLDQVLEVYDVRTSSRAIKELQGLSKLRAVITKGTKECKKILYAAIE 775
Db 714 RVPGRINKLQVLETVTDINRTSSKSVSEELGELIQLKLSVVTQGSTKECKKILTAIQ 773
Qy 776 KLSLSQSIYMAALLSDIETLECLDSISSPPPLARTLGLGSLSEMPNWIQLTHAKFN 835
Db 774 KLSLKLTLNNAHGLDTGTLEWLSHSLPS-LRIIRLIGYMKEMPNWFRELQOLVKIH 832
Qy 836 LWSKLEKGNMILGALPNLMFLSLYHNSYLGEKLVFKTGAPPNLRITLVIFNLDQREI 895
Db 833 LQNSQLEEDKTMEILGELPNLMFLSWRA-----VLIIRNQKQKEV 875
Qy 896 RFEDGSPQLKBIISCCRLESIGIILHPLRKEISLEYKSKVARLQOLGKGVNTHPNR 955
Db 876 RFEBGTSPMERIDIRECLRTSGIAGIKHPLRKEISLEYSAKVVRILQOLEVEMGTHPNR 935
Qy 956 PVLKMDSDRRDHDIG 970
Db 936 PMLRFGERSRDLG 950

RESULT 9
AD157174
ID AD157174 standard; protein; 1054 AA.
AC
XX ADI57174;
XX

22-APR-2004 (first entry)
XX

Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #4.
XX

nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
plant breeding; transgenic plant; plant.
XX

Oryza minuta.
OS

US2004006788-A1.
XX

08-JAN-2004.
XX

27-JAN-2003; 2003US-00352179.
XX

25-JAN-2002; 2002US-0352106P.
PR

01-FEB-2002; 2002US-0353304P.
XX

(WANG/) WANG G.
PA

PA (LTUG/) LIU G.
XX Wang G, Liu G;
XX WPI; 2004-121064/12.
DR N-PSDB; ADI57173.
XX
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
PS Claim 1; SEQ ID NO 91; 136pp; English.
PS
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present amino acid sequence represents an NBS
CC protein encoded by a gene from the Oryza minuta Pi9 locus.
XX
SQ Sequence 1054 AA;

Query Match 46.2%; Score 2427; DB 8; Length 1054;
Best Local Similarity 51.9%; Pred. No. 1.6e-189;
Matches 530; Conservative 144; Mismatches 261; Indels 86; Gaps 21;
Qy 1 MAETVLSMARSLVGSATSKAASAAANETSLLLGVKEKDIWIKDELKTMQAFPLRAEVMKK 60
Db 1 MADTVLSIAKSLVGSASVKASVAADKMIMLLGVQKEIWFIKDELQTLQIAFLIAEA-SK 59
Qy 61 KDELKLVARQIRLSDYIEDSLDEPKVHIESQTLFRQLVKLRERHRIAIRHNKLSRVE 120
Db 60 KSILLKVVQOVRDLYDIEDCLDEFVHVGSQNLSQLMKLKDHRHIAIQIRNLRTIE 119
Qy 121 EVSQRNRYNLVE--PISSGTEDDMSYAEIRNQSARNVDEAEVLVGFSDSKRRLLEMDT 179
Db 120 EVSQRNRYNLVNDLTCTTDERNLFWEDIRNQ-ANNIEADLVGFSGPKRELLDIDV 178
Qy 180 NANGDPAKVICVGMGGLGTALSRTKIFESFEDIRKNPCNAWITVSQSFHRIELKDMI 239
Db 179 HANDGPKVICVGMGGLGKTTIARKIYESKEDIAKPFSCCAWITVSQSFVRVLLKDL 238
Qy 240 RQLGPSLQDLAHLQGVVQVHLSYELIEELKEKRYFVVLDDLWILHDMNWINIEA 299
Db 239 VKLFGEEVLAKKRLRELESGK-VPOVDLASYLRTELNERRYFVVLDNVSTDSWKINSIA 297
Qy 300 FP-KNNKKGSRIVITTRNDVLAEKATASLVYHLDLFLQMDAISLLRKTWNHEDMESN 358
Db 298 FPRNNKSGSRIVITTRDVLGTRKETSSELLTYQLKPLEINYAKELLRLKANKAIGDMESD 357
Qy 359 KMQKQVVERIVNKGRLPLAIIITIGAVLATQKQVSEWEKFEYQLPSELEINPSLEARRMV 418
Db 358 K-MSDIITKIIKGCGYLPALITIGGVLSKREWEWTFYSQIPSELESNPLSAMRRIV 416
Qy 419 TLGYNHLPKPCFLYLSIFPEDFEIQRNRLVGRVIAEGFVRPKVGMTTKOVGESYFNE 478
Db 417 TLSNYLPKPCFLYLSIFPEDFEINRNLVNRVWAEFGIKARTNWTIEDVKSYPKE 476
Qy 479 LINRSMIQSRVGTAGKIKTCRIHDIIRDITVSISROENFVLLPMGDGSDLVQENTRHIA 538
Db 477 LINRSMIQSRAGIRGDFKSCRVDIMRDITISISREENFTLLPDGTDYDVVHGNTRHIE 536
Qy 539 FHGSMSC-KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMURVLDELDVTLITQKDFD 597
Db 537 FHGSKYCSSETSLDWSIIRSLTDMFGRSVLEHSCVSSQLRMLRVLDLTDQAQFSITQNDVD 596
Qy 598 RIALLCHLKYLISIG-----YSSSIYSIPRPS--IGKQGLQTLNMSSTYIAALPSEI 646
Db 597 NIVLCHLKYLKIKIPIPTIYLTSTIHTAWSADIGLSDVHFNFTANSY----- 648
Qy 647 SKIQCLHTLCIRELEFPDNFSLNHPMKCTNTTICLPKFTPLVSRDRNRAKQIAEFHMTK 706
Db 649 --LRSLASLRCKM--EYFSSSLT---TTLTNTLCLPMIFTPFVSTSDRSETIAKLHMTAK 701


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XX Wang G, Liu G;
XX WPI; 2004-121064/12.
XX N-PSDB; ADIS7177.
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX and NBS3, useful for producing plants resistant to Magnaporthe grisea
XX infection.
XX Claim 1; SEQ ID NO 95; 136pp; English.
XX
XX The invention comprises the amino acid and coding sequences of nucleotide
XX binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
XX blight and rice blast resistance genes). The DNA sequences may be used as
XX markers for resistance to infection with Magnaporthe grisea in plant
XX breeding programs. The present amino acid sequence represents an NBS
XX protein encoded by a gene from the Oryza minuta P19 locus.
XX
XX Sequence 451 AA;
XX
XX Query Match 25.4%; Score 1389; DB 8; Length 451;
XX Best Local Similarity 51.7%; Pred. No. 7.5e-105;
XX Matches 282; Conservative 70; Mismatches 95; Indels 98; Gaps 3;
XX
XX 1 MAETVLSMARSLVGSATSKAASAAANETSLLLGVKEDIWIKDELKTWQAFRAAEVWK 60
XX 1 MADTVLSIAKSLVGSANVSKVASVAADKMWILLGVQKEIWFIKDELQIQAFMAEA-SK 59
XX
XX 61 KDELKVAEIQRLSDYDIEDSLDFKVIHESQTLFRQLVKLRERHRIAIRIHNLSKSRVE 120
XX 60 KSILLKVVQVRDLSYDIEDCLOEFTVHVGSQTLRQLMKLKHRIAVQIRNLRTIE 119
XX
XX 121 EVSSRNTRYNLVEPISSGTEDMDSDYAEIRNQSRNVDEAEIVGFSKSKRILEMDTN 180
XX 120 EVSSRNTRYNLIEDLTSITGERNFIMEDIERNESANNIEAEELVGFSGPKRELLDLIDVH 179
XX
XX 181 ANDGPAPKVICVGMGGGLKTALESKIPSEEDIRKNFPCNAWITVSQSFHRIELLDKMWIR 240
XX 180 AKOGFTKVCVGMGGGLKTTIARIKIVESKEDIANKFSCCAWITVSQSFVLELLKDLV 239
XX
XX 241 QLLGPSSLDQLLHLELQGVVQVHHLSEYLIIEELKEKRYFVVLDDLWILHDWNWINEIAF 300
XX 240 KLFGEVLLKRLRELEGG-VQVDDLASYLRTNELNERRYFVVLDDVWVSTDSWKWINSIAF 298
XX
XX 301 PANKKGSRIVITTRNDVLAEKCATASIVYHLDPLQMDAISLILKTKNKHEDMESKN 360
XX 299 PRNNKGSRIVITTRDVLGAKECTSELLIYKLPLEITYAKELLRKANKKIEDKMSDKK 358
XX
XX 361 MOKMVERIVNKCGRPLPLAILTIGAVLATKQVSEWEKPYEQLPSELEINPSLEALRRMVT 420
XX 359 MSDIITKLVKCGVPLPLAILTIGVLA TK----- 387
XX
XX 421 GYNHPLSHLPCFLLYSIFPEDFBIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480
XX 388 ----- 387
XX
XX 481 NRSMIQSRVCTAGKIKTCRIHDIIRDITVTSIQENFVLLPMGDSGLVQENTRHIAFH 540
XX 388 -----DPSRAGVRGEFKSCRIHDIRDIAISIREENFILLPEGTDYDVVHGNTRHIAFH 442
XX
XX 541 GMSMC 545
XX 443 GSKYC 447
XX
XX RESULT 12
XX AAY93135
XX ID AAY93135 standard; protein; 1251 AA.
XX AC AAY93135;
XX DT 08-NOV-2000 (first entry)
```

```
XX Rice blast fungus-resistance protein Pi-b from rice.
XX DE
XX Rice blast fungus; Pyricularia grisea; Magnaporthe grisea;
XX resistance gene.
XX Oryza sativa.
XX OS
XX JP2000125885-A.
XX PN
XX 09-MAY-2000.
XX PD
XX 29-MAR-1999; 99JP-00087305.
XX PF
XX 21-AUG-1998; 98JP-00235884.
XX PR
XX (KAGA-) KAGAKU GIJUTSU SHINKO JICYO DAN.
XX PA (NORQ) NORINSUISANSHO NOGYO SEIBUTSU SHIGEN.
XX FA
XX WPI; 2000-379868/33.
XX DR N-PSDB; AA11349, AA11350.
XX DR
XX A blast-resistant gene and related genes, useful for creating a rice
XX grade of high blast resistance.
XX PT
XX Claim 26; Page 20-23; 36pp; Japanese.
XX PS
XX The invention relates to the isolation of novel rice blast fungus
XX (Pyricularia grisea; also known as Magnaporthe grisea) resistance genes
XX from rice strain BL-1. The genes are designated Pi-b (AA11349) and Pi-b'
XX (AA11351). The genes can be used for creating rice which has high blast
XX fungus resistance. This sequence represents the protein encoded by the Pi
XX -b gene
XX
XX Sequence 1251 AA;
XX
XX Query Match 22.7%; Score 1191; DB 3; Length 1251;
XX Best Local Similarity 27.7%; Pred. No. 6.6e-88;
XX Matches 355; Conservative 208; Mismatches 363; Indels 356; Gaps 39;
XX
XX 1 MAETVLSMARSLVGSATSKAASAAANETSLLLGVKEDIWIKDELKTWQAFRAAEVWK 60
XX 1 MEATALSVGKSLVNGALGYAKSAFAEEVALQGIQKDHFTFVADLEWMSRSPMEAEHQ 60
XX
XX 61 KDELKVAEIQRLSDYDIEDSLDFKVIHESQTLFRQLVKLRERHRIAIRIHNLSKSRVE 120
XX 61 NSKVVTWVQVRDIAVDVEDSLQDFAVHLKRPSPWFRPRTLLEHRHRAVAKMELRNKVE 120
XX
XX 121 EVSSRNTRYNLVEPISSGTEDMDSDYAEIRNQSRNVDEAEIVGFSKSKRILEMDIT 179
XX 121 DVSRNRYHLKGSAAKATINSTEQ--SSVIATAFIGDIDARRAAKQDNQRVDLVQLI-- 176
XX
XX 180 NANDGPAPKVICVGMGG-LGTALSRLKIPSEEDIRKNFPCNAWITVSQSFHRIELDKM 238
XX 177 NSEDQDLKVIADVGTSGDMGQTTIIRMayEN-PDVQIRFPFCRAWVRVWHPSPRDFVQSL 235
XX
XX 239 IRL----- 242
XX 236 VNLHATQGVLEALLEKEKTEODLAKKFGVCNDRKCLIVLNDLSTIEWDQIKKCFQKCR 295
XX
XX 243 -----LGPSSLDQLLH----- 253
XX
XX 296 KGSRIIVSSTQVEVASLCAGESQASLQSLADQTLVAFYDKGSQIIEDSVKPVISDV 355
XX 254 -----ELQG--KVVQVHH 265
XX
XX 356 AITSTNNHTVAHGEIIDDQSDMADEKKVARKSLTRITRSVGASESQLIGREKEISEITH 415
XX 266 L----- 266
XX
XX 416 LILNDSQQVQVIVSWGMGGGLKTKTLVSVYQSPRLSDKPKDYVFTIMRPFILVELLRS 475
XX 267 -----SEYLIEE-----LKEKRYFVWLDDLWILHDW 292
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Db	476	LA	BQ	LH	GK	SS	K	E	E	L	L	N	R	V	S	K	S	L	A	S	M	B	E	T	E	T	G	Q	L	R	L	E	K	S	C	L	I	V	L	D	F	S	D	T	S	E	W	533															
Qy	293	NW	IE	IA	P	P	K	N	K	G	S	R	I	V	I	T	R	N	V	D	L	A	E	K	C	A	T	A	S	-	L	V	Y	H	D	F	L	Q	M	D	A	I	S	L	L	R	K	T	-	N	349												
Db	536	DQ	I	K	P	T	L	P	P	L	-	L	E	K	T	S	R	I	V	I	T	R	K	E	N	I	A	N	I	A	H	C	S	G	K	N	G	V	H	N	L	K	V	L	X	H	D	A	L	C	L	L	E	K	F	E	E	594					
Qy	350	K	N	H	E	M	S	N	K	M	Q	K	V	E	R	I	V	N	K	C	G	R	L	P	L	A	I	T	I	G	A	V	L	A	T	-	-	K	O	V	S	E	W	E	K	F	Y	E	Q	L	P	S	E	L	E	I	407						
Db	595	A	T	I	D	D	Q	N	N	P	E	L	V	E	A	K	Q	L	K	C	D	G	L	P	L	A	I	V	I	G	F	L	A	N	R	P	K	T	P	E	E	R	K	L	N	E	N	I	A	E	L	E	M	654									
Qy	408	N	P	S	L	E	A	R	M	V	T	L	G	N	H	L	P	S	H	L	K	P	C	F	L	S	I	F	P	E	D	P	E	I	Q	R	N	R	L	I	G	R	M	A	E	G	F	V	P	K	V	M	T	467									
Db	655	N	P	E	L	G	M	I	R	T	V	L	E	K	S	Y	D	G	L	F	Y	H	L	K	C	F	L	S	I	F	P	E	D	Q	I	S	R	R	L	V	H	R	A	E	G	S	T	A	A	H	G	K	711										
Qy	468	T	K	D	V	G	S	E	Y	F	N	E	L	I	N	K	S	M	I	-	-	-	Q	R	S	R	V	G	T	A	G	-	I	K	T	C	R	I	H	D	I	R	D	T	S	I	S	R	O	E	N	F	L	L	P	M	523						
Db	715	A	I	E	T	A	N	G	Y	F	N	E	L	K	R	S	M	L	P	Q	S	-	-	G	S	R	K	S	I	D	S	C	K	V	H	D	L	M	R	D	I	A	K	S	T	E	E	N	L	V	P	R	V	E	772								
Qy	524	G	D	G	S	D	L	V	O	E	N	T	R	H	I	A	-	-	-	-	-	-	F	H	G	S	M	S	C	T	G	L	-	D	W	S	I	I	R	S	L	A	I	F	G	D	R	P	K	S	L	A	H	A	V	C	D	L	R	M	578		
Db	773	E	G	S	A	I	T	H	G	A	I	R	H	L	A	I	S	N	N	K	G	D	S	E	P	E	G	I	V	D	L	S	R	I	S	L	S	L	F	G	D	K	W	P	F	V	Y	G	-	-	-	-	-	-	-	-	-	-	K	M	R	F	828
Qy	579	L	R	V	L	D	E	D	V	T	L	I	T	K	O	F	D	R	I	A	L	L	C	H	L	K	Y	L	S	I	G	Y	S	S	I	S	I	P	R	S	I	G	K	L	O	G	L	O	T	T	N	M	S	T	Y	638							
Db	829	I	R	V	D	F	E	G	-	T	R	G	L	E	Y	H	L	D	Q	W	K	N	L	H	K	F	L	S	R	G	C	Y	R	I	D	L	P	D	L	G	N	L	R	Q	L	M	L	D	I	R	G	T	Y	887									
Qy	639	I	A	L	P	S	E	S	K	O	C	L	H	L	R	C	I	R	E	L	F	-	-	-	D	N	F	S	I	N	H	P	M	K	-	-	-	C	I	N	T	T	C	L	P																		

RESULT 13

RESOLUTION
AA49434

AA149434
ID AAY49434 standard; protein; 1205 AA.

XX

AC AAY49434;

XX
DT 17-MAR-2000 (first entry)

DT 17-MAR-2000 (first entry)

XX
DE Blast disease-resistance (Pi-b) protein.

XX Blast disease resistance (t₁ 2), *P*-protein.
KW Blast disease; rice; pi-b gene; blast disease-resistance gene.

XX
OS Orvza sativa.

03 Urya saliv.
XX
PN EP969092-A1.

PN XX PD
EF909092-A1.
05-JAN-2000

FD 05-JAN-2000.

XX PF 11-JUN-1999; 99EP-00111443.
 XX PR 12-JUN-1998; 98JP-00181455.
 XX PA (NORQ) NAT INST AGROBIOLOGICAL RESOURCES.
 XX FI Yano M, Iwamoto M, Katayose Y, Sasaki T, Wang Z, Yamanouchi U;
 FI Ishimaru L;
 XX WP; 2000-064864/06.
 DR NR-PSDB; AAZ46679, AAZ46680.
 XX PT Novel polypeptide and DNA encoding it used to produce plants resistant to
 FT fungal blast disease.
 XX PS Claim 1; Page 8-14; 46pp; English.
 CC The invention provides a protein which confers resistance to blast
 CC disease onto plants. The blast disease-resistance (Pi-b) protein can be
 CC expressed by standard recombinant methodology. The novel Pi-b gene is
 CC used to produce transgenic plants resistant to the rice blast disease,
 CC which will control the disease and increase crop yields. The present
 CC sequence represents the rice Pi-b protein. The resistance gene pi-b is
 CC located at the end of the long arm of rice chromosome 2 and displays
 CC resistance to blast fungi

XX	SQ	Sequence 1205 AA;
	Query Match	20.9%; Score 1100; DB 3; Length 1205;
	Best Local Similarity	27.2%; Pred. No. 1.8e-80;
	Matches 336; Conservative 197; Mismatches 346; Indels 356; Gaps 39	
Qy	48	MQAFPLAAAVNMKKDELLKVNABEQIRLDSYDIEDSLDFEFKVHIESOTLFROLVLKRHRH 107
Db	2	MRSPMEAEHEQDNSSKVVKTWVKQRDTAYDVESLDQFAVHLKRPMSWRPFTLLRHR 61
Qy	108	IATRIHNLSRVREVSSTRNYNLVEPISSCTEDDMDSYAEDIHQNSARNVDDELVGFS 167
Db	62	VAKQMKELRNKVEDVSQRNYHLIKGSAKATINSTQ--SSVIATAIFGIDDDARRAAKQ 119
Qy	168	DSKK-RLEEMIDTNANDGPARKVICVGMGG-LGTALSRLKFSEEDIRKNFPCNAITV 225
Db	120	DNQEVDLVQLI--NSEDDLKVIAWGTSGDMDGOTTIIRMAYEN-PDVQIFPCRAWVRV 176
Qy	226	SQSFRTELKMDIRQL----- 242
Db	177	MHPSPRDFVQLNQLHATQGVEALLEKEKTEQLAKKFNCGVNDRKCLIVLNDLSTIE 236
Qy	243	-----LGPSLQDLH----- 253
Db	237	EWDQIKCFQCKRGSRHIIVSSTQVFASLCAGQESQASELKULSADOTLYAFYDKGSQI 296
Qy	254	-----E 254
Db	297	IEDSVKPVISDVAITSTNNHTVAHGRIIDDQSMADADEKKVARKSLTRIITSVGASESQ 356
Qy	255	LQ--KVVQVHH----- 266
Db	357	LIGREKEISBITHLILNDSQQQVIVSWGVMGGLGKTLTVSGVYQSPRLSDPKFYFVT 416
Qy	267	-----SEYLIEE-----LKEKY 279
Db	417	IMRPFILVELLSLAEOHLKGSSKKEELLENTRVSSKKSLASMEDTELTGQLKRLLEKGC 476
Qy	280	FVVLDDLWLILDWNWINEIAPPKNNKXGRIVITTRNVLDLAEKCATAS-LVYHLDFLOMN 338
Db	477	LIVLDDPSDTSQDWIQPTLPFL-LBKTSRIIVTTRKENIANHCSCGNNGVHNKLKLN 535
Qy	339	DAISLLLRKT--NQNHEDMESNKMQKQVERIVNKCGRPLAULTIGAVLAT--KQVSEW 394
Db	536	DALCLSEKFEFETATYLDQNPNELVKEAQILKKCDGLPAIVVIGGFANRPKTPPEW 595

Qy	866	YLGEKLVFKTGAPFNRLTVIFNLDQLREIRFEDGSSPQLEKIEI-----SCCRLESGII	920
Db	814	KPKEGVIVSSNGFRCLKEFYETCWEIGTGLSFEPGAMPLEKLRIPFNHGVCSLH-GVL	872
Qy	921	--GIIHLPRLBISLEYKSKVARLGOLK	946
Db	873	DSGIWHLCSLRHLHVEIICHGARLKEVE	900

Search completed: February 9, 2005, 08:53:09
Job time : 117.873 secs


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Db 338 EDEAVLFSNKAFFASLEQCRQNTONLEPIARKLVERCOGLPLAIAIASLGSMMSMKFPESEWK 397
Qy 396 KFYEQLPSELEINPSLEALRMVMTGYVNHLPKPCFLYLSIPPEDEFEIQRNRLVGRWI 455
Db 398 KYSTLWELNNHELKIVRSIMFLSFNDLPYPLKRCFLYCSLFPVNTMRKRLRMWM 457
Qy 456 AEGVFRPVKGMVTTKDVGSYFNELINRSMIQSRVGTAGKIKTCRIHDIIRDITVSISRQ 515
Db 458 AORFVEPIRGVKAEBEADSYLNELVYRNMLQVILWNPFGPRKAFKMDHVIWEIALSVSKL 517
Qy 516 ENF--VLLPMGDSGLVQ--EN--TRHIAFHGSMCKTGLDWSIIRSLAIFGDRPKSLAH 569
Db 518 ERFCVDVNDSDGDAETMENYSRHLCIQKEMT--PDSIRATNLHSLLVGSSAKHKM-- 574
Qy 570 AVCDDQLRMRLVLDLEDVTLITQKDFRIALLCHLKVLSIGYSSSIYSLPRSIGKQGL 629
Db 575 ELLP--SLMLLRALDLEDSSI---SKLPDCLVTMFLNLYLNLS--KTQVKELPKNFHKLGNL 629
Qy 630 QTLNMSSTYIAALPSEISKLOCLHTLCIRIELEFDNPSLNPMKCIITNTICLPKVFTPLV 689
Db 630 ETLNTHKSHIEELPLGMWKKLRLVITFRNE----- 662
Qy 690 SRDNRKQIAEFHMATKSFWSSEFGVKPGKIGIKGLDLOVLEYVDVRTSRAIKELGQL 749
Db 663 -----GHDSNMNYVLGTRVVPKIVQLKDLQVM---DCFNAEDELINLQCM 705
Qy 750 SKRLKLAIVITKGTKECKIILYAIEKLSLSQSLYMAALLSDIETLECLDSISSPPLL 809
Db 706 TQLTRISLVM--VRRHGRDLCDSLNTKIRL--FLSLTSDIEBEPLDILITAS--I 759
Qy 810 RTLGINGSLEMPNWIQLTHKFLNWSKKEGKNMLILGALPNLMFLSLYHNSYLGE 869
Db 760 EKLFLAGKLERVPSWNTLQNLTYLGLRGSQLENA--ILSIQTLPRVLWLSFY-NAYMGP 817
Qy 870 KLVFKTGAPPNRLTVIPNLQDLREIRPEDSGSSPOLEKIEISCCR--LBSGIIGIHLPRL 928
Db 818 RLREFAQQ--FQNLKILEIVQMKHLETVIEDGAMFELQKLYVRACRGLEYVPRGIENLNL 876
Qy 929 KEISLEYKSKVARLQGLQKGEVNTHPNR 955
Db 877 QELHLIHVSN--QLVERINGEGSVDRSR 902

RESULT 2
T12977
hypochemical protein T6H20.240 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12977
R;Choiane, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17586
A;Accession: T12977
A;Molecule type: DNA
A;Residues: 1-847 <CH>
A;Cross-references: UNIPROT:Q9SPF7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240
A;Experimental source: cultivar Columbia; BAC clone T6H20
C;Genetics:
C;Gene: ATSP:T6H20.240
A;Map position: 3
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 15.7%; Score 827.5; DB 2; Length 847;
Best Local Similarity 27.7%; Pred. No. 1.6e-39;
Matches 267; Conservative 176; Mismatches 333; Indels 187; Gaps 36;
Qy 8 MARSILVSAISKAASAAANETSLIGVDEKDIWYIKDELTKTQAFILRAAEVMMKKXDELKLV 67
Db 1 MVDATVGFVINKIGGYLINEVALMGVKDDLEELKTELTCIHGYLKQVAREDEREVSKE 60
Qy 68 WAEQIRLDLSYDIENSLDFKVVHIESQTLFRLQVLK-----RRHRTAIRHNLKSRVE 120
Db 61 WTKLVLDIADIEDVLDYTFYFLKLEERSLRRLGLRLTNKIGKRDAYNIVEDIRTLKRRIL 120
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Qy 121 EVSSRNTRYNLVPEISSGTEDDMDSYAEDIRNQSARN-----YDEAEL--VGFSDSKRL 173
Db 121 DITREKRETF-----GIGSFNPRGENITNVVRQLRRAPPVQDEELVGLGDDVKIL 172
Qy 174 L-EMIDTNANDGPAKVICVVMGGLGTALSRKIFESEEDIRKPPCNAMWITSQSFHRI 232
Db 173 LVKLLSDNEKD--KSYIISIFGMGGLGTALARKLYNS--GDVKKRFDICRAWTVYSQEVKTR 230
Qy 233 ELLKDMIRQL--LGPSSLDQLLHLEQKVVVQVHHLSYLLIEELKEKRYFVVLDLWLH 290
Db 231 DILIRIIRSGIVSABEMEKI-----KMFEEDELEVLYLGLLEGKNYVMVDDVMDPD 284
Qy 291 DWNMINBIAPKNNKGSRIVITTRNVDLAEKCATASLVVHLDPLQMNDAISLLIRKTNK 350
Db 285 AWESLKR--ALPCDH--RGSKVITIRIRAIAGVEGTYYAHKRLFTLFEESWTLPERKAFS 342
Qy 351 NHEDMESNMQNMVERIVNKGRLPLAILTIGAVLATKQVSEWEKFYEQLPSELEINPS 410
Db 343 NIEKVD--EDLQRTGKEMVKKCGGLPLAIVLVSLGSLSRKRTNEHVEVCASLWRLKON--S 399
Qy 411 LEALRRMVTILGYNHLPKPCFLYLSIPPEDEFEIQRNRLVGRWIAAGFVRPKVGMWTKD 470
Db 400 IH--ISTVFDLSFKEMRHELKLCFLYFVFPDEYIEKVEKLHLLVAEGFIOEDSEMMEED 458
Qy 471 VGESYFNELINRSMIQSRVGTAGKIKTCRIHDIIRDITVSISRQENFVLL--PMWGDSGD 528
Db 459 VARYCIDELVDRLVKAERI--ERKVMSCRIHDLRLDAIKKAKELAFNVVYNEKHQSSD 517
Qy 529 LVQENTRHIAFHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPD--QLRMLRVLIDEDV 587
Db 518 ICRREVVHLMNDYLLCDRRVN--KRMSFLFIGER--RGFGYVNTNLKLLRLVLMBGL 575
Qy 588 TFL---ITQKDFDRIALLCHLKVLSIGYSSSIYSLPRSIGKLOGLOTLNMSSTYIAALPS 644
Db 576 LFVSKNISNTLPDVGELIHLRYLGIA--DTVVSILPASISNLRFLQTLDAAGNDPFOVTT 634
Qy 645 EISKI-----QC-----LHTRCIRELEFDNFSLNHPMKCIITNTICLPKVF 685
Db 635 DLSKLTSLRHVIGKFVGECLIGEVNLTLSISYSWS--KLNHEL----- 679
Qy 686 TPLVSRDNRKQIAEFHMATKSFWSSEFGVKPGKIGKRLDQVLE-----YVDIRRTS 739
Db 680 -----LRLQDLLEYDHSKVDQRRVP 701
Qy 740 SRAIKELGQLSKRLKLAIVITKGTKECKIILYAIEKLSLSQSLYMAALLSDIETLECL 799
Db 702 LNFV-----SFSKPKNLRVL-----KLE-----MRNFKGJSESRTTIGL 735
Qy 800 DSISPPPLRLRTLGLANG--SLEEMPNIWIEQLTHKKFNLWSSKKEGKNMLILGALPNLMF 858
Db 736 VDVNFPSS--LESLLTVGTLEE-----NNSMPALQKLPLED 769
Qy 859 LSLYHNSYLGEKLV--FKTGAPPNRLTVIPNLQ-----LREIRPEDGSSPOLEKIEISCC 913
Db 770 LVLKDCNYSYGVKIMSAQGFGRUKNLEM--SMERRGHGLDELRIEEEAAMPSLIKLTVK--G 827
Qy 914 RLE 916
Db 828 RLE 830
```

RESULT 3

G96821

probable disease resistance protein F23H11.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: G96821

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

RESULT 4

T45590
hypothetical protein F12A12.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Mar-2000
C:Accession: T45590
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23008
A:Accession: T45590
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-835 <CHO>
A:Cross-references: EMBL:AL13314
A:Experimental source: cultivar Columbia; BAC clone F12A12
C:Genetics:
A:Map position: 3
A:Note: F12A12.50
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein

Query Match	15.2%	Score 798.5;	DB 2;	Length 835;
Best Local Similarity	28.0%;	Pred. No. 7.2e-38;		
Matches 264;	Conservative 169;	Mismatches 360;	Indels 149;	Gaps 33
Qy .	8 MARSLVGSATSKAASAAANETSLLLGVEKDIIWYIKDELKTMQAFLRAAEVWKQDELLKV	67		
Dd	1 MVDAITFVVVGKIGNYLIEEASMPMAVKEDLELKTCLTCIHGYLKQVEAREDEVSK	60		
Qy	68 WAEQIRDSLYDIEDSLDFKHIESOTLFROLVKLRER-----HRTAIRHLNKSRYE	120		
Dd	61 WSKVLDPADVDEVDLTYYHLKEERSQRGLRLTNWIKGRMDAYSIVDDIRILKRILL	120		
Qy	121 EVSSRNTRY---NLVPEISSGTEDDMDSYAEDIRN-QSARNVDAB-LVGFSDSKRRILE	175		
Dd	121 DITRKRETYGGIGLKEPQGGSSTL----RVQLRRARSDVEVVVGLEDDAKILLE	175		
Qy	176 MIDTNAANDGAQVLCVGMGLGTALSARKTFESEEDIRKNPCPNAMITVSQSFRIELL	235		
Dd	176 KL-LDYEEKRFIISIFGMGLGTLAKRLYNLS-RDVKERFEYRAMTYTVSQEYKTDGIL	233		
Qy	236 KDMIROLLGPSSLDOLLAHELQGVVVGVHHLSYELBELKEKRYFVVLDDLWLHDWNVI	295		
Dd	234 MRIIRS-LGMTSGEEL--EKIRKPABE--ELEVLYGLEGKKYLVVVDDIWERENWSL	288		
Qy	296 NEIAFPKNNKKGSRIVITTRNVDLAEKCATASLVYHLDFLQMNDAISLLLRKTNNQHEDM	355		
Dd	289 KR-ALPCNH-EGSRVIIITRIKVAEGVDGRFYAHKLRLFTFESSWELFEQAFENIQ-	344		
Qy	356 ESNNKMGMQWRIVNKCGRLPLAITLTGNVLATKQVSEWEKFYQLPSELINSPLEAR	415		
Dd	345 RKDEDLLTKGEMQKCRGPLCTVWLAGLSRKTPSEWINDVCNSLMRRLL-DDSIHVAP	403		
Qy	416 RWVTLGNYHLPShLKPFLYSIPPEPFQORNRLVGRWIAEGFVRPKVGMTTKDVGESY	475		
Dd	404 IVFDLSFKELRHESKLCFLYSIPPEYEDLEKLIHLLVAEGFIQGDSEMMEDVARY	463		
Qy	476 FNELINRSMIQRSRVGTAGKIKTCRIHDIITDVTSISRQBNFVLLPMGDSGLVQENTR	535		

Db 464 IEELIDRSLLEAVR--RERGVKWSRIHDLRLDVAIKKSELNF-----VNVYND 511
Qy 536 HIAFHGSMCKTGL-----DWSIIRSLAIFGDRPKSLAHAVCPD--QLRMLR 580
Db 512 HVAHSSSTCRREVVHHPQKRYSEKRNKMRGFLYFGE-----FDHLVGLDFETLKLR 567
Qy 581 VLDLEDVFLITQKDFORIALLCILKLYSI--GYSSSIYSLPRISCKLQGLQTLNMSSTYI 639
Db 568 VLDGSLWL-----PFKINGDLHLRYLIGDINSINDFIAAISKRLFLQTLFVSQNYF 622
Qy 640 AALPSEISKLOCLHTLRCIRELEFDNPSLHMPKCIITNTICLPKVFPTPLVSRDNRKQIA 699
Db 623 IEETIDLRKLT-----SLRH-----VIGNPFGLLIGD-----VA 652
Qy 700 EFMATKSFWSFESFGVKPKGIGKLRDLQVLEYVDIRTSRAIK--ELGQSLKRLKLA VI 758
Db 653 NLQTLT--SISFDSWNKLPPELLINLRDIGISE---MSRSKERRVHVSWASLTKLESURL 708
Qy 759 TKGSTKECKILYAAIEKLSLSQSLYMAAALLSDIETLECLDSISSPPPLRLTLGLNGSL 818
Db 709 -----KLATFEVHLS---LESEEA VRSDVIRSLSLESTLVGI--TF 746
Qy 819 EEMPNWIEQLTHLKKFNLWSSKLEGRNMLILGALPNLMFSLYHNSYLGSKLVFKTGAP 878
Db 747 EEDP-----MPFLQKMPRLLEDLILLSCNYSGRKMSVSEQ--F 781
Qy 879 PNARTLVIFNLQDLREIRFEDGSSPOLKIEIKISCCRLESGLI 920
Db 782 GLRLKLDLL--MRSDELQIEEAMPNLITELISVSKRETKLI 822

RESULT 5
T48899
disease resistance protein rpp8 [similarity] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T48899
R;McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl
Plant Cell 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolution
of Arabidopsis thaliana RPP8
A;Reference number: 234999; MUID:99030193; PMID:9811794
A;Accession: T48899
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-308 <MCD>
A;Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AAC78631.1; PID:g3901294
A;Experimental source: Columbia
C;Genetics:
A;Introns: 293/1; 342/1
C;Function:
A;Description: susceptible allele of a gene that promotes resistance to Peronospora para

Query Match 15.2%; Score 796.5; DB 2; Length 908;
Best Local Similarity 25.8%; Pred. No. 1.1e-37;
Matches 267; Conservative 199; Mismatches 360; Indels 209; Gaps 37;

Qy 8 MARSIVGSAISKASAAANETSLILGVKQDIWIYKDELKTQAFIRAAEVWKKXDELKV 67
Db 1 MAEAFVSFGLKLDLLSRESERLQDGLKQRLSRSLQSLKADAKKHGSDRVN 60
Qy 68 WAEQIRDLSDYEDSLDF-----KVHIESQTLFRQLVKLRERHRIAIRIHN 115
Db 61 FLEDVKDLVFAEDTIEISYVNLKSGKGKGVKVRRLACP-----LTDHKKVASDTEGI 115
Qy 116 KSRVEEVSRRNYNLVPISSGTE---DDMDSVAEIDIRNQSAARNVDPAELVGFSDSKR 172
Db 116 TKRISEVIGMQSGFIQIQIDGRSLSLQERQVRQREIR--QTPDSSSDSLVGVEQSVE 174
Qy 173 LL-EMIDTNANDGPAKVTVVGMGGLGKTALSRKLFESSEEDIRKNPFCNANITVSQSFHR 231
Db 175 LVGHLVENDVH----QVVSIAAGMGIGTKTTLARQVHF--HDLVRRHFDGFAWVCVSQQTQ 229

Qy 232 IELLKDMIRQLLQSPSSLDOLLHELQ---GKVV--VQVHHLSEYLIEELKEKRYFVVLDDLM 287
Db 230 KHVWQ-----RILQELQPHGDITLQWDEVALQKLFQLEAGRYLVVLDDVM 276
Qy 288 ILHDWNNINEIAPPKNKKSRIVITRNVDLARKCATASLVYHLDLFQMDAISLLRK 347
Db 277 KKEDWDVIKAV--FPR--KRGWKMLLTSRNEGVGVIHADPTCLTFRASILNPEESKLCERI 333
Qy 348 T--NKNHEDMESNKNMKWVERIVNKGGRPLAIIITIGAVLATKO--VSEWEKFEQLPSE 404
Db 334 VPPRRDETVELDEEMANGKEMWTHCGGLPLAVKALGGLLANKHVTPWKRKRVFNTGSG 393
Qy 405 -----LEINPSLEALRRMVTGYNHLPKPCFLYLSIFPDEFEIQRLNRLVGRWIAEG 458
Db 394 IVGGSWLDN--SLNSVYRILSLSYEDLPTLHKHCFNLNLAHPPEDESEISTYSLFYMAAEG 452
Qy 459 FVRPKVQMTKDVGESYFNELINRSMIORQSRVGTAGKIYTCRIHDIIRDTIVTSIROBNF 518
Db 453 IYD---GSTIEDSGEYYLEELVRNLVIADNLYLSWQSKYQCMHDMRREVCLSKAEEFN 509
Qy 519 ---VLLPMGDSGLVQENTR-----HIAFHGSMCKTGLDWSIIISLAI--- 559
Db 510 LQIITDPTCTSTINAQSPSRRLSIHSGKAFHILGHKN---KTK-----VRSILVPRPE 561
Qy 560 --FGDRPKSLAHAVCPDQLRMLRVLDLEDVTFITQKDFORIALLCILKLYLSIGYSSSIY 617
Db 562 EDYWIRASVFH-----NLTLRVLDLSWVKFEGGKLPCS--IGGLIHLRYLSL--YEAKVS 614
Qy 618 SLPRSIGKLOGLQTLNMSSTYIAALPSEISKLOCLHTLRCIRELEFDNFSLNHPMKCITN 677
Db 615 HLPSTMRNLKLLLYNL-----RVDTEEPHVPNLKEM----- 648
Qy 678 TICLPKVFTPLVSRDNRKQIAEPMATKSFWSFGVKPKGIGKLRDLQVLEVVDIR 737
Db 649 -IQRLYLSLPL--KXMDTKL-----ELGDLNVLNLYLGFS 681
Qy 738 TSSRAIKELGQSLKRLKLVITKSTKEC--KILYAAIEKLSLSQSL----- 783
Db 682 TQHSVTDLRMTKRLVAV---SLSERCNFTLSSSLRELRLNLETINFLFSLETYMVD 737
Qy 784 YMNAAALSDIETLECL-----DSISSPPPLTLTLGLNGSLEEMPWI--EQLTHLK 832
Db 738 YMGFEVLDFHFLKQLGLAVRMSKIPDQHPFPHLFLIYCGMEEDPMPLEKLLHLK 797
Qy 833 KFNLSKKLEKGNMLILGALPNLMFSLYHNSYLGSKLVFKTCGAFPNLRTLVIFNLQDL 892
Db 798 S-----VRLKARFAGSRMVCCKGFFPOLCVIEISKSESL 832
Qy 893 REIRFEDGSSPOLKIEIR--SCRLSEGIIGIHLPLRKEISL-----EYKSKVARLGQLK 946
Db 833 EEWIVEGSMPELTLTIDCKKLKELPDGLKYITSLKELKIEGMKREWKELVPGGEDY 892
Qy 947 GEVNTNRRPVLKMD 961
Db 893 YKVQHIDPVDQFINCD 907

RESULT 6
T51185
resistance protein RPP13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000
C;Accession: T51185
R;Bittner-Eddy, P.D.; Crute, I.R.; Holub, E.B.; Beynon, J.L.
Plant J. 21, 177-188, 2000
A;Title: RPP13 is a simple locus in Arabidopsis thaliana for alleles that specify downy
mildew resistance
A;Reference number: 225333
A;Accession: T51185
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-831 <BIT>
A;Cross-references: EMBL:AF209731; PIDN:AAF42831.1
A;Experimental source: cultivar Rid


```
Db 568 SVFH-----NLTLLRLVLDLYWKF--EGGKLPSSIGGLIHLRYLSL-FLAGVSHLPSTWRN 620
Qy 626 LOGLOTINMSSTYTAALPSEISKLQCLTLRLACIRELEFDNFSLNHPMKCINTTICLPKVF 685
Db 621 LKLLLYNLNS-----VNNKEPIHVPNLVKEM-----TOLRYLS 653
Qy 686 TPLVSRNRAKQIAEFHFMATKSFWSFSGVVPKPGIKGLRDLQVLEVVDIRRTSSRAIK 745
Db 654 LPL-KKDKTKL-----ELGLDVNLEFLPGSTQHSVTD 687
Qy 746 LGQLSKLRKLAVITKGSTKEK--KILYAAIEKLSLQSLYM---NAALLSDIETLECLD 800
Db 688 LLHMTKRLYLAV---SLSERCNPETLSSSLRELRLNLTLYLFSPEIFVMYMGFEVLD 743
Qy 801 SSSPPPLRLTLGLNGLSLEPNWIEQLTHLKKFNLMSSKLKEGKNMILGALPNLMFLS 860
Db 744 HFTH-----LKEGLAVRMKSPDQHLPPHIAQIYICNCRMEEDP-MPILKJLHLKSVK 798
Qy 861 LYHNSYLGEKLVFKTGAPPNLRTLVFNLDQRLREIRFEDGSSPOLEKIEI--SCCLRESGI 919
Db 799 LTFKAFAGRMVCKSGGFTQCALEISEQSELEEWIVEEGSMPCRLTITHDCEKLEKLP 858
Qy 920 IGIHLPLKBEISL-----EYKSVARLGOLKGENVTHPNRPVLRMD 961
Db 859 DGLKYITSLEKLTIEGKMKREWKELVPGGEDYKYVQHIPPVQFINCD 905

RESULT 8
T51186
resistance protein Rpp13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C;Accession: T51186
R;Bittner-Baddy, P.D.; Crute, I.R.; Holub, E.B.; Beynon, J.L.
Plant J. 21, 177-188, 2000
A;Title: Rpp13 is a simple locus in Arabidopsis thaliana for alleles that specify downy
A;Reference number: 225333
A;Accession: T51186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-820 <BIT>
A;Cross-references: UNIPROT:Q9M667; EMBL:AF209732; PIDN:AAF42832.1
A;Experimental source: cultivar Neiderzens
C;Genetics:
A;Gene: RPP13
A;Map position: 3
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 14.9%; Score 782; DB 2; Length 820;
Best Local Similarity 27.7%; Pred. No. 6.2e-37;
Matches 259; Conservative 172; Mismatches 347; Indels 156; Gaps 34;

Qy 8 MARSLSGSAISKAASAAANETSLILGVKEKDIWIYNDELKTMQAFRLRAAEVNMKKDELKRV 67
Db 1 MVDAITFPVVGKIGNYLIEEASMFMAVKEDLEELKTELTCIHGYLKQVEAREDEVSKE 60
Qy 68 WAQIRLDSDYIEDSLDFKVIHSQTLFROLVKLR-----HRIAIRHNLKSRVE 120
Db 61 WSKLVDFAYDVEDVLDYTHLKLSESRQRLRLTNKIGRMADAYSVDVDDIKILKRIL 120
Qy 121 EVSSRNTRY---NLVEPISSTGEDMDSYADIRN-QSARNVDRAE-LVGPSDSKGLLE 175
Db 121 DITKRETYIGGLKEPGGGNTSSL-----RVQLRRARSVDQEEVVVGLADDAKILLE 175
Qy 176 MIDTNANDGPAKVICVWGMGLGTALSRKIFESIEDIRKNFPCNAMITVSQSFRIELL 235
Db 176 KL-LDYDEKNRFIISIFCMGGLGTALKARKLYNS-GDVKRRFEVRAWTVYSQEVKTGDL 233
Qy 236 KDMIRQLLGPSSLQDLLEHLOQKVVVQVHLSYVILIEELKEKRYFVVDLWILHDNWI 295
Db 234 MRIIKS-LGMTSGE-----ELEKIRMFABEEVLEVLHGLLECKYLVVVDWIWERAEWSL 288
Qy 296 NEIAPPKNKKGSRIVITTRNVDLAEKATASLVVHLDFLQMDAISILLIRKTNKNHEDM 355
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Db 289 KR-ALPCNH--EGSRVITITRIKAVAEGLDGRFYAHKRLFLTFFESWELFEQRAFNIQ-- 344
Qy 356 ESNKNQKQWVERIVNKCGRPLPLAITTIGAVLATQVSEWEKFYEQLPSELEINLSLEALR 415
Db 345 KROBDLLTKTKEMVQKCRGLPLCIVLWLAGLSRKTPSEWINDVCNSLRRLK-DDSIHVAP 403
Qy 416 RMVTLGYNHLPShLPCFLYLSIFPPDEFIQNRNLVGRWIAEGFVRPKVGTHTKDVGBESY 475
Db 404 IVFDLSFKELRHESKLCFLYLSIFPPEDYEDLEKILRLVAEGFIQGDDEMMEDVARY 463
Qy 476 FNELINRSMIQSRVGTAGIKTKCIHDIIRDTIVTSISROENFVLLPMGDSGLVQENR 535
Db 464 IEELIDRSLLEAVR--RERGKVMSCRIHDLRLDVAIKSKELNF-----VVVYND 511
Qy 536 HIAFHGSMCKTG-LDWSI-----IRSLAFGDRPKSLAHAVCPDQLRMLRVLDLED 586
Db 512 HVSQHSSTTCRRQVNVNHQIKRFARNKMRSPFLYFEGEL-KFLVR-LDVEKLLRLVLDLEA 569
Qy 587 VTFLITQKDFDRIALLCHLKYLSI-GYSSSIYSLSRSGIKLOGLOTLNMSSTYIAALPSE 645
Db 570 LL-----GPFASNGDLLHLRYLRFDFGSLRFVDFIAALISKRFLOTLDADHV----- 616
Qy 646 ISKLQCLHTLRCIRELEFDNFSNLNHPMKCITNTTICLPKVFTPLVSRDNRAKQIAEFHM-- 703
Db 617 -----CP-----IVDTIDLRK-FTSL--RHVIGKFGVCELLIGD 646
Qy 704 -----ATKSFWSSEFVKVPGKIGKLRDLQVLEVYDVRTSSRAIK-ELGQLSKLRKLV 757
Db 647 AANLQTLRSISSDSSWSKLKHELLINLRDLRI--YEDYNKSKERRVTVSWASLTKLRLSRV 704
Qy 758 ITKGSTKECKILYAAIEKLSLQSLYMNAALLSDIETLECLDSISSPPPLRLTLGLNG- 816
Db 705 LK-----LVADRRVLSLES-----EAVRSMQVIS---PSLESVTLVGI 740
Qy 817 SLEEMPWIEQLTHLKFNLWSSKLKEGKNMILGALPNLMFLSLYHNSYLGEKLVFKTG 876
Db 741 TFEEDP-----MPFLQKMRLEDLIFENCYDYGWGGKMSVSEQ 776
Qy 877 AFPNRLTVFNLDLQRLREIRFEDGSSPOLEKIEI 910
Db 777 GFGRLRKILF-INRLDELQIEEAMPNLIELVV 809

RESULT 9
F96573
protein F12M16.25 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96573
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Chung, M.K.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96573
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1584 <STO>
A;Cross-references: UNIPROT:Q9MAG6; GB:AB005173; NID:g7769860; PIDN:AAF69538.1; GSPDB:GNI
C;Genetics:
A;Gene: F12M16.25
A;Map position: 1

Query Match 14.8%; Score 776; DB 2; Length 1584;
Best Local Similarity 26.5%; Pred. No. 3.5e-36;
Matches 257; Conservative 192; Mismatches 376; Indels 146; Gaps 33;
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Db 614 VSHLPSSLRNVLIIYL-----DIRTDFIVPNVFMGM--RELRYLEL 656
Qy 699 AEF-HMATKSPWSFGVKPGIGKLDIQVLEVDVDIRRTSSRAIKELGOLSKRLKLV 757
Db 657 PRFHEKTKL-----ELSNLEKLEALENFSTKSSLEDLRGWRLRLTVI 701
Qy 758 ITKSTREKCKILYAAIEKLSLQSLYNMAALLSDIETLECLDSISSPPPLRLTGLNGS 817
Db 702 ILSEGT-----SLQTLASVCGLRHLENFK-----IWENAGVNRM 736
Qy 818 LEENPNWIEQTHLKKNFL-----WSSKLGKGNKMLIIGALPNL 856
Db 737 GEE--RMVLDFTYLLKLTLSIEMPRPKIQLHPSHLTVLDLSYCCLEDPMPLEKLIEL 794
Qy 857 MFLSYHNSYLGKLVKFTGAPPNLRTIVFNLDQREIRFEDGSSPOLEKIEISCCRLE 916
Db 795 KDLSDLYLSFGSRKWKVCSAGFPQRLKALDEQBEWEWIVEEGMSRLHTLSIWSSTLK 854
Qy 917 SGIIGIHLPRLEISLEYKSKVARLGQKGEVNTNPNRPVLRMDS 962
Db 855 ELPDGLRPIYSLKXNLIMG-KSWMERLSERGEFYKVNIPKFPSS 899

RESULT 11
F96617
Probable disease resistance protein F9K23.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96617
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96617
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-907 <STO>
A:Cross-references: GB:AE005173; NID:gl1034963; PIDN:AAG27118.1; GSPDB:GN00141
C:Genetics:
A:Gene: F9K23.8
A:Map position: 1

Query Match 14.5%; Score 760; DB 2; Length 907;
Best Local Similarity 26.9%; Pred. No. 1.3e-35;
Matches 255; Conservative 181; Mismatches 399; Indels 114; Gaps 25;
Qy 8 MARSLVGSIAKSAASAAANETSLILGVEKDIWIYIKDELKTMQAFURAAVNMKKDELLKV 67
Db 1 MAGELVSGIKKLDWLLSQEQEQGVEDVTKLRDLNLLSSFLKQADAKKHTTAVVRN 60
Qy 68 WAEQIRLSDYIEDSLDF-----KVHIESQTLFROLVKLRHRHRIAIHNLKSRVE 120
Db 61 VVEBIKEIVYDAEDIIETIYLLKELKWTSGIKMRIRHACIISRDRNALDVGGRIRIS 120
Qy 121 EVSSRNTRYNLAPEPISSTGTEDDMSYADIRNQSARNVDEALGFSDSKRKLLEMDTN 180
Db 121 DVIDMQSGVQQAIVDGGYNQPGDQRQREMRQFTSKDYSDFVGLGVNVKLVGYLVDE 180
Qy 181 ANDGPAKVICVGMGGGLKGTALSRKIFSEEDIRKNFPFCNAWITVSQSFHRIELKQIR 240
Db 181 EN---VQVVSITGNGGLKTTTLARQVF-NHEDVKHQFDRLAWVCVQEFTRKNVQMILQ 236
Qy 241 QLLGSSLDQLLHLELQGVVQVHLSYLLIEELKEKKYFVVDLDLTLHDDWNNINEIAP 300
Db 237 NLTSREKDETLQ-----MEEAEHLKLPQLLETSLKSLIVFDDIKWDEWDLIKPI-F 288

Qy 301 PKNNKSGRIVITTRNVDLAEKCATASLVVHDLFQMDAISLLLRKT--NKNHEDMESN 358
Db 289 PPN--KGMVLLTSQNESVAVRGDIKYILNFKPECLAIEDSTLQRIAPFKDASESKVD 346
Qy 359 KMQQWVERIVNKCGRPLPAILTTIGAVLATK-QVSEWEKPYEQLPSEL--EINFSEALR 415
Db 347 EEMDMGQMLKHCGGLPLAKIVLGGLLAAKYTHDWERLSWNIGSDIVGRTSNNSIY 406
Qy 416 RMVTLGYNHLPKPCFLYLSIPPEDFEIQRNRLVGRWIAEGFVRPK--VGMTTKDVG 472
Db 407 HVLSSFEELPSYLUKHCFLYLAHPEDHKINVEKLSYCAAEGISTAEYNGETIQDVG 466
Qy 473 ESYNELINRSMIQSRVGTAGIKTCRIHDIIRDITVSISRQBNFVLLPMGDSGLVQE 532
Db 467 QSYLEELVRNMIWERDATASRGFTCHLHDMMEVCLFKAKEENFLQIA----- 516
Qy 533 NTRHIAFHGSMSCKTGLDWSIIRSLAIFGRPKSL--AHAVCPQLRLMLRVL--DLEDVT 588
Db 517 ----VKSQVGTSSSTGNSQSPCRSRRLVYQCTTLHVVERDINNPKLRSLLVVLHDLWYEN 572
Qy 589 FLITQKDPDRITALLCHLKYSIGYSSSYSLPRSIGKLGLOTLNMSSTYIAALPSEISK 648
Db 573 WKLGTSFTRKLRLRLDLFYVDFEG--MKLPFGIGNLIHLURLYLSQDAKVSHLPSSLGN 630
Qy 649 LQCLTLRLCIRELEF----DNFSLNHPMKCITNTICLPKVFETPLVSRDNRRAKQIAEPHMA 704
Db 631 LMLLIYLNLDVDTSEFIFVPDVFMRMHELRYLK----LP-----LHMH 668
Qy 705 TKSWFSSSFGVKVPGKIGKRLDQVLEVDVDIRRTSSRAIKELGOLSKRLKLV-ITKGST 763
Db 669 KKTRLS-----LRNLVKLETLYVFTSWHSSKDLGCMTRLTMLTAIRLTRVTS 715
Qy 764 KECKILYAAIEKLSLSQSLYMAALLSDI-ETLECLDSISSPPPLRLTGLNGSLBEMP 822
Db 716 TE---TUSASISGURNLEYLIVGTHSKMKREEIVLDFIH-----LKHLLDLYMPRQQ 767
Qy 823 NWIBQLTHLKFNLWSSKLKEGKNMLILGALPNLMFLSLVHNSYLGKELVKTGAFFNLR 882
Db 768 HFPSRLTFVK--LSECGLEEDP-MPILEKLLHLKGVILLKGSYCGRRMWCSGGFPOLK 823
Qy 883 TLVIFNLDQRLREIRFEGSSPOLSKIEISCCRLESGIIGIHLPRLEI 931
Db 824 KLEIVGLNKWEWLVERGSMPLLETLSILDCE-----ELKEI 860

RESULT 12

B96538
hypothetical protein F14I3.19 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B96538
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96538
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-839 <STO>
A:Cross-references: UNIPROT:Q9SX38; GB:AE005173; NID:g5734781; PIDN:AAD50046.1; GSPDB:GN1
C:Genetics:
A:Gene: F14I3.19
A:Map position: 1

Query Match 14.4%; Score 757.5; DB 2; Length 839;
Best Local Similarity 26.1%; Pred. No. 1.6e-35;

Matches 251; Conservative 173; Mismatches 357; Indels 179; Gaps 31;	
Qy	8 MARSIVGSAISKAASAAANETSLLLGVKEDIWIYIKDELKTWOAFURAAEVMMKKDELKLV 67
Db	1 MAEAIIVSVTKLQGLLEELPLFGIGQVKQLDELKRLNCLFKDADEKHESERVN 60
Qy	68 WAEQIRDLSDYIEDSLDFPKWHIESQT--LFRQLVKLRERHRIAIRHNLSKRVVEVSS 124
Db	61 WYAGIREASYDAEDTLEAFFLKAESRKQKMKVRLRLACLINAEVSLHSGVSEIREITS 120
Qy	125 RNRIRNLVPEITSSGTEDDM-----DSYAEIRNQSANRVDAELVGFSDSKRLLE 176
Db	121 RLSKI-ASMLDFGIKESMGREGLSLSLRB--QRQFPYVVENVLVGLSQSLKLVN- 176
Qy	177 IDTNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELK 236
Db	177 -DLVSGGSEKLARVTSICGMGGLGKTTLAKQIFHHKK-VRRHFDRAFWVTVSQDCRRRHVWQ 234
Qy	237 DMIRQLLGPSSLDQLLHLELQGVVQVHLSYLIEELKEKRYFVVLDDILWLDHWNIN 296
Db	235 DIFNLN-----SYKDENQRILSRDQLGEELHRLPKRNKCLVLVDLWGDQAWDCIK 287
Qy	297 EIAPFNKKNGSRIVITTRNVVDLAEKCATASLVVHLDLQWMDAISLLRLRKNKHEDME 356
Db	288 HV-FP--HETGSEIILTRNKEVALYADPRGVLPQLTCEESWELLEKISLSGRENIE 344
Qy	357 SN--KMQMQRVERIVNKCGRPLAILITIGAVLATKQV-SEWEKFYEQLPSELEINPSLEA 413
Db	345 PMLVKQMEIGKQIIVRCGGPLAITVLGGLATKSTWNEQRCVENIKSVYNGGSSNG 404
Qy	414 LRRWVT-----LQYNHLSHLKPCFLYLSIPEDFEIQRNRLVGRWIAEGFVRP-----KV 464
Db	405 SKNLVADVCLSYELPFPVHKQCFLYFAHPYEDYEVHVGLTVSYCIAEGVMVPVKHTEA 464
Qy	465 GMTTKDVGESYFNEILNRSMTQRVSG-TAGIKTCRIHDIIRDITVSISROENFVLLPM 523
Db	465 GTTIVEDVQDLEELVKKRSMVWGRDITVSEVTCRMHDLRMREVCLOKAKQESFVQVID 524
Qy	524 GDGSDLVQENTRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPQLRMLRLVD 583
Db	525 SRDQDEAB-----AF---ISLSTWTSRRI--SVQLHGGAEH-----556
Qy	584 LEDVTFLITQDFDRIALLCHLKYSIGYSSISYLSRPSIGKLQGLQTLNMSSTYIAALP 643
Db	557 -----HIKSLS-----QSPEREIDKREG-----TVII---578
Qy	644 SEISKLOCLHTLCIRLEFDFNFSLNHPMKCITNTICLPKVTPLVSRDRAKQIAEFHM 703
Db	579 --YWKLVDDYSRLVRE-----RA-----595
Qy	704 ATKSPWSESFGVVKPGIKGLRDQLQVLEYVDIRRTSSRAIKELGQSLKRLKLAIVITKGST 763
Db	596 ---TVYSKHLDPKTKLDLSTLRNLQQLWDPPVGKCNPR---DLLAMTSLRLSLI--NLS 647
Qy	764 KECKKILYAAIEK-LSSLSQSLYMA--ALLSDIETLECLSDISPPPLTLTLGLNGSLE 819
Db	648 QNTDFVWVSSLSKVLKRLRLGLTINVPCEPLPPVDVTQLVSAFTN---LCELELEFLKLE 703
Qy	820 EMPNIEWEQLTHLKKFNWSSKLKEGKNMLILGALPNLMPLSIYHNSYLGEXLVPKTAGFP 879
Db	704 KLPEQSPSSDLGALRLQCGLVDDP-FMVLEKLPNLKILQLFEGSFVSGKLCCSK-----758
Qy	880 NLRTLIVPNLQDLREIRPEDGSSPOLEKIEISCC-RLESGIIGIHLPRLKEISLEYKSK 938
Db	759 -----NLENLEBWTVDGMMWRLVTVELKCCNKLKSVPEGTFPLKNLQVEIGNRTK 810

RESULT 13
G96617
probable disease resistance protein F9K23.7 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G96617

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafai, R.; Marziani, C.A.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96617
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-900 (-STO>
C;Cross-references: GB:AB005173; NID:g11034962; PIDN:AAG27117.1; GSPDB:GN00141
C;Genetics:
A;Gene: F9K23.7
A;Map position: 1
C;Superfamily: disease resistance protein RP82; leucine-rich alpha-2-glycoprotein repeat

Query Match 14.1%; Score 741.5; DB 2; Length 900;	
Best Local Similarity 25.4%; Pred. No. 1.5e-34;	
Matches 247; Conservative 197; Mismatches 389; Indels 139; Gaps 32;	
Qy	8 MARSIVGSAISKAASAAANETSLLLGVKEDIWIYIKDELKTWOAFURAAEVMMKKDELKLV 67
Db	1 MVEAIVSGVKEKLDRLTQYEQGVGEDRIAELKSNLNLKSLFKDAEAKNTSQMVRH 60
Qy	68 WAEQIRDLSDYIEDSLDF---KVHIESQTLFRQLVKLR-----ERHRTAIRHNLSKRV 120
Db	61 CVSEIKIVYDTENMIEFTILKEAARKSGIIRITKLTCTIKVHRWESFASDIGGISKRIS 120
Qy	121 EVSSRNRYNLVPEISGTEDD--MDSYAEIRNQSANRVDAELVGFSDSKRLLEMD 178
Db	121 KVIQDMISFGVQQMISDGSQSHLQEREREMRQTFSRGY-ESDFVGLVENVVKLVGLV- 178
Qy	179 TNANDGPAKVICVVGMGGLGKTALSRKIFESEEDIRKNFPCNAWITVSQSFHRIELKDM 238
Db	179 --VEEDDIQIVSVTGMGLGKTTLARQVF-NHEDVKGQFDRLAWVCVVSQEFTRKNVWQMI 235
Qy	239 IROLGLPSSLDQLLHLELQGVVQVHLSYLIEELKEKRYFVVLDDILWLDHWNINEL 298
Db	236 LQNLTSRETDEILQ-----MEEAELHDELFLLETSKSLIVPDDIWKEDMGLINPI 288
Qy	299 AFPPKN---KXGSRIVITTRNVVDLAEKCATASLVVHLDLQWMDAISLLRLRKNKHEDM 355
Db	289 FPPKKEITAMHGNR-----RYVNFKPECLTI-----LESWILFORIAM-----PRVDESEF 334
Qy	356 ESNKMQMQRVERIVNKCGRPLAILITIGAVLATKQV-SEWEKFYEQLPSEL-----EI 407
Db	335 KVDKEMEMMGQMIKYCGGLPLAVKVLGGLLAAKYTFHDKRLSENIGCHIVGRTDFSDG 394
Qy	408 NPSLEALRRWTLGYNHLPSHLKPCFLYLSIPEDFEIQRNRLVGRWIAEGFVRP--VG 465
Db	395 NNS--SVYHVLSLSEFELPSYLKHCFLYLAHFPEEDHNIKVEKLSYCMAAEGILPRHYHG 452
Qy	466 MTTKDVGESYFNEILNRSMTQRVSGTAGIKTCRIHDIIRDITVSISROENFV---LL 521
Db	453 QTRDVGESYIEELVRRNVIAERDVTTLRFEACHLHDMREVCLLKAKEENFVQIASIL 512
Qy	522 PMGDSGLVQENTRHIA-----FHGSMSCKTGLDWSIIRSLAIFGDRPKS---LAHAYCP 573
Db	513 PPTANSQYPGTSRRFRFVSONPTTLVHSRDINNPKLSL---LIVNERNRKSWKLLGSSFI- 568
Qy	574 DQLRMLRVLDEDVTFLITQKDFDRIALLCHLKYSIGYSSISYLSRPSIGKLQGLQTLN 633
Db	569 -RLELLRVLDLYKAKF-----EGRNLPSPGIGKLIHLRYLN 602
Qy	634 MSSTIYAALPSEISKLOCLHTLCIRLEFDFNFSLNHPMKCITNTICLPKVTPLVSRDN 693
Db	603 LDLARVSRLPSSGNLRLIYL-----DIN-----VCTKSUFVP-----N 637

```
Qy 694 RAKQIAEFHMAKSFWSBSFGVKVPKGIGKGLRDQLVLEYVDIRTSRAIKELQGLSKLR 753
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 638 CLMGHMLRLRLLP---NTSKEIKGLCNLVNLTLENFS---TENSLEDLGMVSLR 691
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 754 KLAV-ITKGSYKCKILYAAIEKLSLSQSLYM-----NAALLSDIETLECLDISISPPPP 807
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 692 TLTTGLFKHISKE---TLFASILGRHLENLSIRTPDGSFKRIMEDGIVLDAIH----- 744
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 808 LLRTGLGLNGSLEEMPNIIEQLTHLKKNLWSSKKEGKNMLILGALPNLMFLSLYHNSYL 867
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 745 -LKQNLRLNPKLPDQEHFFSHLTSISLDCCLVEDP-LPILKLELKEVRDLDFRAC 802
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 868 GEKLVFTKGAPPNRLTLVFNLDQLREIRFDGSSPOLEKIEI-SCCRLESIGIIGIHL 926
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 803 GKRVSSDGGPQLHRLYIWLGAEEWIEVSGSNPRLHTLTWNCKQLKQLPDGLRFYI 862
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 927 RLKEISLEYKSK 938
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 863 SIKDLMDMKWK 874

RESULT 14
T12979
hypothetical protein T6H20.260 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12979
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Catcolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, July 1999
A;Reference number: 217586
A;Accession: T12979
A;Molecule type: DNA
A;Residues: 1-847 <CH>
A;Cross-references: UNIPROT:Q9STE5; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.260
A;Experimental source: cultivar Columbia; BAC clone T6H20
C;Genetics:
A;Gene: ATSP:T6H20.260
A;Map position: 3
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 13.8%; Score 725.5; DB 2; Length 847;
Best Local Similarity 26.7%; Pred. No. 1.1e-33;
Matches 252; Conservative 179; Mismatches 357; Indels 155; Gaps 37;

Qy 8 MARSILVSAISKASAANETSLLGVKEDIWYIKDELTKTQAFIRAAEVMKKDELKLV 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MVDAITFVVGKIDNYLIEEAPMLIGVKDDLEELKLTCTIQVYLKNVECDKREDSKE 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 68 WAEQIRDLSDIEDSLDEFKVIHIESQTLFRQLVKLRER-HRIAI-RHNHLSRVEEVSSR 125
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 WTKLVLDIAYVEDVLDY-----FLKLEKLHLGLMRLTNI-----ISDK 102
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 126 NTRYNLVEPISSGTEDDMD-----SYAEDIRNQSARNVDRAE- 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 KDAYNILDDIKTKRRLTDVTRKLEWYGIGNFNEHVVASTSRVREVR--ARSDQBER 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 163 LVGESDKRLLKLEMDTNDANDPAKIVCWGMGGTALSKTFESEEDIRKNFPCNAW 222
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 VVGUTDPAKVLTKLLDDGDNKNTYMSIFGMEGLGKTSLKARKLFNS-SDVKESFEYRVW 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 223 ITVQSQSHRIELLKDMIRQLLPGSLDQLLHELQCKVVVVQVHHLSVYLIEELKEKRVV 282
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 TNVSGCNTRDILMRIL-----SSLETSSELEKMAAQ--ELEVYLHDLQEKRYLVV 271
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 283 LDDLWLHLDWNWINEIAPPKNKGSRIIVITRNVDIAEKCATASLVYHLDPLQNDNIS 342
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 272 VDDIWESEALSXR-ALP-CSYQSGSVIITTSIRVVAEGRDKRVYTHINIFLTFKESWN 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 343 LLRLKTKNHEDMESNKNMQKWERIYNKCCRLPLATLTIGAVLATQVSEWEKFEYQLP 402
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 330 LFEKKAFR--YILKVDQELKIGEMVQKCGGLTRTTVVLAGLMSRKNPNNDW---- 383
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 403 SELSINPSLEALRMVTLGYNHLPSHLKPCFLYLSIFPEDPEIQIRNLVGRWIAEGFVRP 462
```

```
Db 384 SSLRKKDNDIHVSLFDLSPKDMGHMKLCFLYLSVFPDEYEDVVEKLIQLLAEAGFTQE 443
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 463 KVGWTTTKVGESYFNELINESMIQ---RSRVGTAGKIKTCRIHDIIRDITVISROENFV 519
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 444 DEEMTMEDVARYIETDLYISLVSEVVRKK-----GKLMSPRIHDLVREFTIKSKELNFV 499
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 520 LLPMGDGSGLVQENTRIAHF---GSMSCKTGLDWSIIRSLAIFGDRPKSLAH-A-VCPDQ 575
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 500 --NVYDQHSSTTSRREVHLMDDNYLDCRRVN-TQWRSFLFGKRNDITYVETITLK 556
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 576 LRMLRVLDLBDVTLITQKDFRIALLCHLYKISGYSSTSIYSPRISGKLOGLTNMS 635
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 557 LKLLRVNLGLGHP-----ICQ-----GYSP--WSPLDVIGVLVHLRYLGIA 596
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 636 STYIAALPSEISKLOCLHTLRCI-----RELDFNPF-SLHHPMKCIITNTICLPKVFPPLV 689
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 597 DTVVNNLPDFISNLRFLQTLDASGNSFERMTDLSNLTSLRH-----LTG-----RFIGELL 647
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 690 SRDNRAKQIAEFHMAKSFWSBSFGVKVPKGIGKGLRDQLVLEYVDIRTSRAIKELQQL 749
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 IGD--AVNIQTLRSISSYSWSK---LKHELLI-NLRDLIEYEF-HILNDQIKVPLDLVSL 700
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 750 SKRKLAIVITKGSYKCKILYAAIEKLSLSQ-SLYNNAALLSDIETL-ECLDISISPPPP 807
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 701 SKLKNLRVL-----KIEVVSFLSFSEETVRFELLVKLTLLHCDVRRRLPRMDLIF---P 750
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 808 LLRTGLGLNGSLEEMPNIIEQLTHLKKNLWSSKKEGKNMLILGALPNLMFLSLYHNSYL 867
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 751 SLESLLTNTLQEDP-----MPTLQKQRLNLENLVLYSCVYP 786
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 868 GEKLVFKTGAPPNRLTLVFNLDQLREIRFDGSSPOLEKIEI 910
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 787 GAKMFINAQGFGRLRKLV-IKGLDSELEIEEAMPCLMKLNL 828
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
A86243
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86243
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-821 <STO>
A;Cross-references: UNIPROT:O04093; GB:A5005172; NID:g1931650; PIDN:AAB65485.1; GSPDB:GN
C;Genetics:
A;Map position: 1

Query Match 13.7%; Score 717.5; DB 2; Length 821;
Best Local Similarity 27.2%; Pred. No. 3e-33;
Matches 251; Conservative 180; Mismatches 352; Indels 141; Gaps 32;

Qy 8 MARSILVSAISKASAANETSLLGVKEDIWYIKDELTKTQAFIRAAEVMKKDELKLV 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAEGVVLFGVHKLWELLNRESARLNGIEQVDGLKRLQLGLSKLQADAKKAKKESVRN 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 68 WAEQIRDLSDIEDSLDEFKVIHIESQTLFRQLVKLRERH--RIAIRHNLSRVEEVSSR 125
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 FLEDVRDIVDAEDIIIESFLIN-----EFTKTEGKIKKHARLAC---FLSIGIOEI--- 109
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:34:07 ; Search time 125.377 Seconds
(without alignments)
4215.017 Million cell updates/sec

Title: US-10-656-394A-4
Perfect score: 5255
Sequence: 1 MAETVLSMARSLVGSALSKA.....SQVITLTNDSEIGTAQAG 1032

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2726	51.9	1014	2 Q84KCS	Q84KCS hordeum vul
2	2532	48.2	1007	2 Q9LWV7	Q9LWV7 oryza sativ
3	1319.5	25.1	953	2 Q651S9	Q651S9 oryza sativ
4	1268	24.1	954	2 Q651T2	Q651T2 oryza sativ
5	1254	23.9	1494	2 Q8H5A7	Q8H5A7 oryza sativ
6	1221	23.2	1169	2 Q6WSR3	Q6WSR3 triticum ae
7	1219	23.2	963	2 Q6WMT3	Q6WMT3 oryza sativ
8	1217	23.2	1169	2 Q947C8	Q947C8 triticum mo
9	1215.5	23.1	1226	2 Q84QL0	Q84QL0 oryza sativ
10	1215.5	23.1	1226	2 Q9MBF2	Q9MBF2 oryza sativ
11	1199	22.8	1485	2 Q6U9U8	Q6U9U8 oryza sativ
12	1191	22.7	1251	2 Q6ZNV6	Q6ZNV6 oryza sativ
13	1174.5	22.0	1011	2 Q9LJ70	Q9LJ70 oryza sativ
14	1156	22.0	884	2 Q6ZB12	Q6ZB12 oryza sativ
15	1152.5	21.9	989	2 Q651T0	Q651T0 oryza sativ
16	1124.5	21.4	1205	2 Q84QL4	Q84QL4 oryza sativ
17	1112	21.2	1404	2 Q9LJ11	Q9LJ11 oryza sativ
18	1108.5	21.1	947	2 Q6YVX3	Q6YVX3 oryza sativ
19	1087.5	20.7	774	2 Q84MG3	Q84MG3 oryza sativ
20	1078	20.5	1006	2 Q6ZBT2	Q6ZBT2 oryza sativ
21	1052	20.0	1280	2 Q6Z574	Q6Z574 oryza sativ
22	1046.5	19.9	917	2 Q6PKX5	Q6PKX5 prunus pers
23	1032.5	19.6	905	2 Q7X1I9	Q7X1I9 oryza sativ
24	1028	19.6	945	2 Q6EST1	Q6EST1 oryza sativ
25	1022	19.4	1018	2 Q6ZBT0	Q6ZBT0 oryza sativ
26	1020.5	19.4	880	2 Q6LSR9	Q6LSR9 oryza sativ
27	1017.5	19.4	926	2 Q6ZSH1	Q6ZSH1 brassica na
28	1009.5	19.2	954	2 Q6Z392	Q6Z392 oryza sativ
29	1007.5	19.2	996	2 Q8LM68	Q8LM68 oryza sativ
30	991	18.9	959	2 Q6Z572	Q6Z572 oryza sativ
31	990	18.8	949	2 Q6Z397	Q6Z397 oryza sativ

32 987 18.8 926 1 RPM1_ARATH Q39214 arabidopsis
33 986.5 18.8 966 2 Q6ZDI5 Q6ZDI5 oryza sativ
34 982.5 18.7 927 2 Q9ZSH2 Q9ZSH2 brassica na
35 970 18.5 935 2 Q6H4T9 Q6H4T9 oryza sativ
36 968 18.4 935 2 Q9LJ13 Q9LJ13 oryza sativ
37 957 18.2 927 2 Q7XH20 Q7XH20 oryza sativ
38 957 18.2 927 2 Q9AYH9 Q9AYH9 oryza sativ
39 954 18.2 961 2 Q6Z569 Q6Z569 oryza sativ
40 952 18.1 921 2 Q9XHGO Q9XHGO arabidopsis
41 947 18.0 1072 2 Q6K4U3 Q6K4U3 oryza sativ
42 945 18.0 956 2 Q7Y192 Q7Y192 oryza sativ
43 939 17.9 928 2 Q6ZDI7 Q6ZDI7 oryza sativ
44 935 17.8 876 2 Q8LJY8 Q8LJY8 sorghum bic
45 935 17.8 909 2 Q6ZB32 Q6ZB32 oryza sativ

ALIGNMENTS

RESULT 1
Q84KCS PRELIMINARY; PRT; 1014 AA.
ID Q84KCS
AC Q84KCS;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE NBS-LRR disease resistance protein homologue.
GN Name:rga S-9202;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22600637; PubMed=12715163;
RA Madsen L.H., Collins N.C., Rakwalika M., Backes G., Sandal N.,
RA Krussell L., Jensen J., Waterman E.H., Jahoor A., Pryor A.J.,
RA Langridge P., Schulze-Lefert P., Stougaard J.;
RT "Barley disease resistance Gene analogs of the NBS-LRR class:
RT identification and mapping."
RL Mol. Genet. Genomics 269:150-161(2003).
DR EMBL; AJ507094; CAD45030.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERSIST.
SQ SEQUENCE 1014 AA; 114280 MW; 62C3FE5F04657332 CRC64;

Query Match 51.9%; Score 2726; DB 2; Length 1014;
Best Local Similarity 56.3%; Pred. No. 1.4e-136;
Matches 574; Conservative 156; Mismatches 248; Indels 42; Gaps 14;

Qy 1 MAETVLSMARSLVGSALSKAANAANSTLLGLGVEKDIWYIKDELKTMQAFRAAEVWKK 60
Db 1 MAETVLSMARSLVGSALSKAANAANSTLLGLGVEKDIWYIKDELKTMQAFRAAEVWKK 60
Qy 61 KDELKTMQAFRAAEVWKK 120
Db 61 KDELKTMQAFRAAEVWKK 120
Qy 121 EVSRRNRYNLVEPISGTTEDDMDSYAEDIRNQARNVDEALVGFSDSKRLLEMDTN 180
Db 121 EVSRRNRYNLVEPISGTTEDDMDSYAEDIRNQARNVDEALVGFSDSKRLLEMDTN 180
Qy 181 ANDGPAKVICVGGGGGKTKALSRKIFSEEDIRKPNPCNAWITVSOFHRIELDKMIR 240
Db 181 ANDGPAKVICVGGGGGKTKALSRKIFSEEDIRKPNPCNAWITVSOFHRIELDKMIR 240
Qy 181 SRDGLSKVICVGGGGGKTKTLARKVKYSEKEDIVNFKACCAWITVSOFKIELKEMIR 240
Db 181 SRDGLSKVICVGGGGGKTKTLARKVKYSEKEDIVNFKACCAWITVSOFKIELKEMIR 240


```
Qy 241 QLLGSSLDQLLHELQGVVQVHSLSEYIEELKEKRYFVVLDDLLWILHDMWNIETAF 300
Db 241 QLLGTELLRQCLKELEK-AVVEDLASYLEKLEDMRYFVLDLTDWIDWIKSIAP 299
Qy 301 PKNNKGSRIIVITRNVDLAECATASIVHYHDLQWMDAISLLLRKTKNKHEDMESKN 360
Db 300 PIRNKDSRIILITRDVGLAAKCTSDSLIYHLKHLQIEDATNLLLRKSRKTWEDMKDK 359
Qy 361 MQRVRIKVCGRPLPLAILIGAVLATQVSEWEKPYEQLPSELEINPSLEALRMTVL 420
Db 360 MNAVNNKVKCGGLPLAVLITGGMLANKKVTESIYKQIPSELESNPSLEARRIVTL 419
Qy 421 GYNHLSHLKPCFLYLSIFPDEPTEORNLVGRMTAEGFVRKPGMTTKOVGESYFVELI 480
Db 420 SYNPLPSHLKCFYLSIFPDEPTEIKRRLVDRMTAEGFVRARGSVNIEDVGISYFTELI 479
Qy 481 NRSIQRSRVGTAGKIKTCRIHDIIRDTIVSISQENFVLLPMGDGSDLVQE-NTRHIAF 539
Db 480 NRSIMQPSKVSIEGHVKSCRVDIMRDVMVVISREENFVYL-AGDNSTRVAEGNFRVAY 538
Qy 540 HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLAMRLVLDLVEDVFLITOKDFRI 599
Db 539 HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLAMRLVLDLVEDVFLITOKDFRI 599
Qy 600 ALLCHLKYLSI--GYSSSIYSLPRSIGKLAGLOTLMSSVIAALPSEISKLOCLTLR 656
Db 599 GSLRHLKYLTLRPHLFLNMHKLPAISIGKLAGLOTLMSSVIAALPSEISKLOCLTLR 658
Qy 657 CIRELEDFNLSNHPMKIT--NTICLPKVPPTLVSRDNRKQIAEFHM--ATKSPMS 712
Db 659 C-RNQRSYNYFDNE-SCERWNVCMPLVLAS--EPDQASPPAELPMMCTSGFPKPS 714
Qy 713 FGKVPKIGIKRLDQVLEVDYDRTSSRAIKELGOLSKRLKLAIVYKSTKEKCKILYA 772
Db 715 YGVLPKIGISNLKQLILEYVDIIRTSRAIQELGELTQKLLKLVITKGATEKCELFWE 774
Qy 773 AIELKSSIOSLYMAALLSDIETLECLDSISSPPLLRTGLNGSLSEMPNWIQLTHLK 832
Db 775 AIQKLSLLSYV-----DGENLEWSSVAFAPLMRSKQNSLLLEIPNIGSLMHLV 828
Qy 833 KFNWSSKLKEG-KNMLIGALPALMPLSLYHNSYLGELVKFTGAPFNRLTLVIFNLQ 891
Db 829 KLMVYCDLKEGERSMEMGALPNMLRLGDFDSTIGELKFVFAETFPNRLNGVYVWHG 888
Qy 892 LREIRFEDGSSPQLEKIEISCRLESIGIHIHPLKEISLEYKSVARLQKGEVNT 951
Db 889 LREVRFEAGLPQIAEIRISQGLSVGITGKHLPMLEKISLVGGQVAHLGLVLQGEVNS 948
Qy 952 HPNRPVLRMDSRRDHDIGAEAGSSIEVQADPVPDAQGSVTVAEATDPLPQEGESS 1011
Db 949 HPNHPVLRSLNKLTPQQLG-----DVV--VQGSNAIQVE-----BAMGESS 987

RESULT 2
Q9LWW7
ID Q9LWW7 PRELIMINARY; PRT; 1007 AA.
AC Q9LWW7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to gene for pib.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP001168; BAA90798.1; -.
DR Gramene; Q9LWW7; -.
DR GO; GO:0005524; F:ATP binding; IEA.
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DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PRO0364; DISEASERISIT.
SQ SEQUENCE 1007 AA; 114793 MW; F96F2CE09AE808E3 CRC64;

Query Match 48.2%; Score 2532; DB 2; Length 1007;
Best Local Similarity 52.6%; Pred. No. 2.9e-126;
Matches 541; Conservative 156; Mismatches 289; Indels 42; Gaps 13;

Qy 1 MAETVLSMAWSLVSALSKAASAAANETSLLLGVKEDIWYIKDELKTMQAFRAAEVWKK 60
Db 1 MAETVLSMAWSLVSALSKAASAAANETSLLLGVKEDIWYIKDELKTMQAFRAAEVWKK 60
Qy 61 KDELKVMABQIRDLSDIEDSLDEDFKVHIESQTLFRQLVKLRERHRAIRIHNLSKRV 120
Db 61 KDLKLVMAEQVRSLSYDIEDCLBEFVHVHVGNSQLQLQTLNLDKRRHIAVKIRNLKSRLE 120
Qy 121 EVSSRNTRYNLVPEISSGTEDDMDSYAEDIRNQSARNVDEALVGFSDSKRILLEMIDTN 180
Db 121 EVSSRNTRYNSIIRMEANNTFDEIBS-MEDVRNHSRSDIEAKLVGFDPKKELDKKNMD 179
Qy 181 ANDGP-AKVICVWGMGLGKTALSRKIFESGEEDIRKNFPCNAWITVSQSPHRIELLKDI 239
Db 180 ANDDDHCRVLCVGMGLGKTLLVRKIPESKEDIINNFPHRAWIVVSQSFMSIEMWKDI 239
Qy 240 RQLGPPSLDQLLHELQGVVQVHSLSEYIEELKEKRYFVVLDDLLWILHDMWNIETAF 299
Db 240 SLLGHESLKR---PEGK-PIRAHDLGTHLRDGLKELRYFVVFDDLWNTDHWIREFPA 294
Qy 300 FPKNNKGSRIIVITRNVDLAECATASIVHYHDLQWMDAISLLLRKTKNKHEDMESKN 359
Db 295 LPSKNNKRSRIIVITRDGVANACTTEPFVYRLKLETECAIDLLDKMGESKEDMKNDN 354
Qy 360 NMOQWRIYVNCGRPLPLAILIGAVLATQVSEWEKPYEQLPSELEINPS-LEALRRM 417
Db 355 NLKSIIVQLVKCCCLPLAIVTIGMFANPKSSKWEKCRQLPSELENNPSPGVEAIRV 414
Qy 418 VTLGYNHLSHLKPCFLYLSIFPDEPTEIQNRNLVGRMTAEGFVRKPGMTTKOVGESYFN 477
Db 415 VTLGYHLPSHLKPCFLYLSIFPDEPTEIKRHLVNRVVAEGLVRAVRGWTITSVGESYFD 474
Qy 478 ELNRSIQRSRVGTAGKIKTCRIHDIIRDTIVSISQENFVLLPMGDGSDLVQENRHI 537
Db 475 ELISRSIQRSRVNMGHVSKRVHDIMRDIIVSISKEENFVYSTGDNVSTVIKEFRHL 534
Qy 538 AFHGSMSCKTGLDWSIIRSLAIFGD---RPKSLAHAVCPDQLAMRLVLDLVEDVFLITOK 594
Db 535 SCHGGNYPVGMDFSRVRSITVFGFDPQRPMLVGSSICSAQFTMLRVLDLENVPSVTQK 594
Qy 595 DFDIRIALCHLKYS--IGYSSSIYSLPRSIGKLAGLOTLMSSVIAALPSEISKLOCL 652
Db 595 DINKIGLRLHLYLNTHTRRRTIYALPSSIGKLAGLOTLMSSVIAALPSEISKLOCL 654
Qy 653 HTLRCIRE--LEPDNFSLNHPMKITNTICLPKVPPTLVSRDNRKQIAEFHMAKSPWS 710
Db 655 RILRCSKGPWFYFYPDPDEPIKCLGHTLRLMPLMLTFLVGSAAARNYTAELHRYSSHWS 714
Qy 711 ESFGVKVPKIGIKRLDQVLEVDYDRTSSRAIKELGOLSKRLKLAIVYKSTKEKCKIL 770
Db 715 ETPGVRVPTGISKLKELQVLEVDLKLTKSAIEELGELWQLKLRVSTKGAQDKKRTL 774
Qy 771 YAAIEKLSSLOSLYMAALLSDIETLECLDSIS-SPPLLRTGLNGSLSEMPNWIQLTH 829
Db 775 CEAEIKLSSLOSLCVYEGYFVTGTEWLGPCNPSPPFLRLKLELHGRIRVMPDSFRNLK 834
Qy 830 HLKFFNLWSSKLKEGKNMLILGALPNLMPLSLYHNSYLGELVKFTGAPFNRLTLVIFNL 889
Db 835 QLRKIFLRLSEL-DGRAIEILGTLPMLNLLNDGRAVVGNEAFKGFEPFNLKELRISML 893
Qy 890 DQLREIRFEDGSSPQLEKIEISCRLESIGIITHLPRLKEISLEYKSVARLQKGEV 949
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Db 894 SELGRIRFEKALPHEMERIECCQLRSGIVGIKHLEQNEISL--GCDVAGLDLLEOEY 951
Qy 950 NTHRNPVLRMDSDRRDHLG-----AEAGSSIEVQTADEVPDAQSVTVVAEATDPLP 1004
Db 952 KAHPKTPALRLQDRSKIDGLPVVLTKEGDSNVE-----EAKESVH 994
Qy 1005 EQBESSQ 1012
Db 995 DDAGESSQ 1002

RESULT 3
Q651S9 PRELIMINARY; PRT; 953 AA.
AC Q651S9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to NBS-LRR type resistance gene.
GN Name=P0702F05.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_taxid=33947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0702F05.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005828; BAD46438.1; -.
SQ SEQUENCE 953 AA; 108557 MW; DAFD5081E707261C CRC64;

Query Match 25.1%; Score 1319.5; DB 2; Length 953;
Best Local Similarity 33.7%; Pred. No. 9.3e-62;
Matches 341; Conservative 204; Mismatches 339; Indels 127; Gaps 34;

Qy 1 MAETVLSMARSLVGSASAKAASAAANETSLLLGVKEKDIWIYKDELKTMOAFLRAAEVNMK 60
Db 1 MEGAIFSAEAGTVRSLLSKLSLSSQESWFRVGHGDIQYIKDELSNNAFRLVLTWLED 60

Qy 61 KDELLKWAEGIRLSDYDIEDSLDEPKVHIESQT-----LFRQ-----LVKLRERHRIARIH 113
Db 61 HDTQVRIWMKQVREIAYDAEDCIDQFTHLGSSGIGLYRLIYLILGKLCCHRIAMQLQ 120

Qy 114 NLKSRVEEVSRRNYRLNVEPISSGTEDDMSYAEIRNQSARNVD-----EAEV 164
Db 121 ELKARAQDVSRERRRYEMLP-----KTLQAGPRLTRHASRLDPQLHALFTEEAQLV 175

Qy 165 GFSDSKRLLSMIDTNDANDGPAKVICVVMGGLGKTALSRIKIFSEEDIRKNFPCNAWIT 224
Db 176 GLDEPRDKLVWV--MEADPCERVLAIVGFGLGKTLTARWCVENPWVKGADFCCPLFI 233

Qy 225 VQSQFHRIELKDMIRQLLGPSSLDLL-----HELQ-----KVVQVHHLSYL 270
Db 234 VQTQFNIRTLFOYMIRELIRQPNKAWAVAGCKHGHTMDGNDGMRWEVAVLAEKVRQYL 293

Qy 271 IEELKEKRYFVLLDLWLTHDWNINEIAPFNKKSGSRIVITTRNVDLAEKCAT--SL 328
Db 294 LD-----KYIVIPDDIWTISAWESI--RCALP--DNKKSGSRVITTRNEDVANTCCSGPDQ 346

Qy 329 VYHLDLFQMDAISL--LLRKTNKNHEDMESKNKQKVERIVNKGRLPLAILITIGAVLA 387
Db 347 VYKQK--RLSDASARELPFKRIFGSADISSNEELDEVNSILKCGGLPLAIVIGSLVA 404

Qy 388 TK---QVSEWKEFYQLPSELEINPSLEALRRWTLGYNHLPSHLKPCFLYLSIPDEDFE 444
Db 405 SKTNRTKEWQKICDNLGSELETNPTLEVAQVLTLSYNDLPYHLKACFLYLSIPPENYV 464

Qy 445 IQRNRLVGRVTAEGFVRPKVGTMYTKDVGESYFNELINRSMIQRSRVGTAGKIKTCRIHI 504
Db 445 IQRNRLVGRVTAEGFVRPKVGTMYTKDVGESYFNELINRSMIQRSRVGTAGKIKTCRIHI 504

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Db 465 IRRGPLVRRWTAEGFVNQRHGLSMEEVAESYDFEVSARSIVQPKIDWSGKVRTCRVHDM 524
Qy 505 IRDITVSISROENFVLLPMGDSGLV--QENTRHIAFHGSMSC--KTGLDWSIIRSLAIFG 561
Db 525 MLEVIISKELENFASFLCDNGHPLVCHDKIRRLSIHNSHNSVQTRVSVSHVRSFTW-- 582
Qy 562 DRPKSLAHAVCP---DQLRMLRVLDLDEVDVTLITQKDPDRIALLCALCHLYSIGVSSSIYS 618
Db 583 ----SASVEEVPMPFPQWRLLRVLDLQSSCL--NNSTLNYICKFYQLKYLTL--RKTNI 636
Qy 619 LPRSIGKLGLOTLNMSSTYIAALPSEISKLOCL--HTLRCIREFLEFDFNSLNHPMKCITN 677
Db 637 LPRILGNLKVLETLDIRATRIKRLPASANSULCKHLL-----VCHKVQ--LTR 683
Qy 678 TICLPKVTPLVSRDNRKQIAEFHMAKTSFWSSESFGVKPKGIGK--LRDIQVLEYVDIR 736
Db 684 TTSV--KCFRP-----DSGLEMTAGVVKNMMAQLSLAHIVVK 718
Qy 737 RTSSRAIKELGOLSKLRAVITKSTYKCKIILYAAIEKLSLSQSLYMNMAALSDIE-- 794
Db 719 ERPA--VLSEIGQLQKQKLNVLFRGVEENWNAFLQSLVKLTGSLRSLSIH--ILDEKSHS 775
Qy 795 -TLECLDSISSPPL--LRTLGLNGLSLEMPNWIQLTHLKKFNLWSSKKEGKNMLILGA 852
Db 776 SSLEYLALIAESPPLFIINFLSKGLQRLPPWISLRNVSRITFRDTGL--HAEALGVLD 834
Qy 853 LPNLMFLSLYHNSYLGEKLVFKTGAPNPLRTLVIPLNDQLREIRPEDGSSPOLEKIEISC 912
Db 835 LPNLLCLKLQORSYADDDHIFPAHGNFLKRLMLVIDNMENIRNVHFEKSGSVNLEWLTIAF 894
Qy 913 CR--LESIGIIGIHLPLKEIS-----LEYKSKVARLGQLKGEVNTNRP 956
Db 895 LQEPKDGITGLENLKLKEIEFFDGIILSMVTVKASC-----MKAHENRP 939

RESULT 4
Q651T2 PRELIMINARY; PRT; 954 AA.
AC Q651T2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to NBS-LRR type resistance gene.
GN Name=P0702F05.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_taxid=33947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0702F05.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005828; BAD46435.1; -.
SQ SEQUENCE 954 AA; 108010 MW; 0F8BEBB635D2750 CRC64;

Query Match 24.1%; Score 1268; DB 2; Length 954;
Best Local Similarity 32.9%; Pred. No. 5.1e-59;
Matches 334; Conservative 193; Mismatches 355; Indels 132; Gaps 31;

Qy 1 MAETVLSMARSLVGSASAKAASAAANETSLLLGVKEKDIWIYKDELKTMOAFLRAAEVNMK 60
Db 1 MEGAIFSLTEGAVRSLLCKLCLLTEDTLVQVGHGDIQYIKDELCNNAFLNLITISQI 60

Qy 61 KDELLKWAEGIRLSDYDIEDSLDEPKVHIESQT-----LFRQLVKLRERHRIARI 112
Db 61 HDQVRIWMKQVREIAYDSEDICDEF--IHNLGESSEMGFFGGLISMLRKLACRHRIALQL 119

Qy 113 HNLSRVEEVSRRNYRLNVEPISSGTEDDMSYAEIRNQS-----ARNVDEAEV 164
Db 120 QELKARAQDVGRDRSRVGV--ELAKATHE--EAHPRLTRHASRLHIDPOLHALFABEAQLV 175

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Qy 165 GFSDSKRLLKLEMDITNANDGPAKVICVVMGGLGKTALSRKIFSESEDIRKNFPCNAWIT 224
Db 176 GIDSPNELVSWL--MEEDLRVLVIAVGFGLGKTTLARVCGSPVKSADFQCCPLFI 233
Qy 225 VQSQFPHRIELKDMIRQLLGPSSLDQLLHE-----LQGVVVVQVHHLSE 268
Db 234 ISQTFNIRALFQHMVRELI-----QEPHKAMATAGCKGHLITDYLLEGMERWEVAALTK 287
Qy 269 YLIBELKEKRFVVDLWILHDNWNINEIAPFKNKKGSRIVITTRNVDLAEKCAT--A 326
Db 288 NLRRYFQDKRYIVLDDITWTSAMESI--RCALP-DNLKGSRIIVITRNVADVANTCCSRPQ 345
Qy 327 SLVYHLDPLQWMDAISLLLRKTNKHEDMESKNQKMKVERIVNKKGRPLPLAITIGAVL 386
Db 346 DRIYNIQELSETTSEFFKXIFGFADDKSPDDEFEVSNVLKCGGLPLAIVNIGSL 405
Qy 387 ATK---QVSEWEKPYEQLPSELEINPSLEALRRMVTGYNHLPSHLKPCFLYLFIPEDF 443
Db 406 ASKTRTKKEQKVCNNLGSLENNPTLEGVKVLTLSYNDLPVHLKACFLYLFIPEPNY 465
Qy 444 EIQRNLVGRWIAEGFVVPKVMGTTKQVGSFYFNEILNRSMIQSRVGTAGKITCRHID 503
Db 466 VIKRGPLVRRWIAEGFVSQRHGSMEQALAESYFDEFVARSIVQPVRTDWTGKVRSCRVD 525
Qy 504 IIRDTVSIHQENFVLLPMGDGDLV--QENTRIAPHGS--MSCKTGLDWSIIRSLAIF 560
Db 526 LMLDVIVSRSEENFASPLCDNGSTLASHDKIRLSITHSSYNSQKTSANVSHARSFTM- 584
Qy 561 GDRPKSLAHAVCP---DQLRMLRVLDLVEDVTFLLITQKDFRIALLC---HLKYLISGYSS 614
Db 585 ----SASVEVPVFPQLRELRLVLDLQGCCLSN---ETLHCWCRFPQKYLISL-RNT 634
Qy 615 SIYSLPSIGKLOGLOTLMNSTYIAALPSEISKLOCLHTLRCLRELEFDFNFSLNHPKC 674
Db 635 NVSKPLHLGLNKHLETDIRATILKLPASAGNLSCLKHLFAGHKVQ-----682
Qy 675 ITNTICLPKVTPLVSRNRKQIAEFHMAKTSFWSFGVKVPKGIGK-LRDLQVLEYV 733
Db 683 LTRT-----ASVKFLRQSSGLEVATGVVKNMVALQSLVHI 717
Qy 734 DIRTSRAIKELQSLKRLKAVITKGSTKECKKLYAAIEKL--SSIQSLYMNAAALSD 792
Db 718 -VWKDPSVLRIGLQLNLTKANLLRG--VEENNAFLESLSKLPGLRSLSIHT--LDE 773
Qy 793 IE---TLECLDSISPPPLLTGLNGSLSEMPNWEOLTHLKKFNLWSSKLKSGKNWLI 849
Db 774 KEHSLSLDNLAFVESPPLFITKFSLAGELERLPPMIPSLRNVSRFALRRTEL-HADAIGV 832
Qy 850 LGALPNLMFLSLYHNSYLGEKLVFKTGAPFNRLTIVIFNLDQLEIRPEFGDSSPQLEKIE 909
Db 833 LGDPLNLLCLKLYKHSYADNCIVCHGKFKVLKLLIIDNLERIEKMQPDAGSVTLNRLT 892
Qy 910 ISCCR-LESIGIIGIHLPRLKEIS-----LEYKSKVARLQQLKGEVNTHPNP 956
Db 893 LSFLEPKYIGISLENLPKLEIEBFFGDIILSVVTKVASC-----VKAHNP 940
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RESULT 5

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Q8H5A7 PRELIMINARY; PRT; 1494 AA.
ID AC Q8H5A7;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Putative disease resistance protein RPH8A.
GN Name=QJ1634.B10.108;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
```

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RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:QJ1634.B10.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003840; BAC15497.1; -.
DR Gramene; Q8H5A7; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR008940; Prenyl_trans.
DR Pfam; PF00560; LRR_1; 3.
DR Pfam; PF00931; NB-ARC; 1.
DR Pfam; PF01535; PPR; 4.
DR PRINTS; PRO0364; DISEASERSIST.
DR TIGRFAMs; TIGR00756; PPR; 4.
SQ SEQUENCE 1494 AA; 168313 MW; 15BB15F247C3446B CRC64;
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Query Match 23.9%; Score 1254; DB 2; Length 1494;
Best Local Similarity 31.7%; Pred. No. 5.3e-58;
Matches 337; Conservative 203; Mismatches 364; Indels 158; Gaps 31;

Qy 1 MAETVLSMARSLVGSATSKAASAAANETSLLLGVKEKDIWIYKDELKTMOAFLRAAEVMMK 60
Db 514 MEHAVSAAGAIHTLTKGLTIVLQEAQLGGRIGELHQLKDELESMTAFLODLSGRDE 573
Qy 61 KDELKVAEQIRDSYDIEDSLDEFKVHIESQT-----LFRQ----LVKLRRHR 107
Db 574 CGQVKIWKXHVRIAYDIEDCIDEFKHQLGDSASSAGSGVPVFFRKATHILTQTRVRHQ 633
Qy 108 IATRIHNLKSRVEVSRRNTRNVLVEPISSTEDDMSYAEIRDINQSNVVD-----159
Db 634 IAKIOELKRTMNISARNRYSAHLSITAGNSMAAYDS---QANLLNVDTITALFP 690
Qy 160 -EAEVLGVFSDSKRLLKLEMDITNANDGPAKVICVVMGGLGKTALSRKIFSESEDIRKNFP 218
Db 691 ERRLQVIEPRQGNLVWL-LEAHVQQLRVVSIFFGLGKTLTAMTYTQSLSGRNGFPQ 749
Qy 219 CNAWITVQSFPRIELKDMIRQL-----LGPSSLDOLLHELQGVVVQVHH 265
Db 750 CQAFVTVQSFPVVKVLMRDILLQITQPVNOPSPTGAGKGPMEGLLKGMAMNVVQ---806
Qy 266 LSEVLISELKEKRFVVDLWILHDNWNINEIAPFKNKKGSRIVITTRNVDLAEKCAT 325
Db 807 LASTLROQLNKRKLYLIVLDIWSMTAWEGI-RFSLPDSN-NGSRIVVTTRIRAVAHTCC-863
Qy 326 ASLVYHLDPLQWMDAISLLLRKTNKHEDMESN-----KNMKQKMERIVNK 371
Db 864 -----FHEYDRAYEI-----KPLTDCESRDLFPKRFSGSICPEHLEDISAKILGK 909
Qy 372 CGRLPLAILTIGAVLATKQVSE---WEKFYEQLPSELEINPSLEALRRMVTGYNHLPSH 428
Db 910 CGGTPLSIVSIAGLASKPVHSDLWEKIIYSSLSGEIETNPSLDRKLKILSYNDLPVH 969
Qy 429 LKPCFLYLSIFPEDFEIQRNLVGRWIAEGFVVPKVMGTTKQVGSFYFNEILNRSMIQSR 488
Db 970 LKTCFLYLSIYPEDHNIRKRTILRRWAEARFVTGKGLSVFEVAESYFDEFINRSIIQPV 1029
Qy 489 RVGTAGKITCRHIDITRIVTSIROENFVLLPMGDGDLV-QENTRIAPH--GSMSC 545
Db 1030 TTSTGKVKFRVHDVWMEIIVSKSIEDNFITL-VGEQNTLFPQEKRLRTVHSGVKYI 1088
Qy 546 KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLVEDVTFLLITQKDFRIALLCHL 605
Db 1089 ATREILCHVRSLSIFAD-----GETLQFGWMKMLRILDLEGYEF-LRNRDLKDLRLPQL 1142
Qy 606 KYLSIGYSSSIYSLPSRIGKLOGLOTLMNSTYIAALPSEISKLOCLHTLRCLRELEFDN 665
Db 1143 EYLNL-RRTHITELPAQIGNLKKLETLDIRDTAIKHLPFGPGITNPLHLANLGGRR-----1196
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Qy 666 PSLNHPMKCIINTICLPKVFTPLVSRNRNRAQIAEFHMTKSF--SSFGVKVPKGIGK 723
Db 1197 -SYNHTG-----WPISEFWGLHIPNELRK 1220

Qy 724 LRDLQVLEVDIRTSRAIKELGOLSKRLKLAIVITKSTKECKKILYAAIEKLS-SLOS 782
Db 1221 MDSLTTLAQVELTTSTSHYISLSLRLKRLKGLVLMFVDDSTWASLSALEKLSGSLRS 1280

Qy 783 LYM---NAALSIDIETLCLSDISSPPPLRLTGLNGSLSEPNPNIQOLTHLKKFNLWSS 839
Db 1281 LLLWRPDCAMFN-----VNSLSPPIFTKSMNLRGQLTQLPCWFPLLSNITELTLRAT 1335

Qy 840 KXGKNMLILGALPNLMFLSYHNSYLGEKLVFKTGAPPNLRLLVI-FNLDOQLREIRPE 898
Db 1336 ELSAEDLVKLSPLSLYLRHLHNAVYGTFSASAGEFSPSLRLLVILHDMSEDEWEARFE 1395

Qy 899 DGSSPOLKEIKISCRLES--GIGIHLPLKELSLR-YKSKVARLQO----LKGEVNT 951
Db 1396 EGALPKLARLSLUFERASIOETIGIEFLPSLKEVSRACHSNVNVBEIATSLRADAEK 1455

Qy 952 HPNRPLMDSRRDHDLAGAEGSSIEVQTADVPDQAGSV 993
Db 1456 NINKPIVTFE-----EKQVPMRSRT-DPPLDHMGNL 1486

RESULT 6
ID Q6WSR3 PRELIMINARY; PRT; 1169 AA.
AC Q6WSR3;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Resistance protein T10ga2-1A.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed14645721; DOI=10.1073/pnas.2435133100;
RA Feuillet C., Travella S., Stein N., Albar L., Nublat A., Keller B.;
RT "Map-based isolation of the leaf rust disease resistance gene Lr10
RL from the hexaploid wheat (Triticum aestivum L.) genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:15253-15258(2003).
DR EMBL; AY270159; AAQ01786.1; ..
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 2.
DR Pfam; PF00931; NB-ARC; 2.
DR PRINTS; PR00364; DISEASE_RESIST.
SQ SEQUENCE 1169 AA; 131589 Mw; A64E186A3664C6CA CRC64;

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Query Match 23.2%; Score 1221; DB 2; Length 1169;
Best Local Similarity 28.8%; Pred. No. 2.2e-56;
Matches 356; Conservative 205; Mismatches 333; Indels 342; Gaps 40;

Qy 1 MAETVLSMARSLVGSATSAASAAANETSLLGVEKDIWIYKDELKTWQAFRAAEVMMK 60
Db 1 METTVLSGVKSVINGAVRYAQSATAEVALQLGVRRDQVFTNELEMMQAFMAANDEGD 60

Qy 61 KD-ELLKWASQIRDSYDIEDSLDEFKPHIESOTLFRQLVKLRERHRIAIRIHNLKSRV 119
Db 61 GDSKVVRVWVQVRDLAYDVEDSLQDFAVLEKQPMWR--ILLKDRRQVAKQMKGLRANV 118

Qy 120 EEVSRNRYNLVPEISSGTEDMD-----SYAEDIRNQSR-NVDEALVGFSS 167
Db 119 EDVSQRNRYHLIKGSAGSNPASTDQSGAITGAMTMSSTEDARRQREKAKADLVQLIRKM 178

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Qy 168 DSKRLLLEMDITNANDGPAKVICVVMGGLGKLTALSRKIPESBEDIRK--NPPCNAWITV 225
Db 179 DDLRVIAVMCTSTD-----VGETSVIKRAF--EDLKKCNRFDCCHAWIKL 221

Qy 226 SQSHRIELLKDMIRQ----LLGPSSLDOLLHELOGKVVVVVHLSLEYLIELKEKRVFV 281
Db 222 MCPNSVBFMSRIIRQFYIDLLQDPVENMDAQVLRGMGMKKENDLVDFKSYLNDKSYLI 281

Qy 282 VLDDLWILHDMNNEIAPKNNKKGSRIVITTRNVDLA----- 320
Db 282 VIDGMSITEEDQIKP-CFP-NNKGSRIVISTKQVEVASLCAQPONVAPBHKQPSIDQN 339

Qy 321 ----- 320
Db 340 TLYAFFEKSGDGDSTEVGSSSTNTTASHILVNNKILTRMETTTAAAFKEFQLIGREKE 399

Qy 321 -----EKCATA SL----- 328
Db 400 KSEIIQLVTNGDGCQFEVISVCGMGLGKTTVVRDVYQSELRGKFEKACACVTIMRPFNC 459

Qy 329 ----- 328
Db 460 DELLKNLAGQGYEDVADVMVTHLEGGKCLIVLDDLSTREWDAIIPHTALETSSRIIVT 519

Qy 329 -----VYHLDFLQMDAISLLLRKTNKNHEDM-ESNKNMQMVERIVNK 371
Db 520 TRVEDIGKCHSKKRNIVKLGLELNDADHDLFIQKVPDKTMDLDEQYFELVEQTNNMLKK 579

Qy 372 CGRLPLAILITIGAVLAT--KQVSEWEPYEQ-LPSELEINFSLEALRMVTLGYNHLPSH 428
Db 580 CKGLPLAIVTIGGFANQPKTALEWKKLNEHISAELQMNPELEAIIITVLNKSVDGLPYH 639

Qy 429 LKPCFLYLSIPPEDEIQRNLRVGRWIAEG--VRPKVGTMTKDVGSSEYNELNRSMI 485
Db 640 LKSCFLYLSIPPEIDYNIKRLRRWIAEGYGVVRNK---STEEVASEYFMDLISRMIL 696

Qy 486 ---QRSVGTAGKICTRIHDIIRDITVSISRQENFVLLPMGDGSDL-VQENTRIAPHG 541
Db 697 LPSQRS-ICDGKIGSCOVHDLIREIGISKSMGNLV-LRLEEGCSLTQGTARHLAISS 754

Qy 542 S-----MSCTGLDWSIIRSLAIFGD-RPKSLAHAVCPDQLRMLRVLDLEDVTLITOKD 595
Db 755 NWERDQSAFESIVDMRSVRSITVFEWKPFPLS-----DKMLRLRVLDLEDVTLGLVNH-H 808

Qy 596 FDRITALLCHLYLSIGYSSSYSPRSIGKLOGLQTLNMSSTYIAALPSEISKLQCLHTL 655
Db 809 LEHIGKFLHLYLSRGCEISCHLPDTIGNLRQLETIDIRGTSIVMLPQTIIKQKQHL 868

Qy 656 R-----CIRELEFDNPSLNNHPMKCIINTICLPKVFTPLVSRNRNRAQIAEFHMT 705
Db 869 HAGPPTKGNVLCRHL-LHTYGFNQDAC-TSLCC--GAATPCIMMD----- 911

Qy 706 KSFWSSEFGVKVPKGIOKLDQLVLEVYDTRTSSRAIKELGOLSKRLKLAIVITKSTKYE 765
Db 912 ----KDYGVVLPQGAARKLSLHTIRGVHV-AYGDAVIOETIGRLSGLRKLGMV---GINE 963

Qy 766 KCKTLY-AAIEKLSLOSLYMNAALLSDIETLECLDSTSSPPPLRLTGLNGSLSEPNW 824
Db 964 KNDVKFCSAISNLSRLESL-----SVQSD---KGLDDITSPPKNLSRLKUGRLGVLPDEW 1016

Qy 825 IEQIETHLKKFNL---WSSKLKEGKNMLILGALPNLMFLSYHNSYLGEKLVFKTGAFPNL 881
Db 1017 IKKLONLVKLSLPTTSSQVQDAAMEVLGHLPNLSILRLPGCSFKGELGHFKQDAF--- 1073

Qy 882 RTLVIPLNDQ---REIRFEDSGSPQLEKIEI---SCCRLESGIIGIHLPRKLEISLEYK 936
Db 1074 RSVVFDVEGLGKIKSVNFDQGAPELEQLKVTACKRGGIGFPGFLDILPSIKEVLLSVH 1133

Qy 937 SKVARLG-----QLKGEVNTNPRVLEMD 961
Db 1134 FQMDRAGTELEAREARLKEQFRTQLARNPKPKILKOE 1169

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Query Match	23.2%	Score 1219;	DB 2;	Length 963;
Best Local Similarity	32.8%;	Pred. No. 2.1e-56;		
Matches 332;	Conservative 210;	Mismatches 347;	Indels 122;	Gaps 36;
Qy	1	MASTVLSMBSLVGSAISKAASAAANETSILLGVEXDIWIYKDELTKMQAFZAAEVMVK	60	
Db	1	MEATAVSLAKSVLDGVLNRAAGSADVAEAAALLGVRRVEVEFIRDELDMHRSFLKVATANPD	60	
Qy	61	KDELKVKWASQIRDLSDYIEDSDLEPKVHE-----SQTFLQFLVKLREHRIAIRHNL	115	
Db	61	ADTVRTWVKQVRDLAYDVESDLSLDFALFADTFLSSSSSSSWMLPWIAERHVRVAIRREL	120	
Qy	116	KSRVEEVSRRNRYNLV--EPISS-----GTEDDMDS-----YAEIRNQSARNVDEAE	162	
Db	121	KASVEELNQRFLAYRIVVEHPRASRGCGASDDQQLLHDHGDQVYSAEALAFQ-----ESD	174	
Qy	163	LVGFSOSKRLLEMI DTNANDGPA-----KVTCVGMGGLGTALSRKIFESEEDIRKN	216	
Db	175	IIGRAKEABVTALVLSGCGGDVWGGLGVVSVGMGMGKSSIVRMVY--NDPELLDA	233	
Qy	217	FPNCNMITVSSQFHRELLKDMITROLLGPSSL--DQLLHELQKVVVVVHLLSEYLIEL	274	
Db	234	FDCDAWTVTP--HPLDSADEFVRLRLRHLAGVKQDQVHAY-----L	272	
Qy	275	KKERYFVLDDLWILHDNNWINEIAFPKNNKSGSRIVITTRNVDLAEKATA-----SLV	329	
Db	273	REKRYVIIVDLHRSREWEHIWVP--LHVDGKSGSRVVVTTTTRREDVARHCAGLVREGHGV	331	
Qy	330	YHLDFLQMDAISLLRLKTKWNHEDNESKNQKQWVERIVNKGCRFLPLAITLTIGAVLATK	389	
Db	332	YELRPLGREESKDLFCQKVYKSTFYI--LEKEMEDLAGPILKRCRGLPLAISTIGLLANR	390	
Qy	390	QVS--EWEKPYEQLPSELEINPSLEALRRMVTLYGNHLPshLPCFLYISIPPEDEFIQR	447	
Db	391	PKTGIEWIKLDEHLGAELE--SSDLRNITKVISSYDGLPPLYLKSIFLYLSIPPENHEIRC	449	
Qy	448	NRLVGRWIAAGFVRPKVGMTTTKDVGSYFNELINRSMIQ--RSRVTAGKIKTCRTHDII	505	
Db	450	TRLLRRWMAAGFIAXNRDMPEVEVGORFYNELINRSMIQPSKCRISPSVSDCRVHSMV	509	


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Db 359 VSPVNSDSTKWKSETRSSMEGASTTSDSKTVPDGVQIEDGPKDLPESLPPHLNRDSN 418
Qy 186 -----AKVICVVGSGLGKLTALSRIKPFSEE 211
Db 419 TVSVKELSRSTQIIGRKEKDDVIKLLSDCNPIRQVISVWGMGGIKTTLVRSIYQSS 478
Qy 212 DIRKNFPCNAWITVSQSFHRIELKDMIRQLGLPSSLDQLLHELQGGKVVVQVHHL----- 266
Db 479 LEKLGFERAVVTLRPPQLTELLSRAQLVKDS-----PGKVESIPGLARSL 529
Qy 267 -----SEYLIBELKE-----KRVFVVDLLMIHLDMWNINEIAPPKNNKGSRIVITTRND 318
Db 530 STMGSEELIKLQDLTGKYLIVLDDLSSTTDEWSIIR-NLPINN-NGSRIILTTFRPKL 587
Qy 319 LAEKCATASL-VYHLDPLQMDAISLLLRKTNKHEDMESKNQKQVRIVNVKGRPL 377
Db 588 VAQCHSKKEMMHNIEGLTDGDALEFLTKVRMGDESELKPDLLKBEAKIILKKGRLPL 647
Qy 378 AILTIGAVLAT--KOVSEWEKFFYQLPSELEINPSLEALRMVTLGYNHLPSHLKPCFLY 435
Db 648 AVATVGGFLSARPNILIEWREFSRISSEFPDNNFSLMIKKILASSYEGLYHLKSCFLY 707
Qy 436 LSIFPEPFEIORNLRVGRWIAEGFVRPKVGMWTKDVGESYNFELINSMIORSRVGTAGK 495
Db 708 MSIFPDSDIRYRLLRRWTAEGYSRATNRNSNEKVAEEQFTALINKSMIQOSKTIASGK 767
Qy 496 IKTCRIHDIIRDTIVSISROENFVLLPMGDSGLVQENTRIAHFGSMCKTG-----LD 550
Db 768 TGFQCVNLMHEIISKESEENLVLLDDHITTSRKKVRHLVSVKSRKNDQMNIWD 827
Qy 551 WSIIRSLAIFQDRPKSLAHAVCPQLRMLRVLDLEDVTFLLITQKDFORIALLCHKYLSI 610
Db 828 VSHIRSLTVGEW-KSP---PLSKKQMLRVLDLEDAEGL-QDPDLVPIGKHLHLKYL 882
Qy 611 GYSSISVSLPRSIGKLOGLTNMSSVIAALPSEISKLO----- 650
Db 883 RGSFGVNLPSFGNLLNLETDIRGTWVTKLPATIGRLQNLKYVHAGSLDDEDDQPIIK 942
Qy 651 CLHTLRCTIRELEFDFNFSLNHPMKITNTICLPKVTPLVSRDNRKQIAEPHMTAKFSWS 710
Db 943 LLHQFRSIREMGTRFAVSIMLFIIT-----AWL 971
Qy 711 ESF---GVKPKGIGKRLDQVLEVDIRRTSSRAIKELGOLSKRLKLAIVITGSKTEKC 767
Db 972 RNLDCGVKVPGRIGRLSIIHLSVINAR-GKALLKNLKLTLQCLGV--TGKNNKC 1028
Qy 768 KILYAAIEKSSLOSLYNNAALLSDIETLECLDSISGPPPLRLTLGLNGSLEENPNIEQ 827
Db 1029 KELCSAIADHRLQSLLLRAEGNAGLE--GCLDNNMQPKDLKSLQLYGNLVTLPEWIKD 1086
Qy 828 LTHLKKFNLSKLEKGNMLIIGLNPMLFSLYHNSYLGEKLVFKTGAPNLRTLVIF 887
Db 1087 LKILQKLSRNTNLKADTTMEVGLNPLMLATLRLODNACEEEELCFGPERFTGLTSLLEL 1146
Qy 888 NLDOLREIRPDGSSPOLEKTEISCCRL--BSGIIGIITHLPLKELISL-----EY 935
Db 1147 NWESLSKVFERGATPKLVLLHYCQIHNGGFSIETLSLKEVSILGNYDQTYTEP 1206
Qy 936 KSKVARLGQLKGRVTHPNREVL 958
Db 1207 KE-----QLQKQDMNKNKPNL 1223
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RESULT 10

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Q9MBF2
ID Q9MBF2 PRELIMINARY; PRT; 1226 AA.
AC Q9MBF2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FibH8 protein.
GN Name=FibH8;
OS Oryza sativa (Rice).
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohoku IL-9; TISSUE=Green leaf;
RX MEDLINE=93348180; PubMed=10417726;
RA Wang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L., Hayasaka H.,
RA Katayose Y., Sasaki T.
RT "The Fib gene for rice blast resistance belongs to the nucleotide
RT binding and leucine-rich repeat class of plant disease resistance
RT genes."
RL Plant J. 19:55-64(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohoku IL-9; TISSUE=Green leaf;
RX MEDLINE=11725950; DOI=10.1023/A:1012457113700;
RA Wang Z.X., Yamanouchi U., Katayose Y., Sasaki T., Yano M.;
RT "Expression of the pib rice-blast-resistance gene family is up-
RT regulated by environmental conditions favouring infection and by
RT chemical signals that trigger secondary plant defences."
RL Plant Mol. Biol. 47:653-661(2001).
DR EMBL; AB013451; BAA93618.1; -.
DR Gramene; Q9MBF2; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR 1; 3.
DR Pfam; PF00931; NB-ARC 1.
DR PRINTS; PR0364; DISEASERSIST.
DR SEQUENCE 1226 AA; 138086 MW; F45F3BECF9F0251A CRC64;
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Query Match 23.1%; Score 1215.5; DB 2; Length 1226;
Best Local Similarity 27.5%; Pred. No. 4.5e-56;
Matches 353; Conservative 196; Mismatches 349; Indels 385; Gaps 30;

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Qy 1 MAETVLSMARSLVGSALSKAASAAANETSLLLGVEKDIWIYKDELKTWQAPLRAAEVWK 60
Db 1 MEATAVSVGKSVLGKALSYAQTAAIEGALKLGVQRDQSFIRDELEWMSFLAAD--KE 58
Qy 61 KD---ELLKVAEQIRDSYDIEDSLDEPKVHLESQTLFRQLVKL-RERHRIAIRHNL 115
Db 59 HDGHHHVIRTWKQVRDAYDVEDCLQDYAARLUKPPWMSLPCTVIRERRIRGNEMKEL 118
Qy 116 KSRVEEYSSRNRYNLVE---PISSGTE-----DDMSYAEIDRNQ----- 153
Db 119 RAKVEDVSRQMRVHGVSAAAPQSSSVTAAELLQSTAAIDIDEARRAAKQEKVDLVKL 178
Qy 154 -----SARNVDEA-----ELVGFSDSKKRL----- 174
Db 239 VROPKANSREGTKTPOGTSGVSVLNEMEAQDYNLLHDFTYVTNKKYLVVLNGLSTIE 298
Qy 175 -----EM 176
Db 299 EWDWIKTYLPNNHNGSRVLVCTQQAEEVASCCTCTDDKYKVSEIQHEGFSKPLVFFYKEV 358
Qy 177 IDTNAN-----DGP----- 185
Db 359 VSPVNSDSTKWKSETRSSMEGASTTSDSKTVPDGVQIEDGPKDLPESLPPHLNRDSN 418
Qy 186 -----AKVICVVGSGLGKLTALSRIKPFSEE 211
Db 419 TVSVKELSRSTQIIGRKEKDDVIKLLSDCNPIRQVISVWGMGGIKTTLVRSIYQSS 478
Qy 212 DIRKNFPCNAWITVSQSFHRIELKDMIRQLGLPSSLDQLLHELQGGKVVVQVHHL----- 266
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Db 771 KQDLTGKYLIVLDDSLSTTTEWDFIKTI-PPENS--SSRIIVTTRPKLVAQHCSEEBEYM 827
Qy 331 H-LDFLQWDAISLILRK-----TKNHED-----MESKNKQKQWVERIV 369
Db 828 HRIGDLKDKDALDFLDFKFLYLFGNYKVKCKGDESELKPDMDILKKNPDMIAEALIV 887
Qy 370 NKGRPLAIITIGAVLATK--QVSEWEKPYEQLPSELEINPSELEALRRMVTGLYNHLPS 427
Db 888 KKCGRPLAIVAVGGFISTRPNTREWRKFSHDHISTELDENPSELEMIKKILLISYEGLSY 947
Qy 428 HLKPCFLYLSIFPEDFEIQRNLVGRMIAEGFVRPKVGMTTKDVGESYFNELINRSMIOR 487
Db 948 HLKSCFLYLSIFPEDHDIRYKLLRRWIAEGYSRAKRNNAEKEAEQFTALLNKSMIQQ 1007
Qy 488 SRVGTAGIKTCRTHDIRDTISISQENFVLPMGDGSLDVONTHTIAFHGSM----- 544
Db 1008 SRTVTGKTGFCQVHDLMEISIAKSEENLVLVLDHSISSSKDKVRHLVISQSWREQ 1067
Qy 545 -----CTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDPVTLITQKDFRI 599
Db 1068 KQNDNMQIVDVSHIRSLTVFGEW-KSF---FLSKKVRMLRVLDLED-TDGLDHDIVPI 1122
Qy 600 ALLCHLYLSIGYSSISYSLPRSIGKLGLOTLNMSSTYIAALPSEISKQLCHTLRC-- 657
Db 1123 GKHLHLKYLURGSATILNLPSSFGNLLNLETLDIRGTWTKLPATIGRLQNLKYLHAGM 1182
Qy 658 IRELEFDNFS-LNHPMKCITWTICLPKVTFLVSRDNRKQIAEFHMAKSPWS----- 710
Db 1183 PPDEDDTRSVVTPPSAILEAF-----REYWTNQ-EEVGMGKLFVSVLMFLI 1230
Qy 711 -----ESFGVYKPGKIGKLDQLVLEYDIRTSSRAIKELGOLSKRLKLAIVITKGT 763
Db 1231 SGWRNMDLFGVKVPRRIGRLURSHITLSVNI-SR-GRAMLNKLNKLLQLRKLGV--TGIN 1287
Qy 764 KECKILYAAIEKLSLQSLYNNALSDIETLECLDSISSPPPLRLTLGLNGSLEEMPN 823
Db 1288 KNNCEELCSVIVKHGCLQSLLRABGKDLB--GCLDGLSPPPKDLSESLQLYGNLVKLE 1345
Qy 824 WIEQTLHKFNLSKKLKEGKNMILIGALPNLMPLSLYNSYLGKLVFKTGAPPNLT 883
Db 1346 WVKLENLQKLSLSTNLNLEADATQVGLGPMLDILRLQDKACKENELRHPDCTNLRA 1405
Qy 884 LVIENLQLRIRIEDGSSPOLEKIEISCCRL--ESGIIGHIHLPLKEISL-----EY 935
Db 1406 LELISWSLSKSVIFEEGATPKLEVLLVDHCHSIDBAGPPGIENLATLKEVSLQGYTTF 1465
Qy 936 KSKVARLQQLGVEYTHPNRPVLRM 960
Db 1466 KKK-----LQQLNMITEPRPNLRI 1484
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RESULT 12

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Q9ZNV6
ID Q9ZNV6 PRELIMINARY; PRT; 1251 AA.
AC Q9ZNV6; OS9SV0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Pib.
GN Name=Pib; Synonyms=P1-b;
OS Oryza sativa (Rice);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohoku IL-9; TISSUE=Green leaf;
RX MEDLINE=93348180; PubMed=10417726;
RA Wang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L., Hayasaka H.,
RA Katayose Y., Sasaki T.;
RT "The pib gene for rice blast resistance belongs to the nucleotide
binding and leucine-rich repeat class of plant disease resistance
```

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genes.";
Plant J. 19:55-64 (1999).
[2]
SEQUENCE FROM N.A.
RC STRAIN=BL-1; TISSUE=Green leaves;
RA Jwa N., Tsunoda Y., Akiyama K., Nakamura S., Motomura T., Kamiyama K.,
RA Kodama O., Kawasaki S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB013449; BAA76282.2; -
DR EMBL; AB013448; BAA76281.2; -
DR EMBL; AB026839; BAA85975.1; -
DR Gramene; Q9ZSV0; -
DR Gramene; Q9ZNV6; -
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR00767; Disease_resist.
DR InterPro; IPR01611; LRR.
DR InterPro; IPR02182; NB-ARC.
DR Pfam; PF00560; LRR_1; 2.
DR Pfam; PF00931; NB-ARC.
DR PRINTS; PRO0364; DISEASERISIT.
SQ SEQUENCE 1251 AA; 141638 MW; 011F56630118AB98 CRC64;

Query Match 22.7%; Score 1191; DB 2; Length 1251;
Best Local Similarity 27.7%; Pred. No. 9.4e-55;
Matches 355; Conservative 208; Mismatches 363; Indels 356; Gaps 39;

Qy 1 MAETVLSMARSLVGSALSKASAAANETSLLLGVEKDIWIYKDELKTWQAPLRAAEVKK 60
Db 1 MEATALSVGKSVLNGALGYAKAPAEVALQGIQKDHFTFVADBLEMMRSFMEAEHQD 60
Qy 61 KDELKVAEQIRLSDYIEDSLDEFKVIHIESQTLFQLVKLERHRTAIRIHNLSKSRVE 120
Db 61 NSKVVTWVQVRDTAYDVEDSLQDFAVHLKRSWRRPRTLLERHRVAKQMKELRNKVE 120
Qy 121 EVSRNRYNLVEPISSGTDDMDSYAEDIRNQSRNVDAELVGFSDSKK-RLLEMDIT 179
Db 121 DVSRNVRYHLKGSAKATINSTEQ--SSVIATAI FGIDDDARRAAKQDNQRVDLVQLI-- 176
Qy 180 NANDGPAKVICVGMGG-LGKTALSRKIFSEEDIRKNFPCNAVITVQSFRHIELLKD 238
Db 177 NSEDDQLKVIAMVGTSGDMGQTTIIRMAYEN-PDVQIRFPCRAWVRVMPSPDFVQSL 235
Qy 239 IROL----- 242
Db 236 VNLHATQGVAEALLEKEKTEQDLAKKPGCVNDRKCLIVLNDLSTIEWDQIKCFQKCR 295
Qy 243 -----LGPSSLLDQLLH----- 253
Db 296 KGSRIIVSSTQVEVASLCAQESQASELKQLSADQTLVAFYDKGSQIIEDSVKPSISDV 355
Qy 254 -----ELQG--KVVQVHH 265
Db 356 AITSTNNHTVAHGEIIDDQSDMADEKKVARKSLTRITSVGASESOLIGREKISEITH 415
Qy 266 L----- 266
Db 416 LILNDSQQQVVISVWGMGGLKTLVSGVYQSPRLSDKFDKVFVVTIMRPFILVELLRS 475
Qy 267 -----SEYLIEE-----LKEKRYFVVLDDDLWLHWD 292
Db 476 LAEQHLKSSKCKELLENRVSSKSLASMEDTELTGQLKLEKSCCLIVLDDSDTSEW 535
Qy 293 NWINEIAPPKNKKGSRIVITTRNVDLAEKATAS-LVYHLDLFQMDAISLLRKT--N 349
Db 536 DQIKPTLFP-L-LEKTSRIIVTRKENIANHCSGNGVHNLKVLKHDALCLLSEKVFEE 594
Qy 350 KNHEDMESKNKQKQWVERIVNKCGRPLAIITIGAVLAT--KQVSEWEKPYEQLPSELEI 407
Db 595 ATYLDQDQNPVELVKEAKQILKKCDGLPLAIVIGGFLANRPDTPPEWRKLNENNALEEM 654
Qy 408 NPSLEALRRMVTGLYNHLPSHLKPCFLYLSIFPEDFEIQRNLVGRVIAEGFVRPKVGMT 467
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Db 655 NPELGMITVLEKSDGUPYHLKSCFLYSLIPPEDQIISRRLVHRWAAEGYSTAAHGKS 714
Qy 468 TKDVGESYFNLINRSMI---QSRVGTAGK-IKTCRIHDIIRDITVSISROENFVLLPM 523
Db 715 AIEIANGYFELKNRSMILPQOS--GSRKSIDCKVDLWDLWDLAIKSTEENLVPRVE 772
Qy 524 GDGSDLVQENTRTHA----FHGSMCKTGL-DWSIIRSLAIFGDRPKSLAHAVCPDQIRM 578
Db 773 EGCSAYIHGAIRHLAISSNWNKGDSEFGIIVDLRSIRLSLFGDWKPFVYV---KMRF 828
Qy 579 LRVLDLQVDTFLITQKOPDRALCHLKVLSIGYSSISYLSPRSTGKLGQGLQTLNMSSTY 638
Db 829 IRVLDJFEG-TGLEVYHLDQIWKLNHLKFLSLRGCYRIDLPDLGNLQRLQMLDIRGY 887
Qy 639 IAAIPSEISKQLCHLTLRCIRELEP---DNFSLNHPMK---CITNTICLP---KVFTPLV 689
Db 888 VKALPKTIKQLQYIHAGKTDVYWEKSLMQRCKVGCICATCCPLLCENYGPL- 946
Qy 690 SRDNRAKQIAEFHMATKFSW-----ESFGVKVPGIKGLRDLQVLEYVD 734
Db 947 ---HKA-----LARRDAWTFACCVKPPSMTGVHEBEGAMVPSGIRKLDLHTRLN 996
Qy 735 IRRYSSRAIKELGOLSKRLKAVITKSTKECKLYAAIEKLSLSLOSLYNNALLSDIE 794
Db 997 VGR-GNALRIDGMLTGLHKLGV--AGINKKNGRAFLAISLNKLESLSVSSAGMPL- 1052
Qy 795 TLECLDSSPPPLRLTLGLNGSLSEMPNWEQTLHLKFNLMWSKLKE-GKNMLILGAL 853
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Qy 854 PNLMLSLYHNSYGEKLVFK---TG-APPNRLTVLIFNLDQRLREIFEDGSSPOLEKIE 909
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Qy 910 ISCRLES--CIIGIHLPLKETSLEY-----KSKVARL-----942
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Qy 943 --GOLKGEVN---THNRPVL 958
Db 1229 KGGEIKRKIRQELARNPNQPII 1250

RESULT 13
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AC Q9LJ10;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Oryza sativa gene for Pib.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=339947;
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RX PubMed12447438; DOI=10.1038/nature01184;
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RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuna A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K. Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,

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RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP001073; BAA89580.1; -.
DR Gramene; Q9LJ10; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR000630; Ribosomal_S8.
DR Pfam; PF00560; LRR_1; 2.
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SQ SEQUENCE 1011 AA; 114012 MW; 14EDDBA31A4835C CRC64;

Query Match 22.4%; Score 1174.5; DB 2; Length 1011;
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Matches 334; Conservative 197; Mismatches 365; Indels 179; Gaps 37;

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Qy 59 KKDELKLVAAEQIRDLSYDIEDSLDEPKVHIES-----QTLFRLQVLK 102
Db 61 YHQSQTRTWKQVREYAYDAEDCIDSPRYHVGGDRNHDEGLLVAGLRRRTALRPLTTL 120
Qy 103 RERHRIAIRIHNLSRVEEVSRRTRYNLVPISSGTB-----DMDSVAEDIRNQS 154
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Qy 155 ARNDEALVGFSDSKK---ELLEMDITNANGDA--KVICVVGMGGLGKTALSRIKPS 209
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Qy	105	-----RHRIAIRHNLKSRVEEVSRRNTRY--NLVEPISSTGTEDDMDSYAEDIRNQA 155			
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:53:28 ; Search time 94.0327 Seconds
(without alignments)
3574.555 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4966.5	94.5	1091	15	US-10-352-179-93 Sequence 93, Appl
3	4209.5	80.1	1531	16	US-10-437-963-139799 Sequence 139799
4	3636	69.2	993	16	US-10-437-963-104966 Sequence 104966
5	3080.5	58.2	974	16	US-10-437-963-143499 Sequence 143499
6	3055.5	58.1	979	15	US-10-352-179-85 Sequence 85, Appl
7	2819	53.6	862	16	US-10-437-963-141086 Sequence 141086
8	2595	49.4	993	15	US-10-352-179-87 Sequence 87, Appl
9	2532	48.2	1007	16	US-10-437-963-110261 Sequence 110261
10	2483.5	47.3	1163	16	US-10-437-963-151916 Sequence 151916
11	2427	46.2	1054	15	US-10-352-179-91 Sequence 91, Appl
12	1903	36.2	926	16	US-10-437-963-171923 Sequence 171923
13	1894.5	36.1	812	16	US-10-437-963-177336 Sequence 177336

14	1389	26.4	451	15	US-10-352-179-95	Sequence 95, Appl
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17	1215.5	23.1	1226	16	US-10-437-963-135087	Sequence 135087
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21	1165.5	22.2	1011	16	US-10-437-963-134127	Sequence 134127
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29	1041.5	19.8	953	14	US-10-267-718-36	Sequence 36, Appl
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36	994.5	18.9	911	16	US-10-437-963-198474	Sequence 198474
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44	954	18.2	961	16	US-10-437-963-190153	Sequence 190153
45	948	18.0	780	16	US-10-437-963-174758	Sequence 174758

ALIGNMENTS

RESULT 1

US-10-352-179-89
; Sequence 89, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla.
; FILE REFERENCE: 2272/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 1031
; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-89

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DB 1021 ND 1022

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; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
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; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 1091
; TYPE: PRF
; ORGANISM: Oryza minuta
US-10-352-179-93
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Best Local Similarity 90.4%; Pred. No. 0;
Matches 986; Conservative 20; Mismatches 26; Indels 59; Gaps 1;
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QY 1 MAETVLSMARSLVGSATSKAASAAANETSLLGVEKDIW----- 39
DB 1 MAETVLSMARSLVGSATSKAASAAANETSLLGVEKDIWYIKDELKTMQAFLEAAEVNKK 60
QY 40 -----YIKDELKTMQAFLEAAEVNKK 61
DB 61 KDELKTMQAFLEAAEVNKK 120
QY 62 DELLKVMQAEQIRLDSDYIEDSLDEFKVIHESQTLFROLVKLRERHRAIRIHNLSRVEE 121
DB 121 DELLKVMQAEQIRLDSDYIEDSLDEFKVIHESQTLFROLVKLRERHRAIRIHNLSRVEE 180
QY 122 VSSRTRYNLVPEITSSGTEDDMSYAEIDRNQARNVDEALVGFSDSKLLEMDTNA 181
DB 181 VSSRTRYNLVPEITSSGTEDDMSYAEIDRNQARNVDEALVGFSDSKLLEMDTNA 240
QY 241 NDGPAAKVICVVGGLGKTALSRKIPESEEDIRKNPPCNAWITVSQSFHRIELKDMIRQ 241
DB 241 NDGPAAKVICVVGGLGKTALSRKIPESEEDIRKNPPCNAWITVSQSFHRIELKDMIRQ 300
QY 242 LLGPFSSLDQLLHBLQGVVQVHLSYLFEELKEKRYFVVLDDMLWLDWMWINEIAFP 301
DB 301 LLGPFSSLDQLLHBLQGVVQVHLSYLFEELKEKRYFVVLDDMLWLDWMWINEIAFP 360
QY 361 KNNKGSRIVITRNVDLAECATASLVYHLDLFLQNDALSLLRKTNKKNHDMESKNM 361
DB 361 KNNKGSRIVITRNVDLAECATASLVYHLDLFLQNDALSLLRKTNKKNHDMESKNM 420
QY 421 QKWERIVNKGCGRLPLAILTIGAVLATKQVSEKFEYQLPSELEINPSLEALRRMVTLG 480
DB 421 QKWERIVNKGCGRLPLAILTIGAVLATKQVSEKFEYQLPSELEINPSLEALRRMVTLG 480
QY 481 YNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKOVGESYFNELIN 481
DB 481 YNHLPSHLKPCFLYLSIFPEDFEIQRNRLVGRWIAEGFVRPKVGMTTKOVGESYFNELIN 540
QY 541 RSMIQRSRVGTAGIKITCRTHDIIRDITVSIHQENFVLLPMGGSDLVQENTRHIAFH 541
DB 541 RSMIQRSRVGTAGIKITCRTHDIIRDITVSIHQENFVLLPMGGSDLVQENTRHIAFH 600
QY 601 SMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLVEDVTLITQKDFRIA 601
DB 601 SMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLVEDVTLITQKDFRIA 660
QY 661 LCHLKYSIGYSSSIYSLPRSIGKQLQGLQTLNNSSTVIAALPSEISKQLCHLTLRCIRE 661
DB 661 LCHLKYSIGYSSSIYSLPRSIGKQLQGLQTLNNSSTVIAALPSEISKQLCHLTLRCIRE 720
QY 721 EFNFSNHPMKCITNTICLPKVFTPLVSRDNRKAQIAEFHMAKTSFWSSEFGVKVPKG 721
DB 721 EFNFSNHPMKCITNTICLPKVFTPLVSRDNRKAQIAEFHMAKTSFWSSEFGVKVPKG 780
QY 781 GKLRLDQVLEYVDIIRTSRAIKELGOLSKRLAVITKGTKECKKILYAAIEKLSSLQ 781
DB 781 GKLRLDQVLEYVDIIRTSRAIKELGOLSKRLAVITKGTKECKKILYAAIEKLSSLQ 840
QY 841 SLYVNAALLSDIETLECLDSISSPPPLRLTGLNGSLEEMPNIIEQLTHLKYLRLSK 841
DB 841 SLYVNAALLSDIETLECLDSISSPPPLRLTGLNGSLEEMPNIIEQLTHLKYLRLSK 900
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[illegible]

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RESULT 3
US-10-437-963-139799
; Sequence 139799, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139799
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1.pep
US-10-437-963-139799

```

Query Match	80.1%; Score 4209.5; DB 16; Length 1531;
Best Local Similarity	92.6%; Pred. No. 7.4e-305;
Matches	Conservative 21; Mismatches 42; Indels 3; Gaps 2;
Qy	135 ISSGTED--DWDSVAEQDIRNQSANRVDEAEILVGFSDSKCLLEIMIDTNANDGPAKVICV 192
Db	2 VASGNQSLAIDSVAEDIRNQSANRVDEAEILVGFSDSKCLLEIMIDTNANDGPAKVICV 61
Qy	193 GMSGIGKTALSRKIFESEEDIRKNFPCNAWITVSQSFSHRIFELLDKMI RQLLGPSLSLQQL 252
Db	62 GMSGIGKTALSRKIFESEEDIRKNFPCNAWITVSQSFSHRIFELLDKMI RQLLGPSLSLQQL 121
Qy	253 HELOGKVVVVQVHHLSEYLIIBELKPKRYFVVLDDLIWLHDWNWINEIAPPKNKKGSRIVI 312
Db	122 QELQKVVVVQVHHLSEYLIIBELKPKRYFVVLDDLIWLHDWNWINEIAPPKNKKGSQIVI 181
Qy	313 TTRNVDLAEKCATASLVYHLDPLQMNDAISILLRKTNNKHEDMESNKNMQQVRIYNKC 372
Db	182 TTRNVDLAEKCATASLVYHLDPLQMNDAITULLRKTNNKHEDMESNKNMQQVRIYNKC 241
Qy	373 GRPLAAILTIGAVLATKQVSEWEKFYBQLPSELEINPSLEALRMVTLGYNHLPSHLKPC 432
Db	242 GRPLAAILTIGAVLATKQVSEWEKFYEHLPSELEINPSLEALRMVTLGYNHLPSHLKPC 301
Qy	433 FLYLSIIPPEQFEIQRNLVGRWIAEGFVRPKVGMTTKDVGESYFNEILNISMQRSVGT 492
Db	302 FLYLSIIPPEQFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNEILNISMQRSVGI 361

Qy	493	AGKIKTCRIHDIIRDITVTSISRQENFVLLPMGDSGLVQENTRTHIAFHGSMCKTGLDWS	552
Db	362	AGKIKTCRIHDIIRDITVTSISRQENFVLLPMGDSGLVQENTRTHIAFHGSMCKTGLDWS	431
Qy	553	IIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFILITOKDFDRIALLCHLKYLISIGY	612
Db	422	IIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFILITOKDFDRIALLCHLKYLISIGY	481
Qy	613	SSSIYSLPRSIGKLGQLTLMN SSTYIAALPSEISKLOCLHLTRCIRELEFDFNFSLNHPM	672
Db	482	SSSIYSLPRSIGKLGQLTLMN SSTYIAALPSEISKLOCLHLTRCIGQPHYDNFSLNHPM	541
Qy	673	KCITNTTICLPKVFPLVSRDNRKQIAEFHATKSPWSESGVQKVPKGIGKLRDLQVLEY	732
Db	542	KCITNTTICLPKVFPLVSRDNRKQIAELHATKSCWSESGVQKVPKGIGKLRDLQVLEY	601
Qy	733	VDIIRTSRAIKELGOLSKLRKLAVITKGSTKECKILYAAIEKLSSLSQSLYMAALLSD	792
Db	602	VDIIRTSRAIKELGOLSKLRKLGVTTNGSTKECKILYAAIEKLSSLSQSLHVDVLFSG	661
Qy	793	-IETLECLDSISSPPPLRLTTLGLNGSLEEMPNIWIEQLTHLKKFNLWSSKLEKGNMLILG	851
Db	662	IETLECLDSISSPPPLRLTLRLNGSLEEMPNIWIEQLTHLKKFDLRRSKLEGKTMILG	721
Qy	852	ALPNMFLSLYHNSLYGEKLVFKTGAPNRLTLVIFNLDOLREIRPEDSGSSPOLEKIEIS	911
Db	722	ALPNMFLYLYRNAYLGEKLVFKTGAPNRLTLCIYELDQLREIRPEDSGSSPLLEKIEIG	781
Qy	912	CCRLSEGIIGIHLPLKIEISLEYKSVARLGOLKGEVNTNRPVLRMDSDRRDHDLGA	971
Db	782	CCRLSEGIIGIHLPLKIEIPITVGSKVAGLQGLEGEVNTNRPVLLMYSDRYHDLGA	841
Qy	972	EAEGSSIEVQTADVPVDAQGSVTVVAEATDPLPEQEGESSQSQVITLTITNDSEEI	1026
Db	842	EAEGSSIEVQTADVPVDAQGSVTVVAEATDPLPEQEGESSQSQVITLTITNDNRNL	896

RESULT 4

US-10-437-963-104966

Sequence 104966, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 104966

LENGTH: 993

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_102251C.1.pep

US-10-437-963-104966

	Query Match	59.2%	Score 3636;	DB 16;	Length 993;
	Best Local Similarity	72.6%;	Pred. No. 2.6e-262;		
	Matches 733;	Conservative	78;	Mismatches 120;	Indels 78; Gaps 3;
Qy	1	MAETVLSMARSLVGSIAISKAAASAAANETSLLLGVKEQDIWIYIKDELKTMQAPLRAAEYVMKK	60		
Db	60	MAETVLSMARSLVGSIAISKATSAASAAEASLLGVQKQDIWIYIKDELKTMQAPLRAAEYVMKK	119		
Qy	61	KDELLKVMARQIRDLSDYSDISDLDFPKVHIESOTLFRQLVKLRHRHRIAYIRHNLKSRVE	120		

Db 120 KDELKVAEQRDLSDYIEDCLDEFKVIHIESQNFYQWVKLRKHLLIATQIRNLKSRVE 179
Qy 121 EVSSRNRYNLVPEPISGTTEDMDSYAEDIRNQARVNDDEALVGFSDSKGLLEMDITN 180
Db 180 EVSSRNRYNLVPEPISGTTEDMDSYAEDIRNQARVNDDEALVGFSDSKGLLEMDITN 229
Qy 181 ANDGPAKVICVVGNGGLGKLTALSARKIPESEDIRKNPPCNAWITVSQSFHRIELKKDMIR 240
Db 230 -----IRIELKKDMIR 240
Qy 241 QLLGPPSILDQLLHELQGVVQVHHLSYLIIEELKEKRYFVFLDDLLWLDHWNWINEIAF 300
Db 241 QFLGNSILDQLVQLQGVVQVQIHLSDYLRLKLLKEKRYFVFLDDLLWLDHWNWINEIAF 300
Qy 301 PKNKKGSRIVITRNVDLAEKATASLVYHLDPLQWMDAISLLLRKTNKNHDMESNKN 360
Db 301 PKNKKGSRIVITRNVDLAEKATASLVYHLDPLQWMDAISLLLRKTNKNHDMESNKN 360
Qy 361 MOKMVERIVNKCGRPLAIIITIGAVLATKQVSEWEKFEYQOLPSELEINPSLEALRRMVTL 420
Db 361 MOKMVERIVNKCGRPLAIIITIGAVLATKQVSEWEKFEYQOLPSELEINPSLEALRRMVTL 420
Qy 421 GYNHLPKPCFLYLSIFPPEDFEIQNRNLVGRWIAEGFVRPKVGMITTKDVGESYFNELI 480
Db 421 GYNHLPKPCFLYLSIFPPEDFEIKRSRLVDRWIAEGFVRPKVGMITTKDVGESYFNELI 480
Qy 481 NRSIMQSRVGTAKIKTCRIHDIIRITVISIQENFVLLPMGDGSDLVQENTRHIAFH 540
Db 481 NRSIMQSRVGTAKIKTCRIHDIIRITVISIQENFVLLPMGDGSDLVQENTRHIAFH 540
Qy 541 GMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTELITQKDFRIA 600
Db 541 GMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTELITQKDFRIA 600
Qy 601 LLCHLKLYLSIG--YSSSTYSIPRIGKLGQIQTILNMSSTYIAALPSBISKLCIHLTRCI 658
Db 601 LLRLHKLYLSIGRIFSSCTYTLPRSIGKLGQIQTILNMSSTYIATLPTBISKLCIHLTRCT 660
Qy 659 RELBDFNPSLHMPKCTNTICLPKVTPLVSRDNRAKQIAEFHMAKTSFWSSEFGVKVP 718
Db 661 RVSNNNFNSINHPVKCLTNTMCLPNIETPVSVDNRNRAKQIAEFHMAKTSFWSSEFGVKVP 720
Qy 719 KGICKLADQLVLEVDYDRTSSRAIKELGQSLKRLKLAIVTKGSTKCKILYAAIEKLS 778
Db 721 KGICKLADQLVLEVDYDRTSSRAIKELGQSLKRLKLAIVTKGSTKCKILYAAIEKLS 780
Qy 779 SIQSLYMAALLSDIETLECLDSISSPPPLRTILGLNGSLEEMPNWIEQLTHLKKFNLS 838
Db 781 SIQSLYVDAEGSSNGTILKCLDSISYPLLLKTLKLYGDLSEEMPNWIEQLSHLMKFFLLG 840
Qy 839 SKLKEGNMLITLGPALPNLMFLSLYHNSYLGKLVFKTGAPPNLRTLVIFNLQDLREIRFE 898
Db 841 SKLKEGTMLITLGPALPNLMFLSLYHNSYLGKLVFKTGAPPNLRTLVIFNLQDLREIRFE 900
Qy 899 DGSSPOLKIBISCRLESIGIIGIHLPRKEISLEKVSQVRLGKGVNTHPNRPVL 958
Db 901 NDSSPLLEKIGIRYCRLEIGIIGIISNLMRLKBITLGYRVKGYGLQGLEREVGHNRPVL 960
Qy 959 RMDSDRHDHDLGABEGSSIEVQTADPVPDAQSGVTVAVEATDPLPEOE 1007
Db 961 RMEEDRCHDLRRDGKSAVE-----MEATEPLPPE 992

RESULT 5

US-10-437-963-143499
; Sequence 143499, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 143499
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1.pep
US-10-437-963-143499

Query Match 58.2% Score 3060.5; DB 16; Length 974;
Best Local Similarity 62.8% Pred. No. 2.5e-219;
Matches 610; Conservative 141; Mismatches 217; Indels 3; Gaps 3;

Qy 2 AETVLNARSVLGSAISKAASAAANETSLILGVEKDIWIYKDELKTQWQAFRAAEVKKK 61
Db 3 AETVVSMAVSLGSAVGAASAAAADATLLGIGKEIWIYKDELKTQWQAFRAAEVTKKK 62
Qy 62 DELLKVAEQRDLSDYIEDCLDEFKVIHIESQNFYQWVKLRKHLLIATQIRNLKSRVE 121
Db 63 DELLKVAEQRDLSDYIEDCLDEFKVIHIESQNLAKMLKGERHIAVQIRNLKSRVE 122
Qy 122 VSSRNRYNLVPEPIS--GTEDMDSYAEDIRNSARNVDDEALVGFSDSKRLLEMDITN 180
Db 123 VSNRYSLIKPISITTEDERDYSLEARNQSGSNTDESELVFAKTDELKLLDVTN 182
Qy 181 ANDGPAKVICVVGNGGLGKLTALSARKIPESEDIRKNPPCNAWITVSQSFHRIELKKDMIR 240
Db 183 TNDGPAKVICVVGNGGLGKLTALSARKIPESEDIRKNPPCNAWITVSQSFHRIELKKDMIR 241
Qy 241 QLLGPPSILDQLLHELQGVVQVHHLSYLIIEELKEKRYFVFLDDLLWLDHWNWINEIAF 300
Db 242 QLLGADSLDKLLEKFESEKLVQVHLDHVLGKRYFVFLDDLLWLDHWNWINEIAF 301
Qy 301 PKNKKGSRIVITRNVDLAEKATASLVYHLDPLQWMDAISLLLRKTNKNHDMESNKN 360
Db 302 PKNNRSGRIITKTRDAGLAGRCTSESLLIYHLEPLHDDAIHLLAKTNIRLEDMEDED 361
Qy 361 MOKMVERIVNKCGRPLAIIITIGAVLATKQVSEWEKFEYQOLPSELEINPSLEALRRMVTL 420
Db 362 LGSIVTKLVKRCGYPLAIIITIGAILATKKIMWKGFEYRELPSLESNPSLEAMRRMVTL 421
Qy 421 GYNHLPKPCFLYLSIFPPEDFEIQNRNLVGRWIAEGFVRPKVGMITTKDVGESYFNELI 480
Db 422 SYNHLPSHLKPCFLYLSIFPPEDFEIQNRNLVGRWIAEGFVRATDGVNIEDVGNHFNELI 481
Qy 481 NRSIMQSRVGTAKIKTCRIHDIIRITVISIQENFVLLPMGDGSDLVQENTRHIAFH 540
Db 482 NRSILQPSKYSTDGVVKRCIHDIMRDIIVISIREENFVLLTREKITVVAEESIRHLAFH 541
Qy 541 GMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTELITQKDFRIA 600
Db 542 GSKCKILEWNLHSLVTLFGDRPVGRTPALCSQPFRMLRVLDLEDVAFKFTQNDIRNIG 601
Qy 601 LLCHLKLYLSIGYSSISYLSIPRSIGKLGQIQTILNMSSTYIAALPSBISKLCIHLTRCIRE 660
Db 602 LLRHKYLNFASTIYTLPRSIGKLGQIQTILNMSSTYIAALPSBISKLCIHLTRCIRE 661
Qy 661 LEFDFNS--LNHPMKICTNTICLPKVTPLVSRDNRAKQIAEFHMAKTSFWSSEFGVKVP 719
Db 662 SGSGYFSLIINPKCELMITWCLPMVFLTSINFSRDLVLIPEICMSCTRSWSDTKGVVR 721
Qy 720 GIGKLRDLQVLEVDYDRTSSRAIKELGQSLKRLKLAIVTKGSTKCKILYAAIEKLS 779
Db 722 GIDNLKELQILEVVDINRTSRKAIIEELGELIQLRKLKSLVTTKGTATNKKYQIFCAAIEKLS 781

Qy 61 KDELKVAEQRDLSYDIEDSLDEFKVIHIESOTLFRQLVKLRHRHRIAIHNLKGRVE 120
Db 60 KSILKVVQVRDLSDIEDCLDEFVHVSQTLSQLMKLKHRRHIAIQIRNLRIE 119
Qy 121 EVSSRNRYNLVE-PISSGTDDMDSYAEDIRNQSARNVDAELVGFSDSKKRLLEMDT 179
Db 120 EVSTRNRYNLIENDLTCTTTDERNLFMEDIRNQSANNIEADLVGFGPKRELLDIDV 179
Qy 180 NANGDPAKVICVGMGGGLKGTALSRKIPESBEDIRKPPPCNAWITVSQSFHRIELKDMI 239
Db 180 HANIGPTEVCVGMGGGLKGTIARKIYESKEDIAKNFSCCAMITVSQSFVRLSLKDLM 239
Qy 240 ROLLGPPSSDQLLHELQKVVQVHLSKRYEYLIELKERYFVVLDDWLWLDHWNWINEIA 299
Db 240 MKLFGEEVLKQMELEGK-VQVDDDLASYRLTELNER----- 277
Qy 300 PPKNKKGSRIVITRNVDLAECATASLVYHLDFLQMNDAISLLLRKTNKHEDMESNK 359
Db 278 ---NNKGSWIVITRDVGLAKECTSELLIYQLKPLRISYAKELLRLKANKTTEDIESDK 334
Qy 360 NMQKVERIVNKCGRPLAIIITIGAVLATKQVSEWEKFEYEQLPSELEINPSLEALRMVT 419
Db 335 KMSDIITKIVKCKGYPALAITIGVLTAKREIWEWTFYSQIPSELESNPNEAMRRIVT 394
Qy 420 LGYNHLSHLKPCFLYLSIFPEDFEIQNRNLVGRWIAEGFVRPKVGTTKDVGESYFNEI 479
Db 395 LSYNLSHLKQCFYLSIFPEDFEINRNL----- 425
Qy 480 INRSMIQRSRVGTAGKIKTCHIDIIRDITVSIHQENFVLLPMGDGSDLVQENTRIAF 539
Db 426 ----- 425
Qy 540 HGSMSK-KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTLITQKDFDR 598
Db 426 -GSKYCSKISFDWSIIRSLTFAERPVELEHVSQSLRMLRVLDLRDAQTTIQNDVNN 484
Qy 599 IALLCHUKYLSI---GYSSSIYSIPRSIGKQGLQTLNMSSTYIAALPSEISKLQCLHTL 655
Db 485 IVLCHUKYLIARIYNNASYIYSPKSGIRLDGLQTLDLSTNSTLTPTQITKLRSLSL 544
Qy 656 RCIRELBFNPSLNHPMKCIITNTICLPKVFTPLVSRDNRKQIAEFHFMATKSPWSESFGV 715
Db 545 RCMQYDFSSPT-----TCLDTLCLPMIFTPSVSTSDRAEKIANLHLATKSPRSKNGV 599
Qy 716 KVPKIGIKLRDLQVLEVDIRRTSSRAIKELGQLSKLKLAIVITKGTKECKILYAAIE 775
Db 600 KVPKIGICRLRLQILGVVDIRRTSSRVIKELGQLSKLKLYVVTKGSTKLKCEILYTAIQ 659
Qy 776 KLSLSQSLYNNAAALLSDIETLECLDSISSPPPLRLTLGLNGSLEEMPNIWLBOLTHLKEN 835
Db 660 KLYLSQSLHMDAVCGTGTGLECLDSVSSPPPLRLTLRLNGSLEELPNWIBRLTHLRKFY 719
Qy 836 LWSKLEKGNMLILGALPNLMFLSLYHNSYLGELKVPKGTGAFPNRLTLVFNLDQLEI 895
Db 720 LLRTKLEGTMLILGALPNLMFLHFCNAYLGEKLVFKGTGAFPNRLTLVFNLDQORDI 779
Qy 896 RFEDGSSPQLEKIEISCCRLESIGIIGIHLPRLKEISLEYKSVARLGOLKGEVNTHPNR 955
Db 780 RFEDGSSPQLEKIEIGRCLRLESIGIIGIHLPRLKEISVEYKGVAMLAQLEGEVNAHPNC 839
Qy 956 PVLKMDSDRRDHDIGAEAGS 976
Db 840 PVLKAMDRSDHDLAGNAKS 860

RESULT 8
US-10-352-179-87
; Sequence 87, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Plant
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Oryza minuta
; US-10-352-179-87

Query Match 49.4%; Score 2595; DB 15; Length 993;
Best Local Similarity 55.3%; Pred. No. 1.6e-184;
Matches 539; Conservative 164; Mismatches 242; Indels 30; Gaps 12;

Qy 1 MAETVLSMARSLVGSISAISKAASAAANETSLLLGYEKDIWYIKDELKTMQAFRAAEVYMK 60
Db 1 MTETVVSMAVSLVGSIAIRVASSASSQSMMLIGVQNEIWFIKDELKTMQAFRAAEVRKD 60
Qy 61 KDELKVAEQRDLSYDIEDSLDEFKVIHIESOTLFRQLVKLRHRHRIAIHNLKGRVE 120
Db 61 QDELKVAEQRDLAYDIEDCLQEFVAVHVGHSLSMLIKLCHRRHIAVQIRNLKQORVE 120
Qy 121 EVSSRNRYNLVEPISSGTDDMDSYAEDIRNQSARNVDAELVGFSDSKKRLLEMDTN 180
Db 121 EVSNRNRYNLIKVSPPSSDSDSQNNMELIYQTAHYVNESELVGFDPVKKEILJELVSS 180
Qy 181 ANGDPAKVICVGMGGGLKGTALSRKIPESBEDIRKPPPCNAWITVSQSFHRIELKDMI 240
Db 181 EN-ABEQTIWVGEGLGKTTLAKKVYES-SDVSSKFCRAWITVRSFNVKOLLKNMIK 238
Qy 241 QLLGPPSSDQLLHELQKVVQVHLSKRYEYLIELKERYFVVLDDWLWLDHWNWINEIAP 300
Db 239 QLLGEDSLKLLDE-HKEVIVEKHNLDHLNKLGRGRYFLVLDLWTTQAWDCIKPTSW 297
Qy 301 PKNKKGSRIVITRNVDLAECATASLVYHLDFLQMNDAISLLLRKTNKHEDMESNKN 360
Db 298 -GNMGEGRVVVITRNKNLAGSGST-SPVCLTKLEKEDATKLLRLTKSLHDIKDO- 354
Qy 361 MQKQVERIVNKCGRPLAIIITIGAVLATKQVSEWEKFEYEQLPSELEINPSLEALRMVT 420
Db 355 MKEIFEKILAKCGPLAIIITIGAVLEGDKIKEWEILYALQLPSELESNPAAEPKMKVVT 414
Qy 421 GYNHLSHLKPCFLYLSIFPEDFEIQNRNLVGRWIAEGFVRPKVGTTKDVGESYFNEI 480
Db 415 SYNLPKPCFLYLCIFPEDFQIRKRLVHRWIAEGFIRARGGVGIVDVAQKYPDELI 474
Qy 481 NRSMIQRSRVGTAGKIKTCHIDIIRDITVSIHQENFVLLPMGDGSDLVQENTRIAFH 540
Db 475 NRSMIQRSRVGTAGKIKTCHIDIIRDITVSIHQENFVLLPMGDGSDLVQENTRIAFH 534
Qy 541 GMSCKT-GLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTLITQKDFDR 598
Db 535 DTSKCSNIGMDSHVRSRLTFLGNERPKGLSPFCFQPKMLRVLDLQDVKFGMTQDKIG 594
Qy 599 IALLCHUKYLSIYSSSIYSIPRSIGKQGLQTLNMSSTYIAALPSEISKLQCLHTLRCI 658
Db 595 IGLRLHUKYNNIGHSHIYALPRCIGKIKOLCTLDTIDTSDYITELPTEISKLSILCR 654
Qy 659 RELEFDFNPSLNHPMKCIITNTICLPKVFTPLVSRDNRKQIAEFHFMATKSPWSE- 715
Db 655 GRNPSGDFNLDPKDCLIAFSCPLLMAATDS-DERNKI IAEHLVGCSSQWSPNGYIGV 713
Qy 716 KVPKIGIKLRDLQVLEVDIRRTSSRAIKELGQLSKLKLAIVITKGTKECKILYAAIE 775
Db 714 RVPKIGIKLRDLQVLEVDIRRTSSRAIKELGQLSKLKLAIVITKGTKECKILYAAIE 773
Qy 776 KLSLSQSLYNNAAALLSDIETLECLDSISSPPPLRLTLGLNGSLEEMPNIWLBOLTHLKEN 835
Db 774 KLSLSQSLYNNAAALLSDIETLECLDSISSPPPLRLTLGLNGSLEEMPNIWLBOLTHLKEN 832


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Db 702 GFRSKSNVGVKPGICNKKTRLTNIGSGYKD-----OSNORGVAKQAEIEMCGNKG 755
Qy 763 TREKCKILYAAIEKLSLSQSLYMAALLSIETLECLDS-----ISSPP--- 806
Db 756 HKGMDTLYSPE-----ALPPTISPCCECFRYWNTSVYRPFVFISSPTED 803
Qy 807 -PLRTGLNGSLBEMPNWISQLTHLKFNWSSKLKGGKNMILGALPNLMFSLYHNS 865
Db 804 TQVERKSGDALDAHAAPDEVQ-----LMEEQTKERNHVGTGCGAOPHGPLSSPQCL 854
Qy 866 YLGEKLVKFTGAPNLRVLVFNLDOLREIRFEDGSSPOLEKIBISCCRELSGIHIL 925
Db 855 PWGEASI-QNGSIPKSN---IPDL-QFGAAKRDIGRQLNVGKORNIQGLSGVGIHIL 909
Qy 926 PRLKEISLEYKSKVARLQQLGEVNTNPNRVLPRMDSRRDRHDLGAEAGSSIEVQTADP 985
Db 910 PRLKEISLIGYKSKVARLQQLGEVTRTHNHPVLRMRDRSDHDLACDAEGSPVEATDP 969
Qy 986 V 986
Db 970 V 970

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RESULT 12

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US-10-437-963-171923
; Sequence 171923, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171923
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(926)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70107C.1.pap
US-10-437-963-171923

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Query Match 36.2%; Score 1903; DB 16; Length 926;
Best Local Similarity 41.3%; Pred. No. 6.9e-133;
Matches 431; Conservative 161; Mismatches 270; Indels 182; Gaps 15;

Qy 1 MAETVLSWARSIVGSAISKAASAAANETSILLIGVEKDIWYI----- 41
Db 1 MAETVLSWARSIVGSAISKAASAAANETSILLIGVEKDIWYI----- 41
Qy 42 -----KDELKTQAFRLAAEVNKKDKLLKVAEOIRDSYDIEDSLDEPKVHTESQ 93
Db 61 KETKLLVPSDELKTQAFRLAAEVNKKDKLLKVAEOIRDSYDIEDSLDEPKVHTESQ 120
Qy 94 TLRQLVKLRERHRIAIRHNLKSRVEEVSRNRYNLVPEISSGTEDDMDSYAEDIRNQ 153
Db 121 SLSQQLMKLKHRRIRAIQIRDLKSRVEEVSRNRYNLVPEISSGTEDDMDSYAEDIRNQ 176
Qy 154 SARVDEBELVGFSDSKRLEMDITNDANDGPAKVICVGMGGGLKTKALSIFESSEDI 213

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Db 177 SAKNIDEABELVGFDDAKESILNLIDVHANHGLAKVIFVGMGGGLKTSLVKKVTHS-INI 235
Qy 214 RKNFPCNAWITVSQSFHRIELKDMIRQLLQGLSSLDQLLHLEQKVVVQVHHLSEYLEE 273
Db 236 VNNFSCRAWITVSQSFVRTTELLRGLIKQLLQGLSENHFKGLQS---MQRNEKVEDLVED 292
Qy 274 ----LKEKRPVVDLDDWILHDWNIENIAPPKNNKKGSRIVITRNVDLAEKCNATSLV 329
Db 293 LKQGLKEKRPVVDLDDWMSIDALNWLNESVFPDSNNGSGRIIVTTRDASIIQNCAPSYL 352
Qy 330 YHLDPLQWDAISLLRKTNNKHEDMESNKNMKQKVERIVNKCGRPLAIIITIGAVLATK 389
Db 353 YRLPPLTKDDAKQLLRKSNKSYEDIK----- 379
Qy 390 QVSEWEKFEQLPSELEINPSEALRMVTLGYNHLPKPCFLYLSIPPEDEIQRNR 449
Db 380 -----EARLR-----SIFPEDPIKRRC 397
Qy 450 LVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGTAGIKYTCRIHDIIRIT 509
Db 398 MVRWIAEGFVDKFGMAEDVGNISYFDELINRSMIQCRFYSHGVGVQSCVLHDIRDIA 457
Qy 510 VSIROENFVLLPMGDGSDLVQENTRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAH 569
Db 458 ISISAENFVMTKGVSGIPPENIHLSIDGRQDSYLSFDLSHVRVSUFFTN-PKEQLA 516
Qy 570 AVCPDQLRMLRVLDLEDVTFITQKDFRIALLCHLYLSIGYSSISYSLSPRSICKLOGL 629
Db 517 SLCSPLRMLRVLDLEDLSPSLCRVTQNDISNIGSFCHLRYLSVKKGSYIYHPRIRKLOGL 576
Qy 630 QTLNMSSTYIAALPSEISKLOCLHTLCIRELEFPDNFSLNHPMKCINTTICLPKVFTPLV 689
Db 577 QTLNKRSLITKVPABVTELRSPSLRCSTLGVYSHFEFTTPE---TN----- 621
Qy 690 SRDNRAQIAEFHMAKSPWSESPGVKPGIGIKGLDLOVLYVDIIRTSRAIKELGOL 749
Db 622 -----PRMRSSRVSVPKGIGSLKELQILDELVDIAKSNKKAVHELDEL 666
Qy 750 SKRLKLVITKGTSTKCKILYAAIEKLSLSQSLYMAALLSIETLECLDSISSPPPL 809
Db 667 TQLKGLV--AGVTNRVSYLCEALQKLSLCSLRVEA---KPRGLHMLQLASPPPL 721
Qy 810 RTGLNGSLBEMPNWISQLTHLKFNWSSKLKGGKNMILGALPNLMFSLYHNSYLG 869
Db 722 HTLKLKSLHEIPSWGVKLEKLVQVLFVKLQKTESQVLGELPGLKCLRLXNAVYTK 781
Qy 870 KLVFTKCAPNLRVLVFNLDOLREIRFEDGSSPOLEKIBISCCRELSGIHILPLK 929
Db 782 ELVLCHGKFRGLKTLRLDSLEELKKVTFEERTSPKLETTITIQDCSSELAVCGTVNLQSL 841
Qy 930 EISLEYKSKVARLQQLGEVNTNPNRVLPRMDSRRDRHDLGAEAGSSIEVQTADPVPDA 989
Db 842 KIRFAKGLVK-----RPVQAGQSASAH-----HREDIKAAEIEKS 880
Qy 990 QGSVTVAVEATDPLPEQEGSSQS 1013
Db 881 QTSSL-----EKGGSSQS 893

RESULT 13
US-10-437-963-177336
; Sequence 177336, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 177336

; LENGTH: 812

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_74999C.1.p.ep

US-10-437-963-177336

Query Match 36.1%; Score 1894.5; DB 16; Length 812;

Best Local Similarity 45.5%; Pred. No. 2.4e-132; Indels 265; Gaps 21;

Matches 453; Conservative 87; Mismatches 191; Mismatches 191; Indels 265; Gaps 21;

Qy 48 MQAFLEAAEVKKDELKQWAEQIRDLSDYIEDSLDEFKVIHIESQTLFROLVLRERHR 107

Db 1 MQAFLEAAEVKKDELK-----LVKLRERHR 28

Qy 108 IAIIRHNLKSRVEVSSRNTYNLVPEIISSTGDDMSYAEIDIRNQARNVDEAEVLGFS 167

Db 29 IAIIRHNLKSRVEVSSRNTYNLVPEIISSTGDDMSYAEIDIRNQARNVDEAEVLGFS 88

Qy 168 DSKRLLEMDITNANDGPAKVICVVGGLGKLTALSRKIFESIEDIRKNFPCNAWITVSQ 227

Db 89 DSKRLLEMDITNANDGPAKVICVVGGLGKLTALSRKIFESIEDIRKNFPCNAWITVSQ 148

Qy 228 SFHRIELKDMIRQLLPSSLDQLLHELQGVVQVHHLSYLLSEELKEKRYF-VVLDDL 286

Db 149 SFHRIELKDMIRQLLPSSLDQLLHELQGVVQVHHLSYLLSEELKEKRYF-VVLDDL 208

Qy 287 WILHDMNINEIAPKNNKSGSRIVITRNVDLAEKATASL-----VYHLD----- 333

Db 209 IHFHRFOQLSTVSLPLDLPALPPKLTGVCAAARTSATGRLELGIIGIHLPRLEISL 268

Qy 334 -----FLQMDAI-----SILLRNTKNHEDMESKNM-----QKQVERIVNKKGR- 374

Db 269 EYRSKVARFAQLEGEVCAHPKHPVQMEDSKSYRDLGRHSSWDFDVIISSTGIGSRP 328

Qy 375 -LPLAI-----LFIGAVLATKQVSEWEKFEYQLPSELEINPS 410

Db 329 WLPASVAPSGADLRRLHPLFSIAQLPASMSEACVHGREDIEWEILLYAQLPSELGCPNS 388

Qy 411 LEALRRMTLYGNLHPLSHKPCFLYLSIFPDPEIQRNRLVGRWIAEGFVRPKVGMTYD 470

Db 389 LAAMKVVVALSYNLPKSHVPCFLYLCIFPDPEFVQRRLVHRWIAEGFVRK----- 441

Qy 471 VGESYFNELINRSMIQRSRVGTAGKIKTCRIHDIIRDITVSIHQENFVLLPMGDGDLV 530

Db 442 GGEFWMD-----GDG-ELR 454

Qy 531 QENTRHIAFHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPQLRMLRLVLDLEDVTF 590

Db 455 KE----- 456

Qy 591 ITQKDFRIALLCHLYLSIGYSSISYSLPSIKLQLOTLQNLNMSSTVIAALPSEISKQ 650

Db 457 -----LPPFQVL-----GRDRQGSYDLDITYNRKERVLI----- 486

Qy 651 CLHTLRICIRELEFPNFSLNHPMKITNTICLPKVTPLVSRDNRKQIAEFPHATKSPWS 710

Db 487 -----LSCIPLMA-----LSDSDNRHRLITDHTCCSHWH 518

Qy 711 E-SFGVVKPGKIGKRLDQVLEYVDIRRTSSRAIKELQGLSKRLKLAIVITKGSTKECKI 769

Db 519 RIKDGVVRPGIKNLKLVLEIVDIAVTDKAIQELGELNQLAKLSWTKGSKKCKI 578

Qy 770 LYAAIEKLSLSQSLYMAALLSDIE-TLECLDSSISPPPLRTGLNGSLEEMPNWIEQL 828

Db 579 LCAAIEKLTSPKSLYVDGDHGYSLDGTLECLDSSISHPPS-LKSLRLKGCIKETPNFREL 637

Qy 829 THLKFPNLWSSKLKGGKNMLILGALPNMLFSLYHNSYLGEKLVFTKGAFNRLTLVFN 888

Db 638 KHLVKIYLYKSHL-NGDTWEILGELHNLMDLHFRWYAVVGEKLVFISGAFQNLKLVVET 696

Qy 889 LDQLREIRPDGSSPQLEKIEISCCRLESGIIGIHLPRLKEISLEYKSKVARLGOLKGE 948

Db 697 EDKLEVRFBEGTSPQMEWIEICHCELTSGIVGVKHLPRLKEIGLK-SAKVARLGQLEGE 755

Qy 949 VNTHPNRPVLRMSDRDRDHLGABAEAGSSLEVQTD 984

Db 756 VDTHPNRPILRLSEKSYHDLG-ETHVSVVEVEVAD 790

RESULT 14

US-10-352-179-95

; Sequence 95, Application US/10352179

; Publication No. US20040006788A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Guo-liang

; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla

; FILE REFERENCE: 22727/04108

; CURRENT APPLICATION NUMBER: US/10/352,179

; CURRENT FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/352,106

; PRIOR FILING DATE: 2002-01-25

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: Patent version 3.1

; SEQ ID NO 95

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Oryza minuta

US-10-352-179-95

Query Match 26.4%; Score 1389; DB 15; Length 451;

Best Local Similarity 51.7%; Pred. No. 5.7e-95;

Matches 282; Conservative 70; Mismatches 95; Indels 98; Gaps 3;

Qy 1 MAETVLSWASLSVCSAISKAASAAANETSLLLGVEKDIWYIKDELKTMQAFLEAAEVKK 60

Db 1 MADTVLSIAKSLVGSVSKVASVAADKMLLLGVQKEIWFIKDELQTLQAFMAEA-SK 59

Qy 61 KDELKLVWAEQIRDLSDYIEDSLDEFKVIHIESQTLFROLVLRERHRIAIRHNLKSRVE 120

Db 60 KSILLKVVQVQVRDLYDIEDCLDEFVHVQSTQLSRQLMKLKDHRHIAVQIRNLRTIE 119

Qy 121 EVSSRNTYNLVPEIISSTGDDMSYAEIDIRNQARNVDEAEVLGFSDDSKRLLEMDITN 180

Db 120 EVSSRNTYNLVPEIISSTGDDMSYAEIDIRNQARNVDEAEVLGFSDDSKRLLEMDITN 179

Qy 181 ANDGPAKVICVVGGLGKLTALSRKIFESIEDIRKNFPCNAWITVSQSFHRIELKDMIR 240

Db 180 AKDGFVKVGVGGLGKLTALSRKIFESIEDIRKNFPCNAWITVSQSFHRIELKDMIR 239

Qy 241 QLGLPSSLDQLLHELQGVVQVHHLSYLLSEELKEKRYFVVLDDMLHDMNINEIAP 300

Db 240 XLFGEEVLKRLRELECK-VQVDDLASYLETELNERRYFVVLDDVMSDTSKWNISIAF 298

Qy 301 PKNNKSGSRIVITRNVDLAEKATASLVHLDPLQMDAISLLLRKTNKHEDMESKN 360

Db 299 PRNNKSGSRIVITRNVDLAEKATASLVHLDPLQMDAISLLLRKTNKHEDMESKN 358

Qy 361 MQKVAEIVNKKCGPLPLAILTIGAVLATKQVSEWEKFEYQLPSELEINPSLEALRRVTL 420

Db 359 MSDIITKIVKCGYLPAILTIGAVLATKQVSEWEKFEYQLPSELEINPSLEALRRVTL 387

Qy 421 GYNHLPKPCFLYLSIFPDPEIQRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480

Db 388 ----- 387

Qy 481 NRSMIQSRVGTAGKIKTCRIHDIIRDITVSIHQENFVLLPMGDGSDLVQENTRHIAFH 540

Db 388 -----DPSRVRGFEKSKRICHIMRDIASISREENFILLPEGTYDVVVHGNTRHIAFH 442

Qy 541 GSMSC 545
Db 443 GSKYC 447

RESULT 15
US-10-437-963-197236
; Sequence 197236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197236
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93011C.1.pep
US-10-437-963-197236

Query Match 23.3%; Score 1224; DB 16; Length 978;
Best Local Similarity 32.8%; Pred. No. 4e-82;
Matches 330; Conservative 209; Mismatches 377; Indels 90; Gaps 30;

Qy 1 MAETVLSMARSLVSGSAISAAANETSLLGVEKDIWIYKDELKTWQAFPLRAAEVMKK 60
Db 1 MEATAVSLARTVLDGVLGAGSAAVADAALLGVPREVDPIRSELEMMQSPLRATSGC - 58

Qy 61 KDELKWAQEI RDLSDYDIESLDEFKVIHESQT-----LFRQLVKLRHRIARI 112
Db 59 AGDTARTVVKQVRDLAYDVEDCLDFALHAHAHASSSSCAPPLMLRPWRLAERHVAARI 118

Qy 113 HNLKSRVEVSRRNYNLVPEISGTEDDMDSDVAEDIRNQSARNVD-----EAEIVGP 166
Db 119 RELKASVEELNQRHRYHV -FVLAAGDQQQQQHEPPAAPPAGEQHHLRFRDQVIGR 177

Qy 167 SDSKRLLEMDITNANDGP---AKVICVVGMGGLKTKALSRIKPISEEDIRKNFPCNAWI 223
Db 178 GEESSELAKLISGGDDDAETRRRVVSVGMGMGKSSVARSVY -NDPAIVDGFDCRAWV 236

Qy 224 TVSQSFRIELKDMIRQLLGPSSLDQLLHLOGLQVVVQVHLSYELIEELKEXRYFVVL 283
Db 237 TVP---HPLDSAGEFKRELVA-----QLETEVDG-----CGGGDDVSAWLRQKRYLIW 282

Qy 284 DDLWTLHDWNWINEIAPFNKKNKGSRIVITTRNDVLAEKATA -SLVYHLDPLQWDAIS 342
Db 283 DDVRSLEWEHI -EPCLVESAGGGRVITVTRQVDVQRCVRGMEHAYELKTLAAPHDMR 341

Qy 343 LLRLRTKNKHMESNMKNQKQVRI VNKCGRLPLAILTIGAVLAT--KQVSEWEKPYEQ 400
Db 342 LLCQVYKDPE -YTLQLHMLEANKILGRCRGLPLAIATIGLLANRPKTSAEWKNLRIH 400

Qy 401 LPSELEINPSLEALRMVTLGNHLP SHLKPCLFLYLSIPDPDFEIQNRNLVGRWIAEGFV 460
Db 401 LGSELEFPQDINSINRVITSSYDGLPYHLKSCFLYLSIPFENHETRYRLVRRWIAEGYI 460

Qy 461 RPKVGMTTKDVGESYFNELINRSMTIQ--RSRVGTAGIKTKCRIHDIIRDITVSISSROENP 518
Db 461 AKRRDMTVEEVGQKHYNDLMNRSMIRPMKKKIGASMAVERCQVRGWLQIITLSKSIENQ 520

Search completed: February 9, 2005, 09:16:29
Job time: 99.0327 secs

Qy 519 VLLPMGDSGLVQENTRHIAF-----HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPD 574
Db 521 LFIIDKHCHNEVPQSKIRHLVVRWRKSEKMATNINLSVRSLSLVFGCPASL-----ISP- 576

Qy 575 QLRMLRVLDLSDVTLITQKDPDRIALLCILKYLISIGYSSSIYSIPRISIGKLGLOQLNLM 634
Db 577 KRLRLRVLDLENVLDL-ENDDLKHLGDLHLLYGL-RTNISRUPSSQNLKCLUETLUDV 634

Qy 635 SSTYIAALPSEISKQLCLHTLRCIRELEFDFNF-----SINHHPMKCITNTTICLPK 683
Db 635 QDTKVTHLPDGTAKLEKRLYL-----LAGINFAEDLAEKMQTNAKNKVKNKNGN---LLE 686

Qy 684 VFTPLVSRDNRKQIAEFHMAKTSFWSBSFOVKPKGIGKLRDLQVLYVDIRRTSSRAI 743
Db 687 TLADVVCRCRRG--FSECCSSSSCFAGHFVSRAPEGIEKLRNLHMLGVVRIERDSGVA- 743

Qy 744 KELGOLSKLRKLAIVITKGTKECKILYAAIEKLSLSLQSLYMAALLSDIETLECLDSIS 803
Db 744 QKJGKLSLRRLGV-DLDATGEEGKALCNSIQKLARLERLEVRKSLFLDNLNGL----- 798

Qy 804 SPPPLRLRTGLNGSLEEMPNIWIEQLTHLKFNLMSSKLKEGKNMLILGALPNLMFLSLYH 863
Db 799 -APKHLASLRLYGHLEKLPDAVSSINDLAKVKLLTQL-EQKDINLLGNLSNLTSLGLWG 856

Qy 864 NSYLGEKLVFVTGAPPNLRTLVIFNLDOLREIRFEDGSSPOLEKIEISCRL-----ESGI 919
Db 857 KSPAGVSLHFSRDMFKNLSLHIOGLENLLETINFESAAADRLKLLVKKCFALSDNERGI 916

Qy 920 IGIITHLPRLKEISLEYKSKVARLQ-LKGEVN-----THPNRPVLRM 960
Db 917 SDILFLKNIVETILISGDKPHLQGLQGVSEFELVKNRRPKQI 962

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 22:05:35 ; Search time 8745.62 Seconds
(without alignments)
17170.053 Million cell updates/sec

Title: US-10-656-394A-7
Perfect score: 3099
Sequence: 1 atggcgagacgtgtctgag.....gcacagctcaagtggtgta 3099

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_rts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	2843.4	91.8	138870	8 AP005659	AP005659 Oryza sat
2	1593.8	51.4	3890	8 AK067966	AK067966 Oryza sat
3	1538.6	49.6	122193	2 AP006053	AP006053 Oryza sat
4	1493.2	48.2	3231	8 AK121397	AK121397 Oryza sat
5	1287.4	41.5	3457	8 HVU507094	HVU507094 Hordeum v
6	1205	38.9	4326	8 AK120452	AK120452 Oryza sat
7	1143.2	36.9	147363	8 AP003487	AP003487 Oryza sat
8	1102.4	35.6	176979	8 AP001168	AP001168 Oryza sat
9	811.6	26.2	4248	8 AK070885	AK070885 Oryza sat
10	520.4	16.8	2015	8 AK071029	AK071029 Oryza sat
11	254	8.2	564	8 HVU506137	HVU506137 Hordeum v
12	217	7.0	4949	8 AK101823	AK101823 Oryza sat
13	208.4	6.7	3819	8 AK073612	AK073612 Oryza sat
14	198	6.4	4001	8 AB013451	AB013451 Oryza sat
15	198	6.4	4030	8 AK065693	AK065693 Oryza sat
16	192.6	6.2	145018	8 AP005828	AP005828 Oryza sat
17	192.6	6.2	146776	8 AP007223	AP007223 Oryza sat
18	192.2	6.2	2294	8 AK065372	AK065372 Oryza sat
19	191.4	6.2	164819	8 AC114983	AC114983 Oryza sat

20	179.2	5.8	3329	8 AK103886	AK103886 Oryza sat
21	178.6	5.8	95612	2 AP003862	AP003862 Oryza sat
22	178.6	5.8	150761	8 AP004592	AP004592 Oryza sat
23	178.2	5.8	543	8 AF186640	AF186640 Sorghum b
24	178.2	5.8	149697	8 AC109832	AC109832 Oryza sat
25	176.2	5.7	2947	8 AK101707	AK101707 Oryza sat
26	173.8	5.6	3353	8 AK065775	AK065775 Oryza sat
27	172.6	5.6	168063	8 CNS07YQ8	AL713908 Oryza sat
28	172.2	5.6	2576	8 AK073176	AK073176 Oryza sat
29	171	5.5	3255	8 AK119293	AK119293 Oryza sat
30	171	5.5	149400	8 AC121327	AC121327 Oryza sat
31	167.8	5.4	168063	8 CNS07YQ8	AL713908 Oryza sat
32	165.8	5.4	106970	2 AC124968	AC124968 Medicago
33	165	5.3	3165	8 AK064889	AK064889 Oryza sat
34	164.4	5.3	386	8 TVS249947	AJ249947 Aegilops
35	164.4	5.3	117860	8 AP004648	AP004648 Oryza sat
36	163.4	5.3	4001	8 AK066020	AK066020 Oryza sat
37	162.8	5.3	144207	2 AC120530	AC120530 Oryza sat
38	162.8	5.3	180999	8 AC137924	AC137924 Oryza sat
39	162.8	5.3	197516	8 AC146948	AC146948 Oryza sat
40	160.8	5.2	183990	8 AF114171	AF114171 Sorghum b
41	160.4	5.2	123847	8 AC138002	AC138002 Oryza sat
42	158.8	5.1	3378	8 AK066779	AK066779 Oryza sat
43	158.8	5.1	3534	8 AK103311	AK103311 Oryza sat
44	158	5.1	3886	8 AK064430	AK064430 Oryza sat
45	158	5.1	4561	8 AK099775	AK099775 Oryza sat

ALIGNMENTS

RESULT 1

AP005659

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

AP005659 138870 bp DNA linear PLN 09-APR-2004
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
PAC clone:P0649C11, complete sequence.

AP005659

HTG.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1

Sasaki, T., Matsumoto, T. and Katayose, Y.

Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC

clone:P0649C11

Published Only in Database (2002)

2 (bases 1 to 138870)

Sasaki, T., Matsumoto, T. and Katayose, Y.

Direct Submission

Submitted (21-AUG-2002) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kamondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsaaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

On Apr 8, 2004 this sequence version replaced gi:22415844.

The orientation of the sequence is from SP6 to T7 of the PAC clone.

Location/Qualifiers

1. 138870

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/chromosome="6"

/clone="P0649C11"

ORIGIN

Query Match 91.8%; Score 2843.4; DB 8; Length 138870;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 2901; Conservative 0; Mismatches 56; Indels 4; Gaps 2;

Qy	1966	CGTGTATAGACAGTTTCATATGACAACTTTAGTCTAAACACCCCAATGAATGCGATA	2025
Db	2168	AGATGCAATGAAGCAATATGATTTTCTTCTTCAACA-----TGTTTA	2212
Qy	2026	ACTAACCAATATGCTCCCTAAAGTATTCACACCTTTAGTTCGCGATGATCGTGCA	2085
Db	2213	ACTGACATTTGCTGCTGCCATGATATTCACCTTCGTTAGTACCTCTGATCGTGCT	2272
Qy	2086	AAACAAATTCGTGAATTCACATGCGCCACCAAAAGTTGCTGCTGAATCAATCGGTGTG	2145
Db	2273	GAATAAATTCGTAACCTGCACTTGCCCAACAAAGCTTCCTGTTCAAAATCAATGGCGTC	2332
Qy	2146	AAAGTACCAAGGAATAGGTAAGTTGCGAGCTTCGAGGTTCTAGATATGTAGATATC	2205
Db	2333	AAAGTACCAAGGAATATGTTGGTTGAGAGCTTTACAAATATTTGGGGTGTGATATT	2392
Qy	2206	AGGCGGACCTAGTAGAGCAATCAAGAGCTGGGGCAGTTTAAAGCAAGCTCAGGAATTA	2265
Db	2393	AGAAGGACTACAGTAGAGTAAATAAAGAGTTGGGCGAGTTAAGCGAGCTGAGGAACTA	2452
Qy	2266	GGTGTGACAAACACGGGTCGACAAAGGAAATGTAAAGATCTTTATGACGCCATTGAG	2325
Db	2453	TATGTGTAAACAAAGGAGTCTACAAAGTTAAATGTGAGACTCTATACAGCCATCCAG	2512
Qy	2326	AAGCTCTCTCCCTCCAAATCTCTCATGTGATGCTGCGAGGAATCTGAGATGGGAACA	2385
Db	2513	AAGCTCTATTCCTACAAATCTCTCCATATGATGCTGTGGGATGACACAGGATTGGAACA	2572
Qy	2386	CTTCAGTGCCTAGATCTTATTTATCTCTCTCCCTACCTACCTGAGGACACTCGTGTGGAT	2445
Db	2573	CTTCAGTGCCTAGATCTTATTTATCTCTCTCCCTACCTGAGGACACTCAGGTGGAAT	2632
Qy	2446	GGAAATCTTGAAGGAGATCCCTAACTGGAATGAGCAGCTCACTCACTGAAGAAGATCTAC	2505
Db	2633	GGAAATCTTGAAGGAGTGCCTAACTGGAATGAGCGGCTCACTCACTGAGGAATCTTAC	2692
Qy	2506	TTATTTAGGAGCAAACTAAAGAGAGTTAAACCAATCTGATATCTTTGGGGCACTGCCAAC	2565
Db	2693	TTATTTAGGAGCAAACTAAAGAGAGTTAAACCAATCTGATATCTTTGGGGCACTGCCAAC	2752
Qy	2566	CTCATGTGCTTTCATCTTTATCGGAATGCTTACCTTTGGGGAGAGCTAGTATTCAAAACA	2625
Db	2753	CTCATGTGCTTTCATCTTTATCGGAATGCTTACCTTTGGGGAGAGTTAGTATTCAAAACA	2812
Qy	2626	GGAGCATTTCCCAATCTTAGAACACTTTGGGATTTATGAATTTGATCACTAAGAGAGATC	2685
Db	2813	GGAGCATTTCCCAATCTTAGAACACTTTGGGATTTATGAATTTGATCACTAAGAGATTT	2872
Qy	2686	AGATTTGAGGACGGCAGCTCACCTCTGTTGAAAAGATAGAAAATGAGCGAGTGCGAGTTG	2745
Db	2873	AGATTTGAGGACGGCAGCTCACCTCTGTTGAAAAGATAGAAAATGAGCGAGTGCGAGTTG	2932
Qy	2746	GAATCTGGGATTTACTGTTATCATTCACCTTCCAAAGCTCAGGAGATTTCCAAATAGATAC	2805
Db	2933	GAATCTGGGATTTACTGTTATCATTCACCTTCCAAAGCTCAGGAGATTTCCAAATAGATAC	2992
Qy	2806	GGAAATGAAGTGGCTGGCTGGTTCAGCTGAGGAGAGAGTGAACCGCACACCCCAATCGC	2865
Db	2993	AAAGGTAAAGTGGCGATGCTGCTCAGCTGAGGAGAGAGTGAACCGCACACCCCAATGTT	3052
Qy	2866	CCCGTGTCTTAATGTATACAGTGACCGAAGGTATCAACGCTGGGGGCTGAAGCCGAAGGA	2925
Db	3053	CCCGTGTCTGCAATGGCAATGGACCGAAGGTATCAACGCTGGGGGCTGAAGCCGAAGGA	3112
Qy	2926	TCCTCTATAGAG	2938
Db	3113	TCCTCTCCCTAAG	3125

RESULT 3
AP006053/c 122193 bp DNA linear HTG 30-NOV-2002
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 6 clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
source

ORIGIN

Query Match 49.6%; Score 1538.6; DB 2; Length 122193;
Best Local Similarity 72.9%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches 734; Indels 36; Gaps 6;

Qy	109	GACATCTGGTATATCAAGATGAGCTAAACAGTGAAGCAATTCCTTAGAGCTCTGAA	168
Db	109122	GTCTACAGTTTCATCAAGGAGCAGCTCAAGGATACCAAGCATTTTGTGCTCTGAA	109063
Qy	169	CTTATGAAAAGAAAGATGAACCTATTAAAGTTTGGGCGAGCAAAATACGTGACCTGTCA	228
Db	109062	CCATC---AAGAAAAGCATATTTGAGGTTTGGGTGCGAAGTAAAGGATCTATCC	109006
Qy	229	TATGACATTTGAAGATTCCTTTGATGAATTTAAGGTCATATTTGAAGCAAAACCTATT	288
Db	109005	TATGACATTTGAAGATTTGCTTTGATGAATTTACAGTTTATGTGAGCAGCAAACTTGTG	108946
Qy	289	CGTCAGTTGGTGAACCTCAGAGAACGCCACCGAATTTGCTATCCGTATCCAGACCTTAA	348
Db	108945	AGGCAGTTGATGAAGCTAAAGGATCGGCATCGGATTTGCATCCAGATCCGCAATCTCAG	108886
Qy	349	TCAAGAGTTGAAGAGTGAAGTAGCAGGAACACACGCTACAGTTTGTAGTCAAGCT---ATT	405
Db	108885	ACAAGATTTGAAGAGTGAAGCATAGGACATACGCTACACTTANTAGAGATGACCTC	108826
Qy	406	TCCTCTGCGACAGAGATTGACATGGATTCCTATGCGAAGACATTTGCTTAATCAGTCAGCT	465
Db	108825	ACCTGCACCACTACTGATGAGGGAATTTATTTATGGAAGACATTCGCAACCAATCAGCT	108766
Qy	466	CGCATGTTGATGAGGCTGAGCTTGTGGGTTTCTTGACTCCAGAAAAGGCTGCTTGA	525
Db	108765	AACAACATTTGAGGAGCTGATCTTTGTGGGTTTTTTTGTGGACCCCAAGAGAGTTGTTGAT	108706

QY	526	ATGATCGATACCAATGCTAAATGATGGTCCGGCCCAAGGTAATCTGTGTTGTTGGGATGGGT	585	QY	1606	CACATAGCAATTCATNGGAGATATGTCCTGC---	AAACTGGATTGGATTGGAGCAATTAAT	1662
Db	108705	CTTATAGATGTCATGCCAATATCGGACCTACAGAGTCGTATGTTGTCGGTATGGGT	108646	Db	107628	CACATAGCAATTCAGGGAGTAAGTATTTGCTCTAAGATAAAGCTTTGACTGGAGCAATTATA	107569	
QY	586	GGTTTAGCAAGACAGCTCTTTTCGAGGAAGATCTTTTGAAGCGAAGAAGACATTAGGAAG	645	QY	1663	CGATCATTAGCTAATTTTGGTTCAGAGACCCCAAGAGTCTAGCACATGCAAGTTTGTCCAGAT	1722	
Db	108645	GGTTTGGTAAGACTACTATTTCGAAGGAAATTTATGAAGCAAGAGGACATTGCAAG	108586	Db	107568	CGGTCAATTAATATGTTTGGCCGAGAGGCCCTGAGAACTAGAGCATTCAGTTTGTTCATCT	107509	
QY	646	AACCTCCCTTCGAATGCTTGATACAGTGTCAAGATCATATCTTTTCAGAGATTGACCTACTT	705	QY	1723	CAATTGAGGATGTTTACGGGTCTTGATCTTGAAAGATGTGACATCTTCTTAATCACTCAAAAA	1782	
Db	108585	AAATTTTCTGCTGTGCTTGGATTACTGTTTTCACAGTCCCTTGTGTAGGTTGGAACCTACTA	108526	Db	107508	CAGTTGAGGATGTTTACGGGTCTTGGAATCTAAGAGATGACAAATTTACTATCACACAAAT	107449	
QY	706	AAAGATATGATACGCAACTCTTGGCCCCAGTTCTCTGGATCAACTCTTGCAAGAAATG	765	QY	1783	GAITTCGACCGTATGCAATGTTGTGCCACTTGCAATCTTGAAATCTTGAGTATTGGA	1833	
Db	108525	AAGGATTTGATGATCAAACTTTTGGAGAGGAGTACTGAGAGCCAGATGAGAGACTC	108466	Db	107448	GATGTCAAACATAATAGTGCTCTTGTGCCACTTGAATAACCTACGCAATTCGAAGATACAAT	107389	
QY	766	CAAGGGAAGTGGTGGTCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAG	825	QY	1834	TATTCGTGCATCCATATATTCACTTTCCNAGATCCATTTGTTAACTTACAGGGCTTACAACT	1893	
Db	108465	GAAGGGA---GGTTCACAAGTAGACGACCTCGCCAGTACCTCAGGACAGAGTTAAAT	108409	Db	107388	AATGCATCATATATTTACTCTTCCAAATCCATAGGAAGACTGGATGGTCTGCAGACA	107329	
QY	826	GAGAAGGTAATTTGTTGTTCTAGATGATCTATGGATTTTACATGATTGGAATTTGGATA	885	QY	1894	TTGAACATGCGGAGCACATACATTTGCAGCACTTACCAAGTGAGATCAGTAAACTCCAATGT	1953	
Db	108408	GAAGAAGGTAATTTGTTGCTTGATGACGTGTGGAGTACAGATTCATAGAAATGGAT	108349	Db	107328	TTGCACTTGGATTCGACGACATTTTCAACACTGCCACTCAGATTTACTAAGTTTCGGAGT	107269	
QY	886	AATGAAATTTGCATTTCTTAAGAACAAATAAGAGGCGAGTCGAATAGTAATAACCACTCG	945	QY	1954	CTGCATACCTCTTCGTGTGTATAGGACAGTTTCATTATGACAACTTTTGTCTTAAACCCACA	2013	
Db	108348	ATAGCATTTGCTTCCCTTAGAATAACAAATAAGAGGAGCTGGTGATAGTAACACAGCA	108289	Db	107268	CTCCGAGGCTTTAGATGTCATGAAGCAATATGATTTTCTTTTTCACAACA-----	107218	
QY	946	AATGTTGATCTTGGGGAAGTGGCCACAGCTCACTGGTGTACCACTTTGATTTTCTTG	1005	QY	2014	ATGAAGTGCAATACTTAACACATATGCTGCTGCTTAAAGTATTTACACCTTTTGTAGTCGC	2073	
Db	108288	GATGTGGCTTAGCTAAGGAGTACTTCTGAAATGCTTATCTACCACTTTAAACCCCTG	108229	Db	107217	-----TGTTTAACTGCACATTTGCTGCTGCCCATGATATTTTACACACCTTCCGTTAGTACC	107164	
QY	1006	CAGATGAACGATGCCATBAACCTGCTACTGAGAAACCAAAATTAATAATCATGAACATG	1065	QY	2074	GATGATCTGTCACAAACAAATTTGCTGAATTCACATGGCCACCAAAAGTTGCTGGTCTCAA	2133	
Db	108228	GAATAAGCTATGCGAAAGAGTTGCTTCTTAAGGAAAGCAATAAACAACAGAAAGATATA	108169	Db	107163	TCGATCTGCTGAAAAAAATTTGCTAACTTGCACTTGGCCACCAAAAGCTTCGTTCAAAA	107104	
QY	1066	GAATCAATAAAAAATATCAAAAGAGTGTGAAACGAATTTGTAATAATGTTGGTCTGCTA	1125	QY	2134	TCAATCGGTGTGAAGGTACCCAAAGGAATAGTTAAGTTTGCAGACTTGCAGGTTCTAGAG	2193	
Db	108168	GAAAGTATAAAGATGAGTGACATTAATTAATAATAGTAAGAAGTGTGTTATTTA	108109	Db	107103	TCAAAATGGCGTCAAGGTACCAAAAGGAATAATGTTAGTTTGGAGAGCTTACAAATATTGGG	107044	
QY	1126	CCATTAGCAATCTTACAATAGGAGCTGTGTGCAACTAAACAGGTGTCAAGATGGAG	1185	QY	2194	TATGTAGATATCAGGCGGACAGTAGTAGCAATCAAGAGACTGGGCGAGTTAAGCAAG	2253	
Db	108108	CCGCTGGCTATCTCACAAATAGGGGCGTGTGCCACCAAGAGATAAGAGAGTGGGAA	108049	Db	107043	GTAGTGGATATTAAGAGGACTAGCAGTAGAGTAATAAAAGAGTTGGGCGAGTTAAGCAAG	106984	
QY	1186	AAATTTCTATGAACCTTCTTCAGACTAGAAATTAACCCCAAGCTTGGAGCTTTGAGG	1245	QY	2254	CTGAGGAAATTTAGGTGTGACAAACAAACGGGTGCGACAAAGGAAATGTAAGATCTTTAT	2313	
Db	108048	ACCTTTTATAGTCAGATACCTTCAGAGCTTGAGAGCAACCCCAAACTTTGAAGCAATGAGA	107989	Db	106983	CTGAGGAAACTATATGTGTTGTTAAACAAAGGATCTACAAAGTTTAAATGTGAGATCTCTAT	106924	
QY	1246	AGAAATGGTGACCTAGGTTTACAACCACTACCATCCCAATTTGAAACCAATGCTTTTGTAT	1305	QY	2314	GCAGCCATTTGAGAAGCTCTCTTCCCTCCAATCTCTCCAATGTGGATGTGCGAGGAATCTCA	2373	
Db	107988	AGGATAGTGACCTTAAGTTTACACTACTTGGCCATCTATCTTTAAGCAATGCTTTTGTAT	107929	Db	106923	ACAGCCATCCAGAAGCTCTATTCCTCTCAATCTCTCCATATGGATGCTGTGGGATGCACA	106864	
QY	1306	CTAAGTATCTTTCTGAGGATTTTGAATCAAAAGGAATGCTGTAGTAGGTTAGATGGATA	1365	QY	2374	GATGGTGGAAACACTTGAGTGCCTAGATTTCTATTTTCACTCTCTCCCTACTGAGGACA	2433	
Db	107928	CTAAGCATATTTCTGAGGATTTTGAATTAATAGGAACCTCTGTTAAATAGATGGATG	107869	Db	106863	GGTATTGGAAACACTTGAGTGCCTAGATTTCTGTTTCATCGCTCTCTCCCTTTTGGAGACA	106804	
QY	1366	GCAGAGGGTTTGTAGACCAAGGTTGGGATGACGACTAAGGATGTCCGAGGAAGTTAC	1425	QY	2434	CTCGTGTGGATGGAAATTTCTTGAGGAGATGCTTAACCTGGAATTTGAGCACTCACTCACCTG	2493	
Db	107868	GCAGAGGGTTTATTAAGAGCTAGGCTTAATATGACTATTTGAAGATGTTTGGGAAAGTTAC	107809	Db	106803	CTCAGTTGAAATGGAAGTCTTTGAAGAGTTGCTTAACCTGGAATTTGAGCGGCTCACTCACCTG	106744	
QY	1426	TTTAATGAGCTAATCAACCGAAGTATGATTCACCGATCAAGAGTGGGCATAGCAGGAAATA	1485	QY	2494	AAGAAGATCTCTATTATTGAGGAGCAAACTAAAGGAAGGTAAACCATCTGATACTTGGG	2553	
Db	107808	TTTAAAGACTCATCAACCTGATGATGATTTAGCCATCAAGCGGGGTGACGAGGAG	107749	Db	106743	AGGAAATTTCTACTTTATTGAGGACCAAACTAAAGGAAGGTAAACCATCTGATACTTGGG	106684	
QY	1486	ATTAAGACTTGTGCAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAG	1545	QY	2554	GCATGCCCCAACCTCATGGTCTTCTCACTTTTATCGGAATGCTTACCTTGGGGGAGAAGCTA	2613	
Db	107748	TTTTAGAGTTGTCGAGTCCATGATATATGCTGATATTTACATTTTCAATTTCTAGAGAG	107689	Db	106683	GCATTGGCCCAACCTCATGCTTTCTTCAATTTTGTCAATATGCTTACCTTTGGGGAGAAGTTA	106624	
QY	1546	GAAATTTTGTATTTATACCAATGGGAGATGGCTCTGATTTTGTAGTTCAGGAAACACTCGC	1605	QY	2614	GTATTTCAAAACAGGAGCAATTTCCCAAACTTAGAACAATTTGAGACTTTTCAATTTGGATCAG	2673	
Db	107688	GAAATTTTGTATTTTACCTTAGGGGCACTGACTATATGAAGCAGTACAGGGGAAACACTCGG	107629	Db	106623	GTATTTCAAAACAGGAGCAATTTCCCAAACTTAGAACAATTTGAGACTTTTCAATTTGGATCAG	106564	
				QY	2674	CTAAGAGAGATCAGATTTTGAAGGACGGCAGCTCACCCCTGTTTGGAAAAAGATAGAAATAGGC	2733	

Db 106563 CAAGAGATATTAGATTTTGGAGCCGAGCTCACCCCAATTGGAAAAAGATAGAAATAGGC 106504
 Qy 2734 GAGTCAGGTTGGAACTCTGGGATTACTGGTATCATTTCCCTTCCAAAGCTCAAGGAGATT 2793
 Db 106503 AGGTCAGATTGGATTCAGGGATTATTGGTATCATTTCCCTTCCAAAGCTCAAGGAGATT 106444
 Qy 2794 CCAATTAGATACGGAAGTAAAGTCTGGCTGGCTTGTCTAGCTGGAGGGAGAGTGAACGCA 2853
 Db 106443 TCAGTTGAATCAAAAGGTAAGTGCGGATGCTTGTCTAGCTGGAGGGAGAGTGAACGCA 106384
 Qy 2854 CACCCAAATCGCCCGTCTGCTGCTATGATACAGTACCGAAGTATCACGACCTGGGGCT 2913
 Db 106383 CACCCAAATTTGCCGCTGCTGCGAATGGCAATGGACCGAAGTGATCACGATCTTCTGCTGGC 106324
 Qy 2914 GAAGCCGAAGGATCTTCTATAGAAG 2938
 Db 106323 AAGCCAAAGGATCTCTCCCTTAAG 106299

RESULT 4
 AK121397
 LOCUS
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone.J023131G18, full insert sequence.
 AK121397
 ACCESSION
 VERSION AK121397.1 GI:37991020
 KEYWORDS FLI CDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yabuchi, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Ootomo, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5631), 376-379 (2003)

TITLE
 japonica rice
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 2 12869764

2
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Ootomo, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sasaki, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y.,

Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
 Collection, mapping, and annotation of 28K full-length cDNA clones from japonica rice
 Unpublished
 3 (bases 1 to 3231)
 Kikuchi, S.
 Direct Submission
 Submitted (31-JUN-2003) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Teukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
 This clone is one of the 32K full-length cDNA clones from japonica rice.

URL : http://cdna01.dna.affrc.go.jp/cDNA/NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M. and Nakahama, Y.
 FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Yoshimura, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kouda, M., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ootomo, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

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RESULT 7

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DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
BAC clone:OSJNBa0007020, complete sequence.
ACCESSION AP003487
VERSION AP003487.1 GI:13548703
KEYWORDS HTS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone:OSJNBa0007020
JOURNAL Published Only in Database (2001)
AUTHORS 2 (bases 1 to 147363)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Direct Submission
JOURNAL Submitted (04-APR-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abrr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT The orientation of the sequence is from M13rev to -21M13 of the BAC
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VERSION		AP001168.1 GI:6983854	
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		Ehrhartoidae; Oryzeae; Oryza.	
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REFERENCE		Sasaki, T., Matsumoto, T. and Yamamoto, K.	
AUTHORS		Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC	
TITLE		clone:P0425F02	
JOURNAL		Published Only in Database (2000)	
REFERENCE		2 (bases 1 to 176979)	
AUTHORS		Sasaki, T., Matsumoto, T. and Yamamoto, K.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-FEB-2000) Takuji Sasaki, National Institute of	
		Agrobiological Resources, Rice Genome Research Program; Kamondai	

2-1-2. Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from SP6 to T7 of the PAC clone.
Genes were predicted from the integrated results of the
following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as
SplicePredictor (October1998 version). The genomic sequence was
searched against the non-redundant database NRP(PIR,SWISSPROT,
GENPEPT, PDB) from MAFF DNABank and the cDNA sequence database at
RGP. Protein similarities of the coding regions were searched
against NRP with BLASTP2.0. ESTs represent the identified cDNA
sequences using BLASTN2.0 with the corresponding DDBJ accession no.
and RGP clone ID
Detailed information on assemble quality together with annotation
of this entry at <http://www.dna.affrc.go.jp:82/genomicdata/genomefinished.html>.

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2-1-2. Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from SP6 to T7 of the PAC clone.
Genes were predicted from the integrated results of the
following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as
SplicePredictor (October1998 version). The genomic sequence was
searched against the non-redundant database NRP(PIR,SWISSPROT,
GENPEPT, PDB) from MAFF DNABank and the cDNA sequence database at
RGP. Protein similarities of the coding regions were searched
against NRP with BLASTP2.0. ESTs represent the identified cDNA
sequences using BLASTN2.0 with the corresponding DDBJ accession no.
and RGP clone ID
Detailed information on assemble quality together with annotation
of this entry at <http://www.dna.affrc.go.jp:82/genomicdata/genomefinished.html>.

FEATURES
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1. 176979
/organism="Oryza sativa (japonica cultivar-group)"
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3923. .4483,4546. .4662))
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/codon_start=1
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/db_xref="GI:6983857"
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RCTRAVRGRCGGPTRLSTARGTTRAREGIDRGRLDPALAVLPTWLRGCHAGRRE
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QPAAGEENGDEVGQFPAAARASTRLRESASVGLGTTPEAGDERRFRARAATAA
STRATATEEEEGAPGVPRVLVCTGSSGTHATTNGDGEORERWRRETRETIGGGG
LGKFWAAMSVWERTDIGRSRELAAGACGNGGGRMTNAGRKEKEGKRLAPLP
LWGKGGSGATRGEGGLCLRLPLASARSAGGAENTAMTARGFALKTAATGRSAT
TARGKQRAASARAREHGAAREARRRTRGLGAGLAHAHAARAGSQSGRGA
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DNA"
complement(9848. .12845)
/note="3' LTR"
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/note="Similar to 22 kDa kafirin cluster; Ty3-Gypsy type
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internal stop codon:15317-15319
probably inactive because stop codons are included in CDS"
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complement(join(20711. .20932,23987. .24562))
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/codon_start=1
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LEDVDRLEKELAAKGEAPPKQARIIRTARKRALFVPRYQLAPKVRVVEKEVAPAD
TPVIIISDEGESKRNHSKIEMWATQDDEDEPNPSINLLCSEBLE"
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join(28483. .28975,29105. .30435)
/note="Similar to 22 kDa kafirin cluster; Ty3-Gypsy type
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MKRDVAEVALCDICQVKAERHOPAGLOPLPIPEMKWEIIGMDFITDLRPTSGYD
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KQHEALGDLNSTAYTHPTDGTGRTVQILEDMLRACALDEFGTWDRCUPLYAFESY
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QSRQYADNRRLDLEFGKGDHVLVRSPLGRMRFGMSSKLAPRYIGPYITARRGE
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DKAIROEDKYNRMEQKRIAQFTQOQNNQKRLTIGQSPMPGSGSSVVVRQOQFF
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PAQNASVPASKARVNVHAAEQADPDVILGMDMLARHKGVIDCANRKTPLANSYDGR
VVTVHALSASLSILNLTLEETPIVREYDPDPPDLPDALSRGKVCYCANRKGKAIPL
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EDQGTWLGERICVDPNKKDLKAILKEADHTLSIHPGSTKMYQDLRERFWASMKR
EIVAVCDVQCRVKAERHOPAGLOPLKIPMKWEIIGMDFITGPRTSGGHDSIW
YIDRLTKVAHFPTKVTYSGRSLAELMARIIVCLHGVPKIVSDRGSOFTSNFWKL
QEEMSKLNFSTAYHPQTDGTERVNOILEDMLRACALDEFGSDWKILPYAEFRYNS
YQASLOWPVEALYGRKRTPLLDGTERVQFCTDLREAEKVKVIOERLVAQSR
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complement(38728. .39519)
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internal region (AB014741)"
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/db_xref="GI:6983861"
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PROQSGDRGSYLETEGIENDATTTHLVEMLWAMDESAETVLAQDREDNRGKICK
LEDVDRLEKELAAKGEAPPKQARIIRTARKRALFVPRYQLAPKVRVVEKEVAPQA
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complement(40024. .43033)
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join(45765. .45778,48275. .48378,48699. .48745,49124. .49342,
51652. .51729)
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AU082144 (E20182) correspond to a region of the predicted
gene.
hypothetical protein"
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QY 1716 TCCAGATCAATTGAGGATGTTACGGGCTTGGATCTTGAAGATGACATTCCTTAATCAC 1775
Db 56128 TTCAGTCAATTCACAGTCTGAAGATCTTGGATCTAGAGAAATTTTTCAGTGAC 56069
QY 1776 TCMAAAGATTTGACCGCTATTGCAATTTGTTGCCACCTTGAATACTTGA-----GTAT 1829
Db 56068 ACMAAAGACATAAACAANAATTTGGTTTGGCGCACCTTGAGATATTTTGAATACGCATAC 56009
QY 1830 TGGATATTTCGTCATCATATATTCATTTCCAGATGCCATTCGTTAACTACAGGCGCTTACA 1889
Db 56008 TAGAAGACGGTCCCATATTATATGACATTTCCAGCTCTTCCGGAATTTACAGAACTTACA 55949
QY 1890 AACTTTGAACATGCCGACGACATACATATTGCGAGCACTACCAAGTGGATGATCACTAACTCCA 1949
Db 55948 AGTTTGGACATCAAGAGAGAGTGAATTTTTCACACTACCACTGATATTCAGTAAGCTCTCT 55889
QY 1950 ATGTCCTGCATACTCTTCCGTTGTA-----TAGGACAGTTTTCATTATGACAACTTTAGTCT 2003
Db 55888 TATGCTTCGTATCTCTCGTTGTAGCAAGGACCGTGGTACTTCTACTTCTATTTTGATCC 55829
QY 2004 AAACCCCAATGAAGTGCATATACTAACTAAACACAATATGCTCGCTTAAAGTATTTCACACCTTT 2063
Db 55828 AGATGAACCAATAAATGCTTGAAGCATACGTTGGCGCATGCCCTTGATGTTGACACCAATT 55769
QY 2064 AGTTAGTCGCGATGATCGTGCAAAACAATTTGCTGGAATTCACATGCGCCACCAAAAGTTG 2123
Db 55768 AGTTGGTTCTGCGACGACCAATTTACTATTGCTGAGCTACACAGGGGCTACTCTAGCCA 55709
QY 2124 CTGGTCTCAATCAATCGGTGTGAGGTACCAAGGAATAGTAAAGTTGCGAGACTTGCA 2183
Db 55708 TTGGTCAGAGACACGAGCGGTGAGGTTTCCAAACAGGAATCAGCAAACTAAAGGAGTTGCA 55649
QY 2184 GGTCTAGAGATGTAGATATACGCGGACCAAGTAGTAGAGCAATCAAGAGCTGGGGCA 2243
Db 55648 GGTCTAGAGTTGTAGACCTTAACTAACTAAAGCAAGCAATTAAGAGCTGGGTGA 55589
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Db 55588 ACTTCGCTGGCTACAAAATTTACGGGTGTCAAAAGGGGGGCCAGGACAAAGACGCA 55529
QY 2304 GATATTTTATCAGCAGCTATGAGAGCTCTTCCCTCCCAATCTCTCCATGTTGGATGCTGC 2363
Db 55528 GACACTTTGTGAAGCCATCGAAGAGCTATCATCCCTCCCAATCTCTCTGTTTATGAGGG 55469
QY 2364 AGGAATCTCAGATGCTGGAACACTTTGAGTGCCTAGATTTCT---ATTTTCATCTCTCTCC 2420
Db 55468 TTACTACTTCAATCTGGGACACTTTGAGTGGCTGGTCTTGCAATTTCTCCCTCTCTCC 55409
QY 2421 CCTACTGAGGACACTCGTTGGATGGAAATTTCTTGAGGAGATGCTTAAGTGGATGAGCA 2480
Db 55408 CCTGCTGAGAAAGCTAGAGTTGTCATGGACGTAATTCGCGTGTGTCGCGACTCTTTTAGGAA 55349
QY 2481 GCTCACTCACTGAAGAGATCTACTTATTGAGGAGCAACTTAAGGAGGATTAACCAT 2540
Db 55348 CCTTAAGCAGCTGCGGAAGATTTTTCGCGCTAAGCGAACTA---GATGTAGAGCCAT 55292
QY 2541 GCTGATCTTGGGCGACTGCCCAACTCATGCTCTTCTCATCTTTATCGAATGCTTACCT 2600
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QY 2601 TGGGAGAGCTAGTATTCAAAACAGGAGCAATCCCAATCTTGAACACATTTGGATTTA 2660
Db 55231 TGGGAATGAATTAGCATTTCAAAAACGACGAGTTCCCAATCTCAAGGAGCTTCGTATCAG 55172
QY 2661 TGAATTTGATCAGCTTAAGAGATCAGATTTTGAAGGACGCGAGCTCACCCCTGTTGGAAAA 2720
Db 55171 TATGCTGTCCGAACCTTAAGAGGGATTAAGATTTTGAAGAGACGCCCTTGCCCAATCGGAAG 55112
QY 2721 GATAGAAATAGCGAGTGCAGTTCGGAATCTGGGATTAAGTGTGATTCATTTACCTTTCCAAA 2780
Db 55111 AATGGAATCGAATGTTCCAGTGTGATCAGGATGAGTGTGCGATCAAGCACCTCGAACA 55052
QY 2781 GCTCAAGAGGATTCCAATTAGATACGGAAGTAAAGTGGCTGGCTTGGTACGTGGAGGG 2840

Db 55051 GCTCAACGAGATTTCACTT-----GGGTGATGTGGCGGGCTTGATCTGCTGGAACA 54998
QY 2841 AGAAGTAGAACCCACACCCCAATTCGCTGCTAATGTACAGTGTACCCGAAGGTATCA 2900
Db 54997 GGAAGTAAGCGGACCCCAAGACACCCGCTTGGCGCTTCAAGACCCGAAGCAAAAT 54938
QY 2901 CGACTCTGGG 2910
Db 54937 CGACTCTGGG 54928

RESULT 9
AK070885
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:J023064A19, full insert sequence.
ACCESSION
AK070885
VERSION
AK070885.1
KEYWORDS
FLI_CDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1
The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team., Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ohtsuki, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kuroseki, T., Kodama, T., Maeda, H., Kobayashi, M., Xie, Q., Lu, M., Nariawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Iehi, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Oosato, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

TITLE
japonica rice
JOURNAL
Science 301 (5631), 376-379 (2003)
MEDLINE
22752273
PUBMED
12869764

2 (bases 1 to 4248)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayaishizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Inamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kondo, S., Konno, H., Konno, K., Kouda, M., Koya, S., Kurihara, C., Kuroseki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nomura, M., Namiki, T., Nariawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oosato, N., Oca, Y., Ohtsuki, K., Saitoh, H., Sakai, C., Sakai, K., Sakagawa, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of

Qy	1438	ATCACCGAAGTATGATTCAC	1459
Db	1993	ATCAATGAAGCATGATTCAC	2014
RESULT 11			
LOCUS	HVU506137	564 bp	DNA linear
DEFINITION	Hordeum vulgare partial rga S-9202 gene for NBS-LRR disease resistance protein homologue.		
ACCESSION	AJ506137		
VERSION	AJ506137.1	GI:28555849	
KEYWORDS	NBS-LRR disease resistance protein homologue; rga S-9202 gene.		
SOURCE	Hordeum vulgare		
ORGANISM	Hordeum vulgare		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.		
AUTHORS	1		
TITLE	Madsen,L.H., Collins,N.C., Rakwalaka,M., Backes,G., Sandal,N., Krussell,L., Jensen,J., Waterman,E.H., Jahoor,A., Pryor,A.J., Langridge,P., Schulze-Lefert,P. and Stougaard,J.		
JOURNAL	Barley disease resistance gene analogs of the NBS-LRR class: identification and mapping		
MEDLINE	Mol. Genet. Genomics 269 (1), 150-161 (2003)		
PUBMED	22600637		
REFERENCE	2 (bases 1 to 564)		
AUTHORS	Madsen,L.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-AUG-2002) Madsen L.H., Department of Molecular Biology, Aarhus University, Gustav Wieds Vej 10, DK-8000 C, DENMARK		
FEATURES	Location/Qualifiers		
source	1..564		
gene	/organism="Hordeum vulgare"		
CDS	/mol_type="genomic DNA"		
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ORIGIN			
Query Match	8.2%; Score 254; DB 8; Length 564;		
Best Local Similarity	66.8%; Pred. No. 9.3e-56;		
Matches	378; Conservative 0; Mismatches 185; Indels 3; Gaps 1;		
Qy	577	GGGATGGGTGGTTAGGCAAGACAGCTCTTCGAGGAAGATCTTTGAAAGCGAAGAAGAC	636
Db	1	GGGATGGGGGGTGGGGAAGACGACTCTAGCAGGAAGGTATATGAAGTAAGGAGAT	60
Qy	637	ATTAGGAAGAACTTCCCTTGGCAATGCTTGGATATACAGTGTCAATCATATTTTCACAGGATT	696
Db	61	ATTGTGAATAAATTGCAATGTTGTGCTGGATCACCGTCTCACAGTCATTTTCCAAATA	120
Qy	697	GAGTACTTAAGATATGATACGCCAACTTCTTGCCCCAGTCTCTGGATCAACTCTTG	756
Db	121	GAGATGCTCAAGGAGATGATGAAGACAGCTTTTGGGTACCGAGTGTGCTGAGCAATGCTTG	180
Qy	757	CAAGAATTGCAAGGAAGGTGGTGTGCAAGTACATCATCTTCTTGAGTACTGTAGAA	816
Db	181	AAAGNACTTGAGAGAA---GGCTGTGCACTGAGGAGTCTTGCAGCTACTCTAGAGNA	237
Qy	817	GAGTCAAGGAGAGAGGCTACTTTGTTGTTCTTAGATGATCTATGGATTTTACATGATGG	876

Db	238	AAGCTAGAGGACATGAGATACCTTTTATTGTTCTTGTGACCTTTGTGACCATAGATCTTGG	297
Qy	877	AATTGGATAAATGAAATTTGCATTTTCTTAAGAACAAATTAAGAGGGCAGTTCGAATAGTAATA	936
Db	298	GATTGGATCAATCTATTGCTTTTCTTATTAGAACAAATTAAGACAGCGGAATATTATA	357
Qy	937	ACCACTCGGAATGTTGATCTTGGGAGAGTGTGCGACAGCTCTACTCGTGTACACCTT	996
Db	358	ACAAACAGAGATGTGGGCTTGGCTCGCAAGTGCACCTTCAGATTCACTCATCTACCACTC	417
Qy	997	GATTTCTTGCAGATGAACGATGCCATACATTTGCTACTGAGAAAACAAATAAATAATCAT	1056
Db	418	AAGCACTTGCAAATAGAGGATGCCACAAATTTGCTACTAAGAAAGAGTAGGAAAACATGG	477
Qy	1057	GAAGACATGGAATCAAAATATAAAATATGCANAAAGATGGTTGAACGAATTTGTAATAAATGT	1116
Db	478	GAAGACATGAATAAATGATAGAAATGATGCGCAGTGGTCAACAAATGTTAAGGAAGTGT	537
Qy	1117	GGTCTGTACCATTTAGCAATCTTAC	1142
Db	538	GGTGGTCTCCCTTCGCGCTCATCAC	563
RESULT 12			
LOCUS	AK101823	4949 bp	mRNA linear
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:J033067K01, full insert sequence.		
ACCESSION	AK101823		
VERSION	AK101823.1	GI:32987032	
KEYWORDS	FLI_CDNA; CAP trapper.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	1		
AUTHORS	The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Otsuka,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otsuka,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kuroesaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Haehidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.		
TITLE	japonica rice		
JOURNAL	Science 301 (5631), 376-379 (2003)		
MEDLINE	22752273		
PUBMED	12869764		
REFERENCE	2 (bases 1 to 4949)		
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayaehida,K., Hayaehizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,P., Hotta,I., Iida,J., Ikeda,R., Inamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kondo,S., Konno,H., Kouda,M., Koda,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Maeda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishii,K., Nomura,K.,		

Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: shikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

COMMENT This clone is one of the 48K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Iehikawa, M., Yanada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaiki, T., Kuwamegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

Location/Qualifiers
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ORIGIN

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Best Local Similarity 50.3%; Pred. NO. 8.4e-46;
Matches 838; Conservative 0; Mismatches 740; Indels 87; Gaps 9;

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AB013451
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DEFINITION Oryza sativa PibH8 mRNA, complete cds.

AB013451
ACCESSION

AB013451.1 GI:7415940

VERSION NBS-LRR type resistance gene.

KEYWORDS Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Wang,Z.X., Yano,M., Yamanouchi,U., Iwamoto,M., Momma,L.,

Hayasaka,H., Katayose,Y. and Sasaki,T.

The Pib gene for rice blast resistance belongs to the nucleotide

binding and leucine-rich repeat class of plant disease resistance

genes

Plant J. 19 (1), 55-64 (1999)

MEDLINE

99348180

10417726

REFERENCE

AUTHORS

TITLE

Wang,Z.X., Yamanouchi,U., Katayose,Y., Sasaki,T. and Yano,M.
Expression of the Pib rice-blast-resistance gene family is
up-regulated by environmental conditions favouring infection and by
chemical signals that trigger secondary plant defences

Plant Mol. Biol. 47 (5), 653-661 (2001)

JOURNAL

MEDLINE

21582385

11725950

3 (bases 1 to 4001)

Sasaki,T. and Yano,M.

Direct Submission

Submitted (28-APR-1998) Takuji Sasaki, National Institute of

Agrobiological Resources, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@agr.affrc.go.jp, Tel:0298-38-7441,

Fax:0298-38-7468)

FEATURES

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ORIGIN

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Db 2760 ATTCTTTTGGTAACTCTTGAACCTGGAGACAATAGATATCAGGGGAACATGGGTATCAA 2819
Qy 1922 CACTTACCAGTGAGATCAGTAAATCTCAATGCTCTGCACTCTTCTGTTGTATAGACAGT 1981
Db 2820 AGTTGCCAGCAACATTTGTTAGGCTCCAAACCTGAAATACGTCCATGCCGATCTTTAG 2879
Qy 1982 TTCAATTATGACAACTTTAGTCTAAACCAACCACCAATGAAGTGCATAAATAAATTTGCTGAAT 2041
Db 2880 ATGATGAGGATGA-----TCAGCCGATAATTAATACTACTGCAATC 2918
Qy 2042 TGCCTAAAGTATTCACACCTTTAGTTAGTCCGATGATCGTGCAAAACAAATTTGCTGAAT 2101
Db 2919 AGTTTCAGATCAATCCGAGAGAGATGGGAACAGGTTGCTGTATCATATATCATGTTGT 2978
Qy 2102 TGCAATGGCCACCAAAAGTTGCTGCTGAATCAATCGGTGTAAGGTACCCAAAGGA 2161
Db 2979 TCATCACCGCTTGGTTAAGAAACCTGGATGAT---GTGGTGTAAAGTGCAGAGGA 3035
Qy 2162 TAGTAAAGTTTCGAGACTTTCAGAGTTCTAGAGTATGTAGATATCAGGCGGACCACTAGTA 2221
Db 3036 TTGGACGTTTGAGGTCCATTCACACATCGACATCGTGAACATTTGCACGG---GGAAAGG 3092
Qy 2222 GAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTTAGGTGTGACAAACAAAG 2281
Db 3093 CCTTGTCTCAAAACCTCAAAAGCTTAACCCAACTGTGTAAACTAGGTGTGAC-----TG 3146
Qy 2282 GGTGCAAAAGGAAAAATGTAAGATACATTTATGAGCCATTTGAGAGCTCTCTTCCCTCC 2341
Db 3147 GCATCAACAGAAATTAATGCAAGAGCTCTGTTCTGCCATTTGCCGACCATGGCCGCTTGC 3206
Qy 2342 AATCTCTCCATGTGGATGTGCGAGGAATCTCAGATGTTGGGAACACTTTGAGTGCCTTAGATT 2401
Db 3207 AGTCTTTATTACTCGCGGCAGAGGTA-----ATGCTGGGTAGAAAGTTTGTGGATA 3260
Qy 2402 CTATTTCAATCTCTCTCTCCCTACTGAGGACACTGCTGTTGGATGGAATTTCTTGAGGAGA 2461
Db 3261 ACATGTCCAGCCTCTTAAAGACCTTAAGAGCCTCCAGTTGTAGCGCAATCTGTGACTT 3320
Qy 2462 TGCCTAACTGGATTTGAGCAGCTCACTCACCTGAAGAGATCTATTATTGAGGAGCAAC 2521
Db 3321 TACCAGAAATGGATTAAGGATCTTAAATTTCTAATAAGCTGAGCCTTCGCAACACCAATC 3380
Qy 2522 TAAAGGAAGGTAAACCATGCTGATATCTTGGGGCACTGCCCAACCTCATGTCTCTTCAATC 2581
Db 3381 TGAAGGCAGATACTACCATGGAAGTCTTGGAAACCTTACCAATGCTAGCCATTTCTCGTC 3440
Qy 2582 TTTATCGGAATGCTTATCCTTGGGGAGAGCTAGTATTTCAAACAGAGGAGCATTTCCAAATC 2641
Db 3441 TCCAGGCAATGCGTGTGAGGAGGAGAACTCTGTTTCGGTCCGAGCGTTTTCACAGGTC 3500
Qy 2642 TTAGAAACACTTTGATTTATGAATTTGGATCAGCTTAAGAGAGATCAGATTTTGA 2693
Db 3501 TGACGTCAATTTGGAGCTTCTCAATTTGGGAGAGCCTCAAGTCGGTGAATTTGA 3552

Search completed: February 13, 2005, 07:08:55
Job time : 8765.62 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 22:05:25 ; Search time 1041.76 Seconds
(without alignments)
17609.842 Million cell updates/sec

Title: US-10-656-394A-7
Perfect score: 3099
Sequence: 1 atggcgagagcgtgctgag.....gcacagctcaagctggctga 3099

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3099	100.0	3099	12	Adm72244 O. minuta
2	2951.6	95.2	9090	12	Adm72250 O. minuta
3	2916.2	94.1	3096	12	Adi57171 Oryza min
4	2910.2	93.9	3099	12	Adm72240 O. minuta
5	2850.2	92.0	3276	12	Adi57175 Oryza min
6	2820.4	91.0	76372	12	Adi57166 Oryza min
7	2393.6	77.2	2997	12	Adm72248 O. minuta
8	1621	52.3	2422	12	Adm72252 O. minuta
9	1574.2	50.8	3220	12	Adi57173 Oryza min
10	1562.2	50.4	2940	12	Adi57167 Oryza min
11	1553.4	50.1	2982	12	Adm72238 O. minuta
12	1133.8	36.6	2982	12	Adi57169 Oryza min
13	1040.4	33.6	4147	12	Adm72242 O. minuta
14	918.8	29.6	2265	12	Adi57179 Oryza min
15	838.2	27.0	2351	12	Adi57180 Oryza min
16	546.2	17.6	1355	12	Adi57177 Oryza min
17	413	13.3	1214	12	Adm72251 O. minuta
18	381.8	12.3	1389	12	Adm72246 O. minuta
19	184	5.9	2862	3	Aaz58295 Sorghum r
20	176.8	5.7	2954	3	Aaz58294 Sorghum r

21	176.8	5.7	6760	3	Aaz58293	Sorghum r
22	132.6	4.3	4125	8	ADA70202	Rice gene
23	127	4.1	2739	3	Aaz50262	Coding re
24	127	4.1	2817	3	Aaz50652	Coding re
25	127	4.1	10329	3	Aaz50653	Genomic D
26	127	4.1	10329	3	Aaz50264	Genomic D
27	126.2	4.1	2877	4	ABL50546	Mlai nucl
28	124	4.0	2871	4	ABL50537	Barley M1
29	124	4.0	2871	4	ABL50547	Mla6 nucl
30	124	4.0	3717	4	ABL50538	Barley M1
31	123.8	4.0	2833	4	ABL50549	Rgh1bcd n
32	122.6	4.0	3925	3	Aaz46679	Blaet dis
33	122.6	4.0	4514	3	AA11350	CDNA for
34	122.4	3.9	3434	4	ABL50541	Barley M1
35	120.4	3.9	2904	4	ABL50550	Rgh1a nuc
36	116.8	3.8	2881	4	ABL50548	Mlaih nuc
37	114.4	3.7	3683	4	AA03713	DNA encod
38	113.2	3.7	3989	4	ABL50551	Mlai nucl
39	113.2	3.7	7900	4	ABL50542	Barley M1
40	112.8	3.6	3066	2	AAZ37154	Partial n
41	112.8	3.6	5820	2	AAZ37153	DNA seque
42	111.6	3.6	2613	10	ADD29383	Potato Me
43	111.2	3.6	2885	4	AA03719	DNA encod
44	111.2	3.6	3014	4	AA03715	DNA encod
45	111.2	3.6	3283	4	AA03716	DNA encod

ALIGNMENTS

RESULT 1
ADM72244
ID ADM72244 standard; cDNA; 3099 BP.
AC ADM72244;
XX
DT 03-JUN-2004 (first entry)
XX
DE O. minuta NBS4 polypeptide encoding cDNA.
XX
KW Pi2; NBS4; plant protectant; gene therapy; rice; disease resistance;
KW gene; 88.
XX
OS Oryza minuta.
XX
FH Key Location/Qualifiers
FT CDS 1..3099
FT /*tag= a
FT /product= "NBS4"
XX
XX WO2004022715-A2.
XX
XX 18-MAR-2004.
XX
XX 08-SEP-2003; 2003WO-US027913.
XX
XX 09-SEP-2002; 2002US-0409216P.
XX 18-MAR-2003; 2003US-0455713P.
XX 05-SEP-2003; 2003US-00656394.
XX (OHIS) UNIV OHIO STATE.
XX
XX Wang G;
XX WPI; 2004-257576/24.
XX P-PSDB; ADM72245.
XX
XX New rice Pi2-like disease resistance nucleic acid molecule that confers
XX disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.
XX
XX Claim 1; SEQ ID NO 7; 120pp; English.
XX

CC The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA
XX encoding a rice NBS4 polypeptide.

SQ Sequence 3099 BP; 954 A; 613 C; 743 G; 789 T; 0 U; 0 Other;

Query Match 100.0%; Score 3099; DB 12; Length 3099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCGGAGACGGTCTGAGCATGCGGAGGTCTGCTGGTGGCAGCGCCATCAGCAAGGCC	60
Db	1	ATGCGGAGACGGTCTGAGCATGCGGAGGTCTGCTGGTGGCAGCGCCATCAGCAAGGCC	60
Qy	61	GCCTCCGTGTCGGCAGACGACGACGATTCCTTAGAGCTGCTGAACTTATGAAAAG	120
Db	61	GCCTCCGTGTCGGCAGACGACGACGATTCCTTAGAGCTGCTGAACTTATGAAAAG	120
Qy	121	ATCAAGATGAGCTAATAAAGGTTGGCAGAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	180
Db	121	ATCAAGATGAGCTAATAAAGGTTGGCAGAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	180
Qy	181	AAAGATGAACCTATTAAGGTTGGCAGAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	240
Db	181	AAAGATGAACCTATTAAGGTTGGCAGAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	240
Qy	241	GATTCCTTGATGAATTAAGGTTGGCAGAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	300
Db	241	GATTCCTTGATGAATTAAGGTTGGCAGAGCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	300
Qy	301	AAACTCTGAGAACGCGCAGGATTCCTTAGAGCTGCTGAACTTATGAAAAG	360
Db	301	AAACTCTGAGAACGCGCAGGATTCCTTAGAGCTGCTGAACTTATGAAAAG	360
Qy	361	GAACTGAGTACGAGAAACACGCTACAGTTAGTCAAGCCCTATTCCTTGGCAGAG	420
Db	361	GAACTGAGTACGAGAAACACGCTACAGTTAGTCAAGCCCTATTCCTTGGCAGAG	420
Qy	421	ATTGATGATGATTCCTTAGAGCAAGATTCCTTAGAGCTGCTGAACTTATGAAAAG	480
Db	421	ATTGATGATGATTCCTTAGAGCAAGATTCCTTAGAGCTGCTGAACTTATGAAAAG	480
Qy	481	GCTGAGCTGTTGGGTTTCTGACTCCAAAGAAAGGCTGCTGAACTTATGAAAAG	540
Db	481	GCTGAGCTGTTGGGTTTCTGACTCCAAAGAAAGGCTGCTGAACTTATGAAAAG	540
Qy	541	GCTAATGATGTCGGCCCAAGGTAATCTGTTGTTGGGATGGGTGTTAGGCAAGACA	600
Db	541	GCTAATGATGTCGGCCCAAGGTAATCTGTTGTTGGGATGGGTGTTAGGCAAGACA	600
Qy	601	GCTCTTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAAATTCCTCCCTTGCAT	660
Db	601	GCTCTTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAAATTCCTCCCTTGCAT	660
Qy	661	GCTTGGATTACAGTGTCAATCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	720
Db	661	GCTTGGATTACAGTGTCAATCAATTCCTTAGAGCTGCTGAACTTATGAAAAG	720
Qy	721	CAACTTCTTGGCCCGAGTTCTCTGGATCAAACTCTTGGCAAGAAATTCGAGGAAAGTGGTG	780
Db	721	CAACTTCTTGGCCCGAGTTCTCTGGATCAAACTCTTGGCAAGAAATTCGAGGAAAGTGGTG	780
Qy	781	GTGCAAGTACATCATCTTTCTGAGTACCTGATGAGGCTCAAGGAGAGAGGTACTTT	840
Db	781	GTGCAAGTACATCATCTTTCTGAGTACCTGATGAGGCTCAAGGAGAGAGGTACTTT	840
Qy	841	GTTGTTCTAGATGATCTATGATTTTACATGATTTGGAATTCGATTAATGAAATTCATTT	900
Db	841	GTTGTTCTAGATGATCTATGATTTTACATGATTTGGAATTCGATTAATGAAATTCATTT	900
Qy	901	CCTAAGAACAAATAAGAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGGC	960

Db	901	CCTAAGAACAAATAAGAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGGC	960
Qy	961	GAGAGGTGTCACAGCCTCAGTGTGTACACCTTGATTTCTTTCGAGATCAAGATGCC	1020
Db	961	GAGAGGTGTCACAGCCTCAGTGTGTGTACACCTTGATTTCTTTCGAGATCAAGATGCC	1020
Qy	1021	ATAACATTTGCTGAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1080
Db	1021	ATAACATTTGCTGAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1080
Qy	1081	ATGCAAAAGATGTTGAAACGAAATTTGTAATAAATGTTGGTGTCTTACATTAAGCAATCTT	1140
Db	1081	ATGCAAAAGATGTTGAAACGAAATTTGTAATAAATGTTGGTGTCTTACATTAAGCAATCTT	1140
Qy	1141	ACATAGAGCTGCTGCTGCAATTAACAGGTGTCAAGATGGGAGAAATTCATATGAACAC	1200
Db	1141	ACATAGAGCTGCTGCTGCAATTAACAGGTGTCAAGATGGGAGAAATTCATATGAACAC	1200
Qy	1201	CTTCTCTCAGAACTAGAAATAAACCAAGCTGCAAGCTTTGAGGAGAAATTCGTCACCTA	1260
Db	1201	CTTCTCTCAGAACTAGAAATAAACCAAGCTGCAAGCTTTGAGGAGAAATTCGTCACCTA	1260
Qy	1261	GGTTACAAACCTTACATCCATTTGAAACCAATTCCTTTTGTATCTAAGTATCTTTCCT	1320
Db	1261	GGTTACAAACCTTACATCCATTTGAAACCAATTCCTTTTGTATCTAAGTATCTTTCCT	1320
Qy	1321	GAGGATTTTGAATCAAAAGGATCGTCTAGTAGGTAGATGAGTACGAGAGGTTGTT	1380
Db	1321	GAGGATTTTGAATCAAAAGGATCGTCTAGTAGGTAGATGAGTACGAGAGGTTGTT	1380
Qy	1381	AGACCAAGGTTGGATGACGACTAAGGATGTCGAGAAAGTTACTTTTAATGAGCTAATC	1440
Db	1381	AGACCAAGGTTGGATGACGACTAAGGATGTCGAGAAAGTTACTTTTAATGAGCTAATC	1440
Qy	1441	AACGAAAGTATGATTCACGATCAAGATGAGGCAATAGCAAGAAATTAAGACTTGTGCA	1500
Db	1441	AACGAAAGTATGATTCACGATCAAGATGAGGCAATAGCAAGAAATTAAGACTTGTGCA	1500
Qy	1501	ATTCTCATATCATCCGTGATACACAGTTTCAATCTCGAGACAGGAAATTTTGTATTA	1560
Db	1501	ATTCTCATATCATCCGTGATACACAGTTTCAATCTCGAGACAGGAAATTTTGTATTA	1560
Qy	1561	TTACCAATGGGATGCTCTGATTTAGTTAGTTTCAAGAAACACTCCGCCACATAGCATTCAT	1620
Db	1561	TTACCAATGGGATGCTCTGATTTAGTTAGTTTCAAGAAACACTCCGCCACATAGCATTCAT	1620
Qy	1621	GGGATGATGTCCTGCAAAACTGGATTTGATTTGGAGCATTTATTCGATCATTTAGCTATTTT	1680
Db	1621	GGGATGATGTCCTGCAAAACTGGATTTGATTTGGAGCATTTATTCGATCATTTAGCTATTTT	1680
Qy	1681	GGTGACAGACCCAGAGCTTAGCACATGTCAGTTTGTCCAGATCAATTTGAGGATGTTACGG	1740
Db	1681	GGTGACAGACCCAGAGCTTAGCACATGTCAGTTTGTCCAGATCAATTTGAGGATGTTACGG	1740
Qy	1741	GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTCGA	1800
Db	1741	GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTCGA	1800
Qy	1801	TTGTTTGGCACTTTGAAATACTTTGAGTATTTGATTTGTCGTCATCATATATTCATCTTCCC	1860
Db	1801	TTGTTTGGCACTTTGAAATACTTTGAGTATTTGATTTGTCGTCATCATATATTCATCTTCCC	1860
Qy	1861	AGATCCATTTGGTAACTACAGGCGCTACAACTTTTGAACATGCGGAGCACATATTCGCA	1920
Db	1861	AGATCCATTTGGTAACTACAGGCGCTACAACTTTTGAACATGCGGAGCACATATTCGCA	1920
Qy	1921	GCATCAACAGTACAGTCAAGTAACTCCAACTCTGTCATCTCTTCTGTTGATAGGACAG	1980
Db	1921	GCATCAACAGTACAGTCAAGTAACTCCAACTCTGTCATCTCTTCTGTTGATAGGACAG	1980
Qy	1981	TTTCAATTAAGCAACTTTAGTCTTAAACCAACCAATTAAGTGCATTAACACACAAATATGC	2040
Db	1981	TTTCAATTAAGCAACTTTAGTCTTAAACCAACCAATTAAGTGCATTAACACACAAATATGC	2040

Db	77933	CAGAGATTGACATGGATTCTTATGCGAAGAACATTCGTAATCAGTCAGCTCGCAATGTGG	77992
Qy	476	ATGAGGCTGAGCTGTGTGGGTTTTCTGACTCCAGAAAAGGCTGCTTGAATGATCGATA	535
Db	77993	ATGAAGCTGAGCTGTGTGGGTTTTCTGACTCCAGAAAAGGCTGCTTGAATGATCGATA	78052
Qy	536	CCAAATGCTAATGATGGTCCGCGCCCAAGGTAATCTGTGTTGTTGGGATGGGTGGTTTAGGCA	595
Db	78053	CCAAATGCTAATGATGGTCCGCGCCCAAGGTAATCTGTGTTGTTGGGATGGGTGGTTTAGGCA	78112
Qy	596	AGACAGCTCTTTCCAGGAAGATCTTTGAAACGGAAGAGACATTAAGGAAGAACTTCCTCTT	655
Db	78113	AGACAGCTCTTTCCAGGAAGATCTTTGAAACGGAAGAGACATTAAGGAAGAACTTCCTCTT	78172
Qy	656	GCAATGCTTGAATTACAGTGTCAATCATTTCCACAGATTGAGCTACTTAAAGATATGA	715
Db	78173	GCAATGCTTGAATTACAGTGTCAATCATTTCCACAGATTGAGCTACTTAAAGATATGA	78232
Qy	716	TACGCCAACTTCTTTGGGCCCAAGTTCTCTGGATCAACTCTTGCAAGAAATTGCAAGGGAAGG	775
Db	78233	TACGCCAACTTCTTTGGGCCCAAGTTCTCTGGATCAACTCTTGCAAGAAATTGCAAGGGAAGG	78292
Qy	776	TGGTGGTGCAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGT	835
Db	78293	TGGTGGTGCAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGT	78352
Qy	836	ACTTTGTGTCTAGATGATCATATGGATTTTACATGATTGGAATGGATAAATCAATTTG	895
Db	78353	ACTTTGTGTCTAGATGATCATATGGATTTTACATGATTGGAATGGATAAATCAATTTG	78412
Qy	896	CATTTCTCTAAGAACAAATAAGAAAGGCGAGTCAATAGTAATAACCACTCGGAATGTGTATC	955
Db	78413	CATTTCTCTAAGAACAAATAAGAAAGGCGAGTCAATAGTAATAACCACTCGGAATGTGTATC	78472
Qy	956	TTGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACTTGATTTCTTGAGATGAACG	1015
Db	78473	TTGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACTTGATTTCTTGAGATGAACG	78532
Qy	1016	ATGCCATAACATTCGTACTGAGAAACAAATAAATAAATCATGAAGACATGAATCAATA	1075
Db	78533	ATGCCATAACATTCGTACTGAGAAACAAATAAATAAATCATGAAGACATGAATCAATA	78592
Qy	1076	AAAAATATGCAAAAGATGGTTCGAACGAATTGTAAATAAATGTGGTCTGCTACCATTAGCAA	1135
Db	78593	AAAAATATGCAAAAGATGGTTCGAACGAATTGTAAATAAATGTGGTCTGCTACCATTAGCAA	78652
Qy	1136	TACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAAGATGGAGAAAATTCATAG	1195
Db	78653	TACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTGTCAAGATGGAGAAAATTCATAG	78712
Qy	1196	AACACCTTCTTCAGNACTAGAAATTAACCCAGCCTGGAGCTTTCGAGGAGATGGTGA	1255
Db	78713	AACACCTTCTTCAGNACTAGAAATTAACCCAGCCTGGAGCTTTCGAGGAGATGGTGA	78772
Qy	1256	CCCTAGGTTACAAACCACTACCATCCCATTTGAAACCACTGCTTTTGTATCTAAGTATCT	1315
Db	78773	CCCTAGGTTACAAACCACTACCATCCCATTTGAAACCACTGCTTTTGTATCTAAGTATCT	78832
Qy	1316	TTCTCTAGGATTTTGAATCAAAAAGGAATCGCTAGTAGGTAGATGGATAGCAGAAAGGT	1375
Db	78833	TTCTCTAGGATTTTGAATCAAAAAGGAATCGCTAGTAGGTAGATGGATAGCAGAAAGGT	78892
Qy	1376	TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCCGGAAGCTTACTTTAATGAGC	1435
Db	78893	TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCCGGAAGCTTACTTTAATGAGC	78952
Qy	1436	TAATCAACCGAAGTATGATTCAAACGATCAAGATGGGCATAGCAGGAAAATTAAGACTT	1495
Db	78953	TAATCAACCGAAGTATGATTCAAACGATCAAGATGGGCATAGCAGGAAAATTAAGACTT	79012
Qy	1496	GTCGAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAATTTTG	1555
Db	79013	GTCGAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAATTTTG	79072
Qy	1556	TATTTATTACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAAACACTCGCCACATAGCAT	1615
Db	79073	TATTTATTACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAAACACTCGCCACATAGCAT	79132
Qy	1616	TCCAATGGAGATATGTCCTGCAAAAACCTGGATTTGGATTCGAGCATTTATTCGATATTAGCTA	1675
Db	79133	TCCAATGGAGATATGTCCTGCAAAAACCTGGATTTGGATTCGAGCATTTATTCGATATTAGCTA	79192
Qy	1676	TTTTTGTGTACAGACCCCAAGAGTCTAGCACATGCGAGTTTTGTCCAGATCAATTTGAGGATGT	1735
Db	79193	TTTTTGTGTACAGACCCCAAGAGTCTAGCACATGCGAGTTTTGTCCAGATCAATTTGAGGATGT	79252
Qy	1736	TACGGGTCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCACCCGTA	1795
Db	79253	TACGGGTCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCACCCGTA	79312
Qy	1796	TTGCATTTGTGTGCCACTTGAAAATPACTTGTAGTATGTGATATTCGTCAATATATTTCAC	1855
Db	79313	TTGCATTTGTGTGCCACTTGAAAATPACTTGTAGTATGTGATATTCGTCAATATATTTCAC	79372
Qy	1856	TTCCAGATCCATTTGGTAAACTACAGGCCCTTACAAAATTTTGAACATGCCGAGCACATACA	1915
Db	79373	TTCCAGATCCATTTGGTAAACTACAGGCCCTTACAAAATTTTGAACATGCCGAGCACATACA	79432
Qy	1916	TTGCAGCATCTACCAAGTGAGATCAGTAAACTCCAAATGCTCTGCATACCTTTCGTTGTATAG	1975
Db	79433	TTGCAGCATCTACCAAGTGAGATCAGTAAACTCCAAATGCTCTGCATACCTTTCGTTGTATAG	79492
Qy	1976	GACATTTTCATTTATGACAACTTTTAGTCTAAACCAACCAATGAAGTGCATATCTAACACAA	2035
Db	79493	GACATTTTCATTTATGACAACTTTTAGTCTAAACCAACCAATGAAGTGCATATCTAACACAA	79552
Qy	2036	TATGCCCTGCCTAAAGTATTTACACCTTTTAGTTAGTCCGATGATCGTGCAAAAACAAATTTG	2095
Db	79553	TATGCCCTGCCTAAAGTATTTACACCTTTTAGTTAGTCCGATGATCGTGCAAAAACAAATTTG	79612
Qy	2096	CTGAATTTGCACATGGCCACCAAAAATTTGCTGGTCTGAAATCAATCGGTGTGAAGTACCCCA	2155
Db	79613	CTGAATTTGCACATGGCCACCAAAAATTTGCTGGTCTGAAATCAATCGGTGTGAAGTACCCCA	79672
Qy	2156	AAGGAATAGGTAAAGTTCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGCGGACCA	2215
Db	79673	AAGGAATAGGTAAAGTTCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGCGGACCA	79732
Qy	2216	GTAGTAGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTAGGTCTGACAA	2275
Db	79733	GTAGTAGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTAGGTCTGACAA	79792
Qy	2276	CAAAACGGTTCGACAAAAGAAAAATGTAAGATACCTTTATCGAGCCATTGAGAAGCTCTCTT	2335
Db	79793	CAAAACGGTTCGACAAAAGAAAAATGTAAGATACCTTTATCGAGCCATTGAGAAGCTCTCTT	79852
Qy	2336	CCCTCCAATCTCTCATGTGGATGCTCAGGAATCTCAGATGGTGGAAACACTTGAGTGCC	2395
Db	79853	CCCTCCAATCTCTCATGTGGATGCTCAGGAATCTCAGATGGTGGAAACACTTGAGTGCC	79912
Qy	2396	TAGATTTCTATTTCTATCTCCCTCCCTACTGAGGACACTCGTCTTGATGGATGGAATTTCTTG	2455
Db	79913	TAGATTTCTATTTCTATCTCCCTCCCTACTGAGGACACTCGTCTTGATGGATGGAATTTCTTG	79972
Qy	2456	AGGAGATGCTTAACCTGGAATGAGCAGCTCACTCACCTGGAAGAAGATCTACTTTATTGAGGA	2515
Db	79973	AGGAGATGCTTAACCTGGAATGAGCAGCTCACTCACCTGGAAGAAGATCTACTTTATTGAGGA	80032
Qy	2516	GCAAACTAAAGGAAGGTAAACCAATGCTGATATCTTGGGGCACTGCCCAACCTCATGFTCC	2575
Db	80033	GCAAACTAAAGGAAGGTAAACCAATGCTGATATCTTGGGGCACTGCCCAACCTCATGFTCC	80092
Qy	2576	TTCAATCTTTATCGGAATGCTTACCTTTGGGGAAGAGCTAGTATTTCAAAACAGGACATTTCC	2635
Db	80093	TTCAATCTTTATCGGAATGCTTACCTTTGGGGAAGAGCTAGTATTTCAAAACAGGACATTTCC	80152

QY 2636 CAATCTTAGACACTTTGGATTATGAATGGATCAGCTAAGAGAGATCAGATTTGAGG 2695
Db 80153 CAATCTTTAGAACACTTTTGGATTTATGAATTTGGATCAGCTAAGAGAGATCAGATTTGAGG 80212
QY 2696 ACGGCGAGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTTTGGAAATCTGGGA 2755
Db 80213 ACGGCGAGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTTTGGAAATCTGGGA 80272
QY 2756 TTACTGGTATCATTCACCTTCCAAAGCTCAAGGAGATTTCCAATTAGATACGGAAGTAAAG 2815
Db 80273 TTACTGGTATCATTCACCTTCCAAAGCTCAAGGAGATTTCCAATTAGATACGGAAGTAAAG 80332
QY 2816 TGGCTGGGCTTGGTTCAGCTGAGGAGGAAGTGAACGACACCCAAAATCGCCCCGTGCTGC 2875
Db 80333 TGGCTGGGCTTGGTTCAGCTGAGGAGGAAGTGAACGACACCCAAAATCGCCCCGTGCTGC 80392
QY 2876 TAATGTACAGTGACCGAAGGTATCAGACCTGGGGGCTGAAGCCGAAGATCTTCTATAG 2935
Db 80393 TAATGTACAGTGACCGAAGGTATCAGACCTGGGGGCTGAAGCCGAAGATCTTCTATAG 80452
QY 2936 AAGTGCAAACAGCAGATCTCTGTTCTGATGCCGAAGGATCAGTCACTGTAGCAGTGAAG 2995
Db 80453 AAGTGCAAACAGCAGATCTCTGTTCTGATGCCGAAGGATCAGTCACTGTAGCAGTGAAG 80512
QY 2996 CAACGGATCCCTTCCCGAGCAGGAGGAGAGAGCTCCGAGTCCGAGGTATCAGTTGA 3055
Db 80513 CAACGGATCCCTTCCCGAGCAGGAGGAGAGAGCTCCGAGTCCGAGGTATCAGTTGA 80572
QY 3056 CGACGAATGATAGCGNAG 3073
Db 80573 CGACGAATGATAGGTGAG 80590

RESULT 3

ADI57171
ID ADI57171 standard; DNA; 3096 BP.
XX
AC ADI57171;
XX
DT 22-APR-2004 (first entry)
XX
DE Oryza minuta P19 locus nucleotide binding site (NBS) gene #3.
XX
KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; gene; ds.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PP 27-JAN-2003; 2003US-00352179.
XX
PR 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX
PA (WANG/) WANG G.
PA (LIU/) LIU G.
XX
PI Wang G, Liu G;
XX
DR WPI; 2004-121064/12.
DR P-PSDB; ADI57172.
XX
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
infection.
XX
PS Claim 3; SEQ ID NO 88; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial

CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents an NBS gene from
CC the Oryza minuta P19 locus.

SQ Sequence 3096 BP; 960 A; 606 C; 730 G; 800 T; 0 U; 0 Other;

Query Match 94.1%; Score 2916.2; DB 12; Length 3096;

Best Local Similarity 96.8%; Pred. No. 0;

Matches 2975; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATGCGGAGAGCGTCTGAGCATGCGAGGTGCGTGGTGGCGAGCGCATCAGCAAGGCC 60
Db 1 ATGCGGAGAGCGTCTGAGCATGCGAGGTGCGTGGTGGCGAGCGCATCAGCAAGGCC 60
QY 61 GCCTCCGCTGTCGCCGACGAGACGAGCTCTCTGCTGGCGCTCGAGAAAGACATCTGGTAT 120
Db 61 GCCTCCGCTGTCGCATGAGACGAGCTCTCTGCTGGCGCTCGAGAAAGACATCTGGTAT 120
QY 121 ATCAAGATGAGCTTAAAGCATGCAAGCATTCCTTAGAGCTGTGAACTTATGAAAAG 180
Db 121 ATCAAGATGAGCTTAAAGCATGCAAGCATTCCTTAGAGCTGTGAACTTATGAAAAG 180
QY 181 AAAGATGAATTTAAAGGTTTGGGACAGCAATACTGACCTGTCTATGACATTTGAA 240
Db 181 AAAGATGAATTTAAAGGTTTGGGACAGCAATACTGACCTGTCTATGACATTTGAA 240
QY 241 GATTCCCTTGTATGAATTTAAGTCCATATTGAAAGCCAAACCTTATTCGTCAGTTGTG 300
Db 241 GATTCCCTTGTATGAATTTAAGTCCATATTGAAAGCCAAACCTTATTCGTCAGTTGTG 300
QY 301 AAACCTCAGAGAACGCCACCGAATTTGCTATCCGTATCCACCACTTAAATCAAGAGTTGAA 360
Db 301 AAACCTCAGAGAACGCCACCGAATTTGCTATCCGTATCCACCACTTAAATCAAGAGTTGAA 360
QY 361 GAAGTGTAGTAGCAGGAACACACGCTACAGTTTAGTCAAGCCTATTTCCTCTGGCAGAG 420
Db 361 GAAGTGTAGTAGCAGGAACACACGCTACAGTTTAGTCAAGCCTATTTCCTCTGGCAGAG 420
QY 421 ATTGACATGATTCCTATGACAGAGACATTCGTATCATGAGCTCGCAATTTGATGATGAG 480
Db 421 ATTGACATGATTCCTATGACAGAGACATTCGTATCATGAGCTCGCAATTTGATGATGAG 480
QY 481 GCTGAGCTTGTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAATATGATACCAAT 540
Db 481 GCTGAGCTTGTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAATATGATACCAAT 540
QY 541 GCTAATGATGGTCCGGCAAGGTTAATCTGTGTTGTTGGGATGGGTGTTTGAAGCAAGACA 600
Db 541 GCTAATGATGGTCCGGCAAGGTTAATCTGTGTTGTTGGGATGGGTGTTTGAAGCAAGACA 600
QY 601 GCTCTTTTCGAGGAAGATCTTTGAAAGCGAAGACACATTTAGGAAGACTTCCCTTGCAT 660
Db 601 GCTCTTTTCGAGGAAGATCTTTGAAAGCGAAGACACATTTAGGAAGACTTCCCTTGCAT 660
QY 661 GCTTGGATTACAGTGTACCAATCATTTTCAGAGGATTCAGCTACTTAAAGATATGATACGC 720
Db 661 GCTTGGATTACAGTGTACCAATCATTTTCAGAGGATTCAGCTACTTAAAGATATGATACGC 720
QY 721 CAACCTCTTGGCCCCAGTTCTCTGGATCAACTCTTTCGCAAGAAATTCGAAGGAAGTGGTG 780
Db 721 CAACCTCTTGGCCCCAGTTCTCTGGATCAACTCTTTCGCAAGAAATTCGAAGGAAGTGGTG 780
QY 781 GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGGCTCAAGGAGAGAGGTACTTTT 840
Db 781 GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGGCTCAAGGAGAGAGGTACTTTT 840
QY 841 GTTGTCTTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGAATTTGGAATTTGCA 900
Db 841 GTTGTCTTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGAATTTGGAATTTGCA 900
QY 901 CCTAAGAACCAATGAAGAGGCGAGTCGAATAGTAATAACCACTCGGAATTTGATCTTGGC 960
Db 901 CCTAAGAACCAATGAAGAGGCGAGTCGAATAGTAATAACCACTCGGAATTTGATCTTGGC 960

Db 901 CCTAAGAAACAATAAGAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTAGCG 960
Qy 961 GAGAAGTGTGCCACAGCCTCTAGTGTACACCTTGATTTCTTCGAGTGAACGATGCC 1020
Db 961 GAGAAGTGTGCCACAGCCTCTAGTGTACACCTTGATTTCTTCGAGTGAACGATGCC 1020
Qy 1021 ATAAACATTGCTACTGAGAAAAACAATAAATAATCATAGAACATGGAATCAAAATAAAAT 1080
Db 1021 ATAAACATTGCTACTGAGAAAAACAATAAATAATCATAGAACATGGAATCAAAATAAAAT 1080
Qy 1081 ATGCAAAAGATGGTTGAACGAATTTGTAATAATGTGGTCTGTCAACATAGCAATACTT 1140
Db 1081 ATGCAAAAGATGGTTGAACGAATTTGTAATAATGTGGTCTGTCAACATAGCAATACTT 1140
Qy 1141 ACAATAGGAGTGTGCTTGCAACTAAACAGAGTGTCAAGATGGGAGAAATTTCTATGAACAC 1200
Db 1141 ACAATAGGAGTGTGCTTGCAACTAAACAGAGTGTCAAGATGGGAGAAATTTCTATGAACAA 1200
Qy 1201 CTTCCCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTGAGAGAAATGGTGACCCCTA 1260
Db 1201 CTTCCCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTGAGAGAAATGGTGACCCCTA 1260
Qy 1261 GGTTACAAACCACTCAACATCCCAATTTGAAACCACTGCTTTTGTATCTTAAGTATCTTTCCCT 1320
Db 1261 GGTTACAAACCACTCAACATCCCAATTTGAAACCACTGCTTTTGTATCTTAAGTATCTTTCCCT 1320
Qy 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATGAGAGGGGTTGTT 1380
Db 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATGAGAGGGGTTGTT 1380
Qy 1381 AGACCAAAAGTTGGGATGACCACTAAGGATGTGCGAGAAAGTTACTTTAATGAGCTAATC 1440
Db 1381 AGACCAAAAGTTGGGATGACCACTAAGGATGTGCGAGAAAGTTACTTTAATGAGCTAATC 1440
Qy 1441 AACCAGAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGGA 1500
Db 1441 AACCAGAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGGA 1500
Qy 1501 ATTCATGATATCATCCGATGATACAGTTTCAATCTCGACACAGGAAAAATTTGTATTA 1560
Db 1501 ATTCATGATATCATCCGATGATACAGTTTCAATCTCGACACAGGAAAAATTTGTATTA 1560
Qy 1561 TTACCAATGGAGATGGCTCTGATTTAGTTAGTCAGGAAAAACATCGCCACATAGCATTTCCAT 1620
Db 1561 TTACCAATGGAGATGGCTCTGATTTAGTTAGTCAGGAAAAACATCGCCACATAGCATTTCCAT 1620
Qy 1621 GGGAGTATGCTCTGCAAACTGGATGGATTTGGAGCAATTAATCGATCAATTAGCTATTTT 1680
Db 1621 GGGAGTATGCTCTGCAAAACAGGATTTGGATTTGGAGCAATTAATCGATCAATTAGCTATTTT 1680
Qy 1681 GGTGACAGACCAAGAGTCTAGCACATGCGATTTGTCCAGATCAATTCAGGATGTTACGG 1740
Db 1681 GGTGACAGACCAAGAGTCTAGCACATGCGATTTGTCCAGATCAATTCAGGATGTTACGG 1740
Qy 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
Db 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
Qy 1801 TTGTTGTGCCACTTGAATACTTGAGTAATTCGATATTCGATCCATATATTCATCTCCC 1860
Db 1801 TTGTTGTGCCACTTGAATACTTGAGTATTCGATATTCGATCCATATATTCATCTCCC 1860
Qy 1861 AGATCCATTGGTAACACTACAGGCGCTACAACTTTGAAATGCGCGAGCACATACATTGCA 1920
Db 1861 AGATCCATTGGTAACACTACAGGCGCTACAACTTTGAAATGCGCGAGCACATACATTGCA 1920
Qy 1921 GCATCTACCAAGTGTAGATCAGTAATACTCCAAATGTCTGCATCTCTTCGTTGTATAGGACAG 1980
Db 1921 GCATCTACCAAGTGTAGATCAGTAATACTCCAAATGTCTGCATCTCTTCGTTGTATAGGAAAG 1980
Qy 1981 TTTCTATTATGACAACTTTAGTCTAAACCAACCAATGAAGTGCATAAATCAACAAATATGC 2040
Db 1981 TTTGTTTATGACAACTTTAGTCTAAACCAACCAATGAAGTGCATAAATCAACAAATATGC 2040

Qy 2041 CTGCTAAAGTATTTCAACACCTTTAGTTAGTCGCGATGATCGTGCAAAAACAAATTTGCTGAA 2100
Db 2041 CTGCTAAAGTATTTCAACACCTTTAGTTAGTCGCGATGATCGTGCAAAAACAAATTTGCTGAA 2100
Qy 2101 TTGCACATGGCCACCAAAAGTTGCTGCTGTAATCAATTCGCTGTGAAGGTACCCAAAGGA 2160
Db 2101 TTGCACATGGCCACCAAAAGTTGCTGCTGTAATCAATTCGCTGTGAAGGTACCCAAAGGA 2160
Qy 2161 ATAGGTAAGTTGCGAGACTTTCAGGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2220
Db 2161 ATAGGTAAGTTGCGAGACTTTCAGGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2220
Qy 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTAAGTGTGCAACAACAAAC 2280
Db 2221 AGAGCAATCAAAAGAGCTGGGCGACTTAAGCAAGTTGAGGAAATTAAGTGTGATACAAAA 2280
Qy 2281 GGGTCGACAAAGGAAAAATGTAGATATCTTTATCGACCAATTTGAGAAAGCTCTCTTCCCTC 2340
Db 2281 GGGTCGACAAAGGAAAAATGTAGATATCTTTATCGACCAATTTGAGAAAGCTCTCTTCCCTC 2340
Qy 2341 CAATCTCTCATGTGGATGTGCGAGGAATCTCAGATGGTGGAAACACTTTGAGTGCCTAGAT 2400
Db 2341 CAATCTCTCTATGTGAATGTGCGGTTATATCAGATATTTGAACAACACTTTGAGTGCCTAGAT 2400
Qy 2401 TCTATTTTCATCTCTCCCTACTCGAGGACACTCGTGTGGATGGAATTTCTTTGAGGAG 2460
Db 2401 TCTATTTTCATCTCTCCCTACTCGAGGACACTCGGTTGGAATTTGGAAGTCTTTGAAGAG 2460
Qy 2461 ATGCCTAACTGGATTGAGCAGCTCACTCAGCTGAAGAGATCTACTTTATTTGAGGAGCAAA 2520
Db 2461 ATGCCTAACTGGATTGAGCAGCTCACTCAGCTGAAGAGATCTACTTTATTTGAGGAGCAAA 2520
Qy 2521 CTAAAGGAAGGTAATAACATGCTGATCTTTGGGCGACTGGCCACCTCATGGTCTTTCTAT 2580
Db 2521 CTAAAGGAAGGTAATAACATGCTGATCTTTGGGCGACTGGCCACCTCATGGTCTTTCTAT 2580
Qy 2581 CTTTATCGGAATGCTTACTCTTTGGGAGAGCTAGTATTTCAAAACAGAGACATTTCCCAAT 2640
Db 2581 CTTTATTTGGAATGCTTACTCTTTGGGAGAGCTAGTATTTCAAAACGGGAGCATTTCCCAAT 2640
Qy 2641 CTTAGAACACATTTTGGATTTATGAATTCGATCAGCTAAGAGAGATCAGATTTGAGGACGGC 2700
Db 2641 CTTAGAACACATTTCTGATTTTACGAATTCGATCAGCTAAGAGAGATGAGATTTGAGGATGCGC 2700
Qy 2701 AGCTCACCCCTGTTGGAAAAAGATAGAAATAGGCGAGTGCAGGTTTGGAACTCTGGGATTTACT 2760
Db 2701 AGCTCACCCCTGTTGGAAAAAGATAGAAATCTCTTTGCTGCGAGTTTGGAACTCAGGGATTTAT 2760
Qy 2761 GGTATCAATTCACCTTTCCAAAGCTCAAGGAGATTTCCAAATTAGATACGGAAGTAAAGTGGCT 2820
Db 2761 GGTATCAATTCACCTTTCCAAAGCTCAAGGATTTCCAAAGTAAAGTAAAGTGGCT 2820
Qy 2821 GGGCTTGGTCAAGCTGGAGGAGAGTGAACGCAACCAAAATCGCCCGTCTGCTTAATG 2880
Db 2821 AGGCTTGGTCAAGCTGGAGGAGAGTGAACACACACCAAAATCGCCCGTCTGCGAATG 2880
Qy 2881 TACAGTACCGAAGGTATCAGGACTGGGGCTGAGCGGAGGATCTTCTTATAGAGTGT 2940
Db 2881 GACAGTACCGAAGGATCAGGACTGGGGCTGAGCGGAGGATCTTCTTATAGAGTGT 2940
Qy 2941 CAAACACGAGATCTGTTCTGATGCCGAGATTCAGTCACTGTAGCAGTGGAAAGCAACG 3000
Db 2941 CAAACACGAGATCTGTTCTGATGCCGAGGATTCAGTCACTGTAGCAGTGGAAAGCAACG 3000
Qy 3001 GATCCCTTCCGAGCAGGAGGAGAGAGTCTCGAGTCCGAGGTGATCAGCTTGAAGACG 3060
Db 3001 GATCCCTTCCGAGCAGGAGGAGAGAGTCTCGAGTCCGAGGTGATCAGCTTGAAGACG 3060
Qy 3061 AATGATAGCGAAG 3073
Db 3061 AACGATAGGTGAG 3073

Db 1321 GAGGATTTTGAATAACAAAGGAATCGTCTAGTAGTAGATGGATAGCAGAGGGTTTGT 1380
Qy 1381 AGACCAAGGTTGGATGACCACTAAGAGTCTCGGAGAAAGTTACTTTAATGAGCTAATC 1440
Db 1381 AGACCAAGGTTGGATGACCACTAAGAGTCTCGGAGAAAGTTACTTTAATGAGCTAATC 1440
Qy 1441 AACCGAAGTAGATTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGGA 1500
Db 1441 AACCGAAGTAGATTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGGA 1500
Qy 1501 ATTCAATGATCATCCGATGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATTA 1560
Db 1501 ATCCATGATATCATCCGATGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATTA 1560
Qy 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAACACTCGCCCATAGCAATTCAT 1620
Db 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAACACTCGCCCATAGCAATTCAT 1620
Qy 1621 GGGAGTAGTCTCTGCAAAACTGGATTTGGATTTGGAGCAATTAATTCGATCATTAAGCTATTTTT 1680
Db 1621 GGGAGTAGTCTCTGCAAAAACAGGATTTGGATTTGGAGCAATTAATTCGATCATTAAGCTATTTTT 1680
Qy 1681 GGTGACAGACCCAAAGAGTCTAGCACAATGCAATTTGTCTCAGATCAATTTGAGGATGTTACGG 1740
Db 1681 GGTGACAGACCCAAAGAGTCTAGCACAATGCAATTTGTCTCAGATCAATTTGAGGATGTTACGG 1740
Qy 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
Db 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCA 1800
Qy 1801 TTGTTTGGCCACTTTGAAATACCTGAGTATTGGATATTGTCATCCATATATTCACTTTCCC 1860
Db 1801 TTGTTTGGCCACTTTGAAATACCTGAGTATTGGATATTGTCATCCATATATTCACTTTCCC 1860
Qy 1861 AGATCCATTTGTAACCTACAGGGCTACAGACTTTGAAACATGTCAAGCACATATGCA 1920
Db 1861 AGATCCATTTGTAACCTACAGGGCTACAGACTTTGAAACATGTCAAGCACATATGCA 1920
Qy 1921 GCATTCAGTAGTGCAGTAACTCCAAATGTCGCATCTCTCGTTGATAGGACNG 1980
Db 1921 GCATTCAGTAGTGCAGTAACTCCAAATGTCGCATCTCTCGTTGATAGGAG 1980
Qy 1981 TTTCAATTATGACAACTTTAGTCTAAACCACCCCAATGAAGTCATAAATCAACAAATATGC 2040
Db 1981 CTGGAATTTGACAACTTTAGTCTAAATCACCCCAATGAAGTCATAAATCAACAAATATGC 2040
Qy 2041 CTGCTAAAGTATTACACCTTTAGTCTAGTCGCGATGATCTGTGCAAAAACAAATTTGCTGAA 2100
Db 2041 CTGCTAAAGTATTACACCTTTAGTCTAGTCGCGATGATCTGTGCAAAAACAAATTTGCTGAA 2100
Qy 2101 TTGCACATGGCCACCAAAAGTTGCTGTCTGAATCAATCCGTTGGAAGGTACCCAAAGGA 2160
Db 2101 TTGCACATGGCCACCAAAAGTTTCTGTCTGAATCAATCCGTTGGAAGGTACCCAAAGGA 2160
Qy 2161 ATAGTAAGTTGCAGACTTCAGGTTCTAGATATGTAGATATCAGGCGACCAAGTAGT 2220
Db 2161 ATAGTAAGTTGCAGACTTCAGGTTCTAGATATGTAGATATCAGGCGACCAAGTAGT 2220
Qy 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTAAGTGTGACAAAC 2280
Db 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTAAGTGTGATAACAAA 2280
Qy 2281 GGGTCGACAAAGGAAATGTAAAGTACTTTATTCAGCCCATTTGAGAGCTCTCTCCCTC 2340
Db 2281 GGGTCGACAAAGGAAATGTAAAGTACTTTATTCAGCCCATTTGAGAGCTCTCTCCCTC 2340
Qy 2341 CAATCTCTCATATGAATGCTGCGTTATATCAGATATTGAAAACACTTGAGTGCTTAGAT 2400
Db 2341 CAATCTCTCATATGAATGCTGCGTTATATCAGATATTGAAAACACTTGAGTGCTTAGAT 2400
Qy 2401 TCTATTTCACTCTCTCCCTACCTGAGGACACTCGGTTGGATGGAATTTTGGAGAG 2460
Db 2401 TCTATTTCACTCTCTCCCTACCTGAGGACACTCGGTTGGATGGAATTTTGGAGAG 2460

Qy 2461 ATGCTAACTGGATTGAGCAGCTCACTCACCTGAAGAAGATCTACTTTATTGAGGAGCAAA 2520
Db 2461 ATGCTAACTGGATTGAGCAGCTCACTCACCTGAAGAAGTTCACTTTATGAGTAGTAAA 2520
Qy 2521 CTTAAGGAAGGTAAAAACCATGCTGATACTTTGGGGCACTGCCCAACCTCATGGTCCCTCAT 2580
Db 2521 CTTAAGGAAGGTAAAAACATGCTGATACTTTGGGGCACTGCCCAACCTCATGTTCTCTTCT 2580
Qy 2581 CTTTATCGGAATGCTTACCTTTGGGGAAGCTAGTATTCAAAACAGAGCATTTCCCAAT 2640
Db 2581 CTTTATCATTAATTTTATCTTTGGGGAAGCTAGTATTCAAAACGGGAGCATTTCCCAAT 2640
Qy 2641 CTTAGAACACCTTTGGATTATGAAATTCGATCAGCTAAGAGAGATCAGATTTGAGGACGGC 2700
Db 2641 CTTAGAACACCTTTGGATTATGAAATTCGATCAGCTAAGAGAGATCAGATTTGAGGACGGC 2700
Qy 2701 AGCTCACCCCTGTTGGAAAAAGATAGAAATAGGCGAGTTGAGGTTGGAATCTGGGATTAAT 2760
Db 2701 AGCTCACCCCTGTTGGAAAAAGATAGAAATCTCTTCTGCTGAGGTTGGAATCAGGATTAAT 2760
Qy 2761 GGTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCCAATTTAGATACGGAAGTAAAGTGGCT 2820
Db 2761 GGTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCACTTGAATCAAAAAGTAAAGTGGCT 2820
Qy 2821 GGGCTTGGTCAAGTGGAGGAGAAAGTGAACGACACCCAAATCGCCCGCTGCTCTAATG 2880
Db 2821 AGGCTTGGTCAAGTGGAGGAGAAAGTGAACACACCCAAATCGCCCGCTGCTGCGAATG 2880
Qy 2881 TACAGTACCCAAAGGTATACGACCTGGGGGCTGGAAGCCCAAGGATCTTCTATAGAGTG 2940
Db 2881 GACAGTACCCAAAGGATACGACCTGGGGGCTGGAAGCCCAAGGATCTTCTATAGAGTG 2940
Qy 2941 CAAAACAGCAGATCTGTTCTGATCGCAAGGATCAGTCACTGTAGCAGTGGAGCAACG 3000
Db 2941 CAAAACAGCAGATCTGTTCTGATCGCAAGGATCAGTCACTGTAGCAGTGGAGCAACG 3000
Qy 3001 GATCCCTTCCGAGCAGGAGGAGAGAGCTCGCAGTCGCGAGGTGATCAGCTTACGACG 3060
Db 3001 GATCCCTTCCGAGCAGGAGGAGAGAGCTCGCAGTCGCGAGGTGATCAGCTTACGACG 3060
Qy 3061 AATGATAGCGAAGAGATAGGACAGCTCAAGCTGGCTGA 3099
Db 3061 AATGATAGCGAAGAGATAGGACAGCTCAAGCTGGCTGA 3099

RESULT 5

ADI57175
ID ADI57175 standard; DNA; 3276 BP.

AC ADI57175;

XX ADI57175;

DT 22-APR-2004 (first entry)

DE Oryza minuta Pi9 locus nucleotide binding site (NBS) gene #5.

XX nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;

XX plant breeding; transgenic plant; plant; gene; ds.

OS Oryza minuta.

OS US2004006788-A1.

PN 08-JAN-2004.

XX 27-JAN-2003; 2003US-00352179.

PD 25-JAN-2002; 2002US-0352106P.

XX 01-FEB-2002; 2002US-0353304P.

XX (WANG/) WANG G.

PA (LIUG/) LIU G.

XX

PI Wang G, Liu G;
XX WPI; 2004-121064/12.
DR P-PSDB; ADI57176.
XX
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
PS Claim 3; SEQ ID NO 92; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the *Oryza minuta* Pi9 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with *Magnaporthe grisea* in plant
CC breeding programs. The present DNA sequence represents an NBS gene from
CC the *Oryza minuta* Pi9 locus.
XX
SQ Sequence 3276 BP; 1028 A; 531 C; 770 G; 847 T; 0 U; 0 Other;
Query Match 92.0%; Score 2850.2; DB 12; Length 3276;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2900; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 117 GTATATCAAGATGAGCTAAACAGATGCAAGCATTCCTTAGAGCTGCTGAACATTATGAA 176
DB 294 GTATATCAAGATGAGCTAAACAGATGCAAGCATTCCTTAGAGCTGCTGAACATTATGAA 353
QY 177 AAAGAAAGATGAACATTAATAAGGTTTGGCGAGCAAAATACGTGACCTGTCATATGACAT 236
DB 354 AAAGAAAGATGAACATTAATAAGGTTTGGCGAGCAAAATACGTGACCTGTCATATGACAT 413
QY 237 TGAAGATTCCCTTGTATGAATTAAGGTCCATATTGAAGCCAAACCCCTATTTCGTGAGTT 296
DB 414 TGAAGATTCCCTTGTATGAATTAAGGTCCATATTGAAGCCAAACCCCTATTTCGTGAGTT 473
QY 297 GGTGAACCTCAGAAAGCCGACCGAATTCGTATCCGTATCCAAACCTTAATAATCAAGAGT 356
DB 474 GGTGAACCTCAGAAAGCCGACCGAATTCGTATCCGTATCCAAACCTTAATAATCAAGAGT 533
QY 357 TGAAGATGTAGTACAGGACACACGCTACAGTTTGTAGTCAAGCTATTCCTCTGGCAC 416
DB 534 TGAAGATGTAGTACAGGACACACGCTACAGTTTGTAGTCAAGCTATTCCTCTGGCAC 593
QY 417 AGAGATTGACATGGAATTCCTATGCAAGAGACATTCGTATCAGTCAGCTCGCAATGTGGA 476
DB 594 AGAGATTGACATGGAATTCCTATGCAAGAGACATTCGTATCAGTCAGCTCGCAATGTGGA 653
QY 477 TGAGCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATAC 536
DB 654 TGAAGCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGGTTGCTTGAATGATCGATAC 713
QY 537 CAATGCTAATGATGTCCGGCCAAAGTAACTCTGTGTTCTGGGATGGGTGTTAGGCCAA 596
DB 714 CAATGCTAATGATGTCCGGCCAAAGTAACTCTGTGTTCTGGGATGGGTGTTAGGCCAA 773
QY 597 GACAGCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACATTAAGGAAGAACTTCCCTTTG 656
DB 774 GACAGCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACATTAAGGAAGAACTTCCCTTTG 833
QY 657 CAATGCTGGATTAACAGTGCATATCAATATTTCAAGGATGAGCTACTTAAGATATGAT 716
DB 834 CAATGCTGGATTAACAGTGCATATCAATATTTCAAGGATGAGCTACTTAAGATATGAT 893
QY 717 AGCCCAACTCTTGGCCCCAGTTCTCTGGATCAACTCTTGCAGAAATTCGAAGGAAGGT 776
DB 894 AGCCCAACTCTTGGCCCCAGTTCTCTGGATCAACTCTTGCAGAAATTCGAAGGAAGGT 953
QY 777 GGTGTGCAAGTACATCATCTTCTGTAGTACCTGATAGAGAGCTCAAGGAGAGAGGTA 836
DB 954 GGTGTGCAAGTACATCATCTTCTGTAGTACCTGATAGAGAGCTCAAGGAGAGAGGTA 1013
QY 837 CTTTGTGTTCTPAGATGATCTATGGATTTTACATGATTTGGAAATTTGGAATTAATTTGC 896

DB 1014 CTTTGTGTTCTPAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATTAATTTGC 1073
QY 897 ATTTCTTAAGAAACAATAAGAAAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCT 956
DB 1074 ATTTCTTAAGAAACAATAAGAAAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCT 1133
QY 957 TGGGAGAAAGTGTGCCACAGCCTCAGCTGGTGTACCACTTGATTTCTTGGCAGATGAACGA 1016
DB 1134 AGCGGAGAAAGTGTGCCACAGCCTCAGCTGGTGTACCACTTGATTTCTTGGCAGATGAACGA 1193
QY 1017 TGCCATTAACATTTGCTTACGAGAAACAAATATAAAATCATAGACATGGAATCAAAATA 1076
DB 1194 TGCCATTAACATTTGCTTACTAAGAAACAAATATAAAATCATAGACATGGAATCAAAATA 1253
QY 1077 AAATATGCAAAAGATGTTGAAACGAATTTGTAATAAATGTCGTCTGCTACCAATAGCAAT 1136
DB 1254 AAATATGCAAAAGATGTTGAAACGAATTTGTAATAAATGTCGTCTGCTACCAATAGCAAT 1313
QY 1137 ACTTACAATAGGAGCTGTGCTTGGCAACTAAACAGGTGTGAGATGGGAGAAATTTCTATGA 1196
DB 1314 ACTTACAATAGGAGCTGTGCTTGGCAACTAAACAGGTGTGAGATGGGAGAAATTTCTATGA 1373
QY 1197 ACACCTTCTCTCAGAACTAGAAATATAACCCCAAGCTTGAAGCTTTTGAGGAGAAATGCTGAC 1256
DB 1374 ACACCTTCTCTCAGAACTAGAAATATAACCCCAAGCTTGAAGCTTTTGAGGAGAAATGCTGAC 1433
QY 1257 CCTAGGTTTACAAACCACTTACCCTCCATTTGCAACCACTGCTTTTGTATCTTAAGTATCTT 1316
DB 1434 CCTAGGTTTACAAACCACTTACCCTCCATCCATCTGAAACCACTGCTTTTGTATCTTAAGTATCTT 1493
QY 1317 TCCTGAGGATTTTGAATCAAAAGGAATTCGTCTAGTAGGTAGATGAGTAGCAGAAAGGTTT 1376
DB 1494 TCCTGAGGATTTTGAATCAAAAGGAATTCGTCTAGTAGGTAGATGAGTAGCAGAAAGGTTT 1553
QY 1377 TGTTAGACCAAGGTTGGGATGACGACTTAAGGATGTCCGAGAAAGTTTACTTTAATGAGCT 1436
DB 1554 TGTTAGACCGCAGGTTGGGATGACGACTTAAGGATGTCCGAGAAAGTTTACTTTAATGAGCT 1613
QY 1437 AATCAACCGAAGTATGATTCAACCGATCAAGAGTGGGATAGCAGGAAATAATTAAGACTTG 1496
DB 1614 AATCAGCGAAGTATGATTCAACCGATCAAGAGTGGGATATCAGGAAATAATTAAGACTTG 1673
QY 1497 TCGAATTCATGATATCATCCGTGATATCAGAGTTTCAATCTCGAGACAGGAAATTTTGT 1556
DB 1674 TCGAATTCATGATATCATCCGTGATATCAGAGTTTCAATCTCGAGACAGGAAATTTTGT 1733
QY 1557 ATTAATTACCAATGGGAGATGGCTCTGATTTAGTTTACAGGAAACACTCCGCCACATAGCAAT 1616
DB 1734 ATTGTTACCAATGGGAGATGGCTCTGATTTAGTTTACAGGAAACACTCCGCCACATAGCAAT 1793
QY 1617 CCATGGGAGTATGCTCGCAAAACCTGGATTCGATTCGATTCGAGCAATTTCCATCATTTAGCTAT 1676
DB 1794 CCATGGGAGTATGCTCGCAAAACAGGATTCGATTCGATTCGAGCAATTTCCATCATTTAGCTAT 1853
QY 1677 TTTTGGTGACAGACCCCAAGAGCTTAGCAGCTGAGTTTGTCCAGATCAATTTGAGGATGTT 1736
DB 1854 TTTTGGTGACAGACCCCAAGAGCTTAGCAGCTGAGTTTGTCTAGATCAATTTGAGGATGTT 1913
QY 1737 ACGGGTCTTGATCTTGAAGATGTGACATTTCTTAATCTCACTCAAAAGATTTTCGACCGTAT 1796
DB 1914 ACGGGTCTTGATCTTGAAGATGTGACATTTCTTAATCTCACTCAAAAGATTTTCGACCGTAT 1973
QY 1797 TGCAATGTTGTCACCTTGAATACTTGAATTTGGATTTGGATATTTCCATCATATTTTCACT 1856
DB 1974 TGCAATGTTGTCACCTTGAATACTTGAATTTGGATATTTGGATATTTCCATCATATTTTCACT 2033
QY 1857 TCCAGAGTCCAATTCGTAAAATAACAGGCTTACAACTTTTGAACATTCGCCGAGACATACAT 1916
DB 2034 TCCAGAGTCCAATTCGTAAAATAACAGGCTTACAACTTTTGAACATTCGCCGAGACATACAT 2093
QY 1917 TGCAGCACTACCAAGTGAAGATCAGTAACTCCAATGCTGCAATCTCTTCTGTTGATAGG 1976

Db 2094 TGCAGCACTACCAAGTGAGATCAGTAATACTCCAAATGCTGCATATCTCTTCGTTGTAGTAG 2153
Qy 1977 ACAGTTTCATTATGACAACTTTAGTCTAAACACCCCAATGAAGTGCATAAATCAACACAAAT 2036
Db 2154 AAAGTTTGTTTATGACAACTTTAGTCTAAACACCCCAATGAAGTGCATAAATCAACAAAT 2213
Qy 2037 ATGCTGCTCTAAAGTATTTACACCTTTTATGTCGCGATGATCGTCAAAACAAATTCG 2096
Db 2214 ATGCTGCTCTAAAGTATTTACACCTTTTATGTCGCGATGATCGTCAAAACAAATTCG 2273
Qy 2097 TGAATTCGACATGCGCACAAAGTGTGCTGTGTAATCAATCGGTGGAAGGTACCCAA 2156
Db 2274 TGAATTCGACATGCGCACAAAGTGTGCTGTGTAATCAATCGGTGGAAGGTACCCAA 2333
Qy 2157 AGGAATAGTAAAGTTGCGAGACTTGCAGGTCTTAGAGTATGATGATATCAGCGGACAG 2216
Db 2334 AGGAATAGTAAAGTTGCGAGACTTGCAGGTCTTAGAGTATGATGATATCAGCGGACAG 2393
Qy 2217 TAGTAGAGCAATCAAGAGCTGGGCACTTAAAGCAAGCTGAGGAAATTAGGTGTGACAA 2276
Db 2394 TAGTAGAGCAATCAAGAGCTGGGCACTTAAAGCAAGCTTAAAGCAAGCTTAAAGGTGATA 2453
Qy 2277 AAACGGGTGCAAAAGGAAATGTAAGTACTTTATGACGCCATTTGAGAGCTCTCTTC 2336
Db 2454 AAAGGGCTCGACAAAGGAAATGTAAGTACTTTATGACGCCATTTGAGAGCTCTCTTC 2513
Qy 2337 CCTCCATCTCTCATGTGGATGCTGCAGGATCTCAGATGCTGGAACACATTTAGTGCCT 2396
Db 2514 CCTCCATCTCTCATGTGAATGCTGCGTTATATCAGATATGAAACACATTTAGTGCCT 2573
Qy 2397 AGATTCTATTTCACTCTCTCCCTACTGAGGACACTCGTGTGGAATGGAATTTCTGA 2456
Db 2574 AGATTCTATTTCACTCTCTCCCTACTGAGGACACTCGGTTGGAATGGAATTTCTGA 2633
Qy 2457 GGAGATGCTAACTGGAATGAGAGCTCACTCACTGAAAGAGTCTACTTATTGAGGAG 2516
Db 2634 AGAGATGCTAACTGGAATGAGAGCTCACTCACTGAAAGAGTCTACTTATTGAGGAG 2693
Qy 2517 CAATAAGAGAGTAAACCATGCTGATACTTTGGGCACTGCCCACTCATGTTGCT 2576
Db 2694 CAATAAGAGAGTAAACCATGCTGATACTTTGGGCACTTGCCCACTCATGTTGCT 2753
Qy 2577 TCATCTTTATCGGAATGCTTACCTTTGGGGAAGCTAGTATTTCAAAACAGGAGCATTTCCC 2636
Db 2754 TTATCTTTATGGAATGCTTACCTTTGGGGAAGCTAGTATTTCAAAACAGGAGCATTTCCC 2813
Qy 2637 AAATCTTAGAACACTTTGGATTTATGAATTTGATCAGCTAAGAGAGTCAAGTTGAGGA 2696
Db 2814 AAATCTTAGAACACTTCGTATTTACGAATTTGGATCAGCTAAGAGAGTCAAGTTGAGGA 2873
Qy 2697 CGGAGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTTGGAAATCTGGGAT 2756
Db 2874 TGGCAGCTCACCCCTGTTGGAAAGATAGAAATCTTTGCTGCGAGTTGGAAATCAGGAT 2933
Qy 2757 TACTGGTATCATTCACCTTTCCAAAGCTCAAGAGATTTCCAAATTAGATACGGAAGTAAAGT 2816
Db 2934 TATTGGTATCATTCACCTTTCCAAAGCTCAAGAGATTTCACTTGAATACAAAGTAAAGT 2993
Qy 2817 GGCTGGGCTTGCTCAGCTGGAGGAGAGTGAAGTGAACGACACCCCAATGCCCGCTGCTGCT 2876
Db 2994 GGCTAGGCTTGCTCAGCTGGAGGAGAGTGAACGACACCAATGCCCGCTGCTGCTGCTGCG 3053
Qy 2877 AATGTACAGTACCGAAGGTATCAGACCTGGGGCTGGAAGCGAAGGATCTTCTATAGA 2936
Db 3054 AATGTACAGTACCGAAGGATTCAGACCTGGGGCTGGAAGCGAAGGATCTTCTATAGA 3113
Qy 2937 AGTGCAAACAGCAGATCTCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAGC 2996
Db 3114 AGTGCNAACAGCAGATCTCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAGC 3173
Qy 2997 AACGGATCCCTTCCCGAGCAGGAGGAGAGTGTGCGAGTGTGCGAGGTGATCACTGTGAC 3056
Db 3174 AACGGATCCCTTCCCGAGCAGGAGGAGAGTGTGCGAGTGTGCGAGGTGATCACTGTGAC 3233

Qy 3057 GACCAATGATAGCGAAGATAGGACAGCTCAAGCTGAGCTGGA 3099
Db 3234 GACCAAGATAGCGAAGATAGGACAGCTCAAGCTGAGCTGGA 3276

RESULT 6
ADIS7166
ID ADIS7166 standard; DNA; 76272 BP.
XX
AC ADIS7166;
XX
DT 22-APR-2004 (first entry)
XX
DE Oryza minuta P19 locus genomic DNA sequence.
XX
KW nucleotide binding site; NBS; P19; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; ds.
XX
OS Oryza minuta.
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JAN-2003; 2003US-00352179.
XX
PR 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX
(WANG/) WANG G.
PA (LIU/) LIU G.
XX
PI Wang G, Liu G;
XX
DR WPI; 2004-121064/12.
PT
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
PS Disclosure; SEQ ID NO 83; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents the Oryza minuta
CC P19 locus.
SQ Sequence 76272 BP; 22112 A; 16049 C; 16316 G; 21795 T; 0 U; 0 Other;

Query Match 91.0%; Score 2820.4; DB 12; Length 76272;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2872; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 116 GGTATATCAAGATGAGCTAAAGAGATGCAAGCATTCCTTAGAGCTGCTGAACCTATGA 175
Db 62061 GGTATATCAAGATGAGCTAAAGAGATGCAAGCATTCCTTAGAGCTGCTGAACCTATGA 62120
Qy 176 AAAAGAAAGATGAACTATTAAAGGTTTGGGAGAGCAAAATACGTGACCTGTCATATGACA 235
Db 62121 AAAAGAAAGATGAACTATTAAAGGTTTGGGAGAGCAAAATACGTGACCTGTCATATGACA 62180
Qy 236 TTGAAGATTCCTTGATGAATTTAAGGTCCATATTGAAGCCAAACCCCTATTTCGTCAGT 295
Db 62181 TTGAAGATTCCTTGATGAATTTAAGGTCCATATTGAAGCCAAACCCCTATTTCGTCAGT 62240
Qy 296 TGGTGAAGTACAGAGAGCGCCAGCAATTCGATTCGATCCGATCCCAACCTTAAATCAAGAG 355
Db 62241 TGGTGAAGTACAGAGAGCGCCAGCAATTCGATTCGATTCGATCCCAACCTTAAATCAAGAG 62300
Qy 356 TTGAAGAAAGTGAAGTAGCAGGAGCAACACGCTACAGTTTAGTCAAGCCTATTTCCTCTGGCA 415

Db	62301	TTGAAGAGTGTAGTAGCAGGAACACACGCTACAGTTTGTAGTCAAGCCTATTTCCCTCTGGCA	62360
Qy	416	CAGAGATTGAACATGATTTCTATGACAGGAACATTCGTAATCAGTCAGCTCGCAATGTGG	475
Db	62361	CAGAGATTGACATGATTTCTATGACAGGAACATTCGTAATCAGTCAGCTCGCAATGTGG	62420
Qy	476	ATGAGCTGAGCTTGTGGGTTTCTGACTCAAGAAAAGGTGCTGGAATGATCGATA	535
Db	62421	ATGAAGCTGAGCTTGTGGGTTTCTGACTCAAGAAAAGGTGCTGGAATGATCGATA	62480
Qy	536	CCAAATGCTAAATGATGCTCCGCCAAGTAATCTGTGTTGGATGGGTGTTAGGCA	595
Db	62481	CCAAATGCTAAATGATGCTCCGCCAAGTAATCTGTGTTGGATGGGTGTTAGGCA	62540
Qy	596	AGACAGCTCTTTTCAGGAAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTT	655
Db	62541	AGACAGCTCTTTTCAGGAAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTT	62600
Qy	656	GCAATGCTTGGATTACAGTGTCAACATCTTTCACAGATTTAGACTCTTAAAGATATGA	715
Db	62601	GCAATGCTTGGATTACAGTGTCAACATCTTTCACAGATTTAGACTCTTAAAGATATGA	62660
Qy	716	TACGCCAACTCTTGGCCCGAGTCTCTGGATCACTCTTCGCAAACTTTCGCAAGATTTGCAAGGGAAG	775
Db	62661	TACGCCAACTCTTGGCCCGAGTCTCTGGATCACTCTTCGCAAACTTTCGCAAGATTTGCAAGGGAAG	62720
Qy	776	TGGTGGTGCAAGTACATCATCTTTCTGAGTAGTACCTGATAGAGAGCTCAAGGAGAAAGGT	835
Db	62721	TGGTGGTGCAAGTACATCATCTTTCTGAGTAGTACCTGATAGAGAGCTCAAGGAGAAAGGT	62780
Qy	836	ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGAAATTTG	895
Db	62781	ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGAAATTTG	62840
Qy	896	CATTTCCTTAAGAACATTAAGAGGCGAGTCGAAATAGTAATAACCACTCGGAATGTTGATC	955
Db	62841	CATTTCCTTAAGAACATTAAGAGGCGAGTCGAAATAGTAATAACCACTCGGAATGTTGATC	62900
Qy	956	TTGCGGAGAAGTGTGCCACAGCTCACCTGGTGTACCACTTGATTTCTGACAGATGAACG	1015
Db	62901	TAGCGGAGAAGTGTGCCACAGCTCACCTGGTGTACCACTTGATTTCTGACAGATGAACG	62960
Qy	1016	ATGCCATAACATTTGCTACTGAGAAAACAAATAAAAAATCATCAAGACATGGAATCAATA	1075
Db	62961	ATGCCATAACATTTGCTACTGAGAAAACAAATAAAAAATCATCAAGACATGGAATCAATA	63020
Qy	1076	AAATATATCAAAAGATGTTGAAACGAATTTGAAATTAATTAATGTTGCTCTACATAGCAA	1135
Db	63021	AAATATATCAAAAGATGTTGAAACGAATTTGAAATTAATTAATGTTGCTCTACATAGCAA	63080
Qy	1136	TACTTTACAAATAGGAGCTGTCTTGCAACTTAACACAGTGTCAAGATGGGAGAAAATTTCTATG	1195
Db	63081	TACTTTACAAATAGGAGCTGTCTTGCAACTTAACACAGTGTCAAGATGGGAGAAAATTTCTATG	63140
Qy	1196	AACACCTTCTTTTCAGAACTAGAAAATAAACCCCAAGCTTGGAAAGCTTTGAGGAGAAATGTTGA	1255
Db	63141	AACACCTTCTTTTCAGAACTAGAAAATAAACCCCAAGCTTGGAAAGCTTTGAGGAGAAATGTTGA	63200
Qy	1256	CCCTAGGTTACAAACACCTACATCCCATTTGAAACCATGCTTTTGTGTATCTAAGTATCT	1315
Db	63201	CCCTAGGTTACAAACACCTACATCCCATTTGAAACCATGCTTTTGTGTATCTAAGTATCT	63260
Qy	1316	TTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAGGGT	1375
Db	63261	TTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAGGGT	63320
Qy	1376	TTGTTAGACCAAGGTGCGGATGACGACTTAAGGATGTCGGGAAAGTTACTTTTAAATGAGC	1435
Db	63321	TTGTTAGACCGAGGTGCGGATGACGACTTAAGGATGTCGGGAAAGTTACTTTTAAATGAGC	63380
Qy	1436	TAATCAACCGAAGTATGATTTCAACGATCAAGTGGGCATGACGAGAAAATTTAAGACTT	1495

Db	63381	TAATCAGCCGAAGTATGATTTCAACGATCAAGAGTGGGCATATCAGGAAAAAATTAAGACTT	63440
Qy	1496	GTGGAATTCATGATATCATCCGTGATATCAAGATTTCAATCTCGAGACAGAAAAATTTTG	1555
Db	63441	GTGGAATTCATGATATCATCCGTGATATCAAGATTTCAATCTCGAGACAGAAAAATTTTG	63500
Qy	1556	TATTTATACCAATCGGAGATGGCTCTGATTTAGTTTCAGGAAAAACACTCGCCACATAGCAT	1615
Db	63501	TATTTATACCAATCGGAGATGGCTCTGATTTAGTTTCAGGAAAAACACTCGCCACATAGCAT	63560
Qy	1616	TCCATGGAGTATGCTCTGCAAAAACAGTATGGAATTTGAGCATTTATTCGATCTTAGCTA	1675
Db	63561	TCCATGGAGTATGCTCTGCAAAAACAGTATGGAATTTGAGCATTTATTCGATCTTAGCTA	63620
Qy	1676	TTTTTGGTGACAGACCCAAAGAGCTTAGCACATGCAAGTTTGTCCAGATCAATTTGAGGATGT	1735
Db	63621	TTTTTGGTGACAGACCCAAAGAGCTTAGCACATGCAAGTTTGTCTAGATCAATTTGAGGATGT	63680
Qy	1736	TACGGGTCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTA	1795
Db	63681	TACGGGTCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTA	63740
Qy	1796	TTGCATTTGTTGTGCCACTTGAAATACCTTGAGTAATGGATATTTGTCATCCATATATTAC	1855
Db	63741	TTGCATTTGTTGTGCCACTTGAAATACCTTGAGTAATGGATATTTGTCATCCATATATTAC	63800
Qy	1856	TTCCAGATTCATTTGGTAAACTACAGGGCTTACAAACTTTGAACTGCGGAGCACATACA	1915
Db	63801	TTCCAGATTCATTTGGTAAACTACAGGGCTTACAAACTTTGAACTGCGGAGCACATACA	63860
Qy	1916	TTGACGACATACCAAGTGAGATTCAGTAAATCTTCAATGTCGCATATCTCTTCGTTGTATAG	1975
Db	63861	TTGACGACATACCAAGTGAGATTCAGTAAATCTTCAATGTCGCATATCTCTTCGTTGTATAG	63920
Qy	1976	GACATTTTCAATTAAGACAACTTTTAGTCTTAAACCAACCACTTAAAGTGCATATACTAACAA	2035
Db	63921	GAAAGTTTGTTTTAGACAACTTTTAGTCTTAAACCAACCACTTAAAGTGCATATACTAACAA	63980
Qy	2036	TATCCCTGCCTTAAAGTATTTCAACCTTTAGTTAGTTCGCGATGATCGTSCAAAAACAATTTG	2095
Db	63981	TATCCCTGCCTTAAAGTATTTCAACCTTTAGTTAGTTCGCGATGATCGTSCAAAAACAATTTG	64040
Qy	2096	CTGAATTTGCACATGGCCACCAAAAAGTTGCTGGTCTGAAATCAATCGGTGTGAAGGTACCCA	2155
Db	64041	CTGAATTTGCACATGGCCACCAAAAAGTTGCTGGTCTGAAATCAATCGGTGTGAAGGTACCCA	64100
Qy	2156	AAGGAATAGGTAAAGTTCGGAGACTTGCAGAGTTCTAGAGTATGTAGATATCAGGCGGACCA	2215
Db	64101	AAGGAATAGGTAAAGTTCGGAGACTTGCAGAGTTCTAGAGTATGTAGATATCAGGCGGACCA	64160
Qy	2216	GTAGTAGAGCAATCAAAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAAATTAGGTGTGACAA	2275
Db	64161	GTAGTAGAGCAATCAAAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAAATTAGGTGTGATAA	64220
Qy	2276	CAAAACGGGTGCACAAAAGGAAAAATGTAAGATACTTTATGACAGCCATTGAGAAGCTCTCTT	2335
Db	64221	CAAAACGGGTGCACAAAAGGAAAAATGTAAGATACTTTATGACAGCCATTGAGAAGCTCTCTT	64280
Qy	2336	CCCTCCAATCTCTCCATGTCGATGCTCAGGAATCTCAGATGGTGGACACTTCAGTGTGCC	2395
Db	64281	CCCTCCAATCTCTCTATGTGAATCTCGGTTATTTATCAGATATTGAAACACTTCAGTGTGCC	64340
Qy	2396	TAGATTTCTATTTCACTCTCCCTCTCTGAGGACACTCGTGTGGATGGAAATTTCTTTG	2455
Db	64341	TAGATTTCTATTTCACTCTCTCCCTCTCTGAGGACACTCGGTTGAAATGGAAAGTCTTTG	64400
Qy	2456	AGGAGATGCTTAATCTGATGAGCAGCTCACTCACTGAAAGAAATCTTACTTTATTTAGGA	2515
Db	64401	AAGAGATGCTTAATCTGATGAGCAGCTCACTCACTGAAAGAAATCTTACTTTATTTAGGA	64460
Qy	2516	GCAAACTTAAGGAGGTAAACCACTGATCTATTTGGGGCACTGCCCACTCATGGTCC	2575
Db	64461	GCAAACTTAAGGAGGTAAACCACTGATCTATTTGGGGCACTGCCCACTCATGGTCC	64520

QY 2576 TTTCATCTTTATCGGAATGCTTACCTTGGGGAAGCTAGTATTCAAAACAGGAGCATTC 2635
DB 64521 TTTATCTTTATGGATGCTTACCTTGGGGAAGCTAGTATTCAAAACAGGAGCATTC 64580
QY 2636 CAAATCTTAGAACACTTGGTATTTATGAAATGGATCAGCTAAGAGAGATCAGATTTGAGG 2695
DB 64581 CAAATCTTAGAACACTTGGTATTTACGAATTTGGATCAGCTAAGAGAGATGAGATTTGAGG 64640
QY 2696 ACGGAGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTTGGAATCTGGGA 2755
DB 64641 ATGGCAGCTCACCCCTGTTGGAAAGATAGAAATCTTGTGTCAGGTTGGAATCAGGGA 64700
QY 2756 TTACTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATCCAAATTAGATACGGAAGTAAAG 2815
DB 64701 TTATTTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCACTTGAATACAAAGTAAAG 64760
QY 2816 TGGCTGGGCTTTGGTCAGCTGGAGGAGAGTGAACGCAACCCAAATCGCCCGTGTGTC 2875
DB 64761 TGGCTAGGCTTTGGTCAGCTGGAGGAGAGTGAACACACACCCAAATCGCCCGTGTGTC 64820
QY 2876 TAATGTACAGTCACCGAAGGTATCACGACCTGGGGGCTGAAGCCGAGGATCTTCTATAG 2935
DB 64821 GAAATGGACAGTGAACGAAGGATCACGACCTGGGGGCTGAAGCCGAGGATCTTCTATAG 64880
QY 2936 AAGTGCAAAACAGCAGATCCTGTTCTGATGCGAAGGATCAGTCACTGTAGCAGTGGAAAG 2995
DB 64881 AAGTGCAAAACAGCAGATCCTGTTCTGATGCGAAGGATCAGTCACTGTAGCAGTGGAAAG 64940
QY 2996 CAACGGATFCCCTTTCCGAGCAGGAGGAGAGAGCTCGCAGTCGCGAGGTGATCAGTTGA 3055
DB 64941 CAACGGATFCCCTTTCCGAGCAGGAGGAGAGAGCTCGCAGTCGCGAGGTGATCAGTTGA 65000
QY 3056 CGACGAATGATAGCGAAG 3073
DB 65001 CGACGAACGATAGGTGTCAG 65018

RESULT 7

ADM72248
ID ADM72248 standard; cDNA; 2997 BP.

XX AC ADM72248;

XX DT 03-JUN-2004 (first entry)

XX DE O. minuta NBS6 polypeptide encoding cDNA.

XX KW Pi2; NBS6; plant protectant; gene therapy; rice; disease resistance;
XX KW gene; ss.

XX OS Oryza minuta.

XX FH Key Location/Qualifiers
XX FT CDS 1. .2997
XX FT /*tag= a
XX FT /product= "NBS6"

XX FN WO2004022715-A2.

XX PD 18-MAR-2004.

XX PP 08-SEP-2003; 2003WO-US027913.

XX PR 09-SEP-2002; 2002US-0409216P.

XX PR 18-MAR-2003; 2003US-0455713P.

XX PR 05-SEP-2003; 2003US-00656394.

XX PA (OHIS) UNIV OHIO STATE.

XX PI Wang G;

XX DR WPI; 2004-257576/24.

DR P-PSDB; ADM72249.

XX New rice Pi2-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.

XX Claim 1; SEQ ID NO 11; 120pp; English.

XX The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA
CC encoding a rice NBS6 polypeptide.

XX Sequence 2997 BP; 874 A; 607 C; 723 G; 793 T; 0 U; 0 Other;

Query Match 77.2%; Score 2393.6; DB 12; Length 2997;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 2453; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 422 TTGACATGGATTCTCTATGCAAGACACATTCTGTAATCAGTCAGCTCGCAATGTGATGAGG 481
DB 197 TAGCAATAGATTCTATGCAAGACATTTCGAATCAATCAGCTCGAAATGTGATGAG 256
QY 482 CTGAGCTGTGTGGGTTTTCTGACTCCAAGAAAAGGCTCTTGAATGATCGATACCAATG 541
DB 257 CTGAGCTGTGTGGGTTTTCTGACTCCAAGAAAAGGCTCTTGAATGATCGATACCAATG 316
QY 542 CTAAATGATGGTCCGGCCAAAGTAAATCTGTGTTGGGATGGGTGGTTTAGGCAAGACAG 601
DB 317 CTAAATGATGGTCCGGCCAAAGTAAATCTGTGTTGGGATGGGTGGTTTAGGCAAGACAG 376
QY 602 CTCTTTTCGAGGAAGATCTTTGAAGCGAAGACATTAGGAAGAACTTCCCTTTGCAATG 661
DB 377 CTCTTTTCGAGGAAGATCTTTGAAGCGAAGACATTAGGAAGAACTTCCCTTTGCAATG 436
QY 662 CTTGGATTACAGTGTCAATCTTTACAGGATTTGAGCTACTTTAAAGATATGATACGCC 721
DB 437 CTTGGATTACAGTGTCAATCTTTACAGGATTTGAGCTACTTTAAAGATATGATACGCC 496
QY 722 AACTTCTTGGCCCGAGTTCTCTGGATCAACTCTTTGCAAGAAATTCGAAGGAGGTGGTG 781
DB 497 AACTTCTTGGCCCGAGTTCTCTGGATCAACTCTTTGCAAGAAATTCGAAGGAGGTGGTG 556
QY 782 TGCAAGTACATCATCTTTCTGAGTACCTGTAGAAGAGCTCAAGGAGAGGTACTTTTG 841
DB 557 TGCAAGTACATCATCTTTCTGAGTACCTGTAGAAGAGCTCAAGGAGAGGTACTTTTG 616
QY 842 TTGTTCTAGATGATCTATGGATTTTACATGATTGGAATTTGGATAAATGAAATTCATTTTC 901
DB 617 TTGTTCTAGATGATCTATGGATTTTACATGATTGGAATTTGGATAAATGAAATTCATTTTC 676
QY 902 CTAAGAAACAATAAGAGGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGGCG 961
DB 677 CTAAGAAACAATAAGAGGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGGCG 736
QY 962 AGAAGTGTGCCACAGCTCACTGGTGTACCACCTTGTATTTCTTCAGATGAACGATGCCA 1021
DB 737 AGAAGTGTGCCACAGCTCACTGGTGTACCACCTTGTATTTCTTCAGATGAACGATGCCA 796
QY 1022 TAACATTTGCTACTGAGAAAAACAAATAAAATCAATGAAGACATGGAATCAAAATAAATA 1081
DB 797 TAACATTTGCTACTGAGAAAAACAAATAAAATCAATGAAGACATGGAATCAAAATAAATA 856
QY 1082 TGC AAAAGATGGTTGAACGAATTTGTAATAAATGTTGTTGCTCTACCATTAGCAATACTTAA 1141
DB 857 TGC AAAAGATGGTTGAACGAATTTGTAATAAATGTTGTTGCTCTACCATTAGCAATACTTAA 916
QY 1142 CAATAGGAGCTGTGCTTTGCAACTAAACAGGTGTGAGAAATTTCTTATGAACACC 1201
DB 917 CAATAGGAGCTGTGCTTTGCAACTAAACAGGTGTGAGAAATTTCTTATGAACACC 976
QY 1202 TTCCTTCAGAACTAGAAAAAACCACCGCTGGAAAGCTTTTGAGGAGAAATGGTGACCCCTAG 1261

Db 977 TTTCTTTCAGAACTAGAAATAAACCCAGCCTGGGAAGCTTTGAGGAGAATGGTGACCCTAG 1036
Qy 1262 GTTAAACACCACTACCATCCCATTTGAAACCACTGCTTTTGTGTATCTAAGTATCTTTCTCTG 1321
Db 1037 GTTAAACACCACTACCATCCCATCTGAAACCACTGCTTTTGTATCTAAGTATCTTTCTCTG 1096
Qy 1322 AGGATTTTGAATCAAAAAGGAATCGTCTAGTAGGTAGATGATGATAGCAGAGGGTTTGTGA 1381
Db 1097 AGGATTTTGAATCAAAAAGGAATCGTCTAGTAGGTAGATGATGATAGCAGAGGGTTTGTGA 1156
Qy 1382 GACCAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTTACTTTTAATCAGCTAATCA 1441
Db 1157 GACCAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTTACTTTTAATCAGCTAATCA 1216
Qy 1442 ACCGAAGTATGATTCACACGATCAAGAGTGGGATAGCAGGAAATAAAGACTTTGTGAA 1501
Db 1217 ACCGAAGTATGATTCACACGATCAAGAGTGGGATAGCAGGAAATAAAGACTTTGTGAA 1276
Qy 1502 TTATGATATCATCGGTGATATCAAGTTTCAATCTCGAGACAGGAAATTTTGTATAT 1561
Db 1277 TTATGATATCATCGGTGATATCAAGTTTCAATCTCGAGACAGGAAATTTTGTATAT 1336
Qy 1562 TACCAATCGGAGATGGCTCTGATTTAGTTTCAAGGAAACACTCGCCACATAGCATTTCCATG 1621
Db 1337 TACCAATCGGAGATGGCTCTGATTTAGTTTCAAGGAAACACTCGCCACATAGCATTTCCATG 1396
Qy 1622 GGAGTATGCTCTGCAAACTGGATTTGGATTTGGAGCATTTATTCGATCATTAGCTATTTTGTG 1681
Db 1397 GGAGTATGCTCTGCAAAACAGATTTGGATTTGGAGCATTTATTCGATCATTAGCTATTTTGTG 1456
Qy 1682 GTGACAGACCAAGAGTCTAGCACATGCAATGTTTGTCCAGATCAATTTAGGAGTTTACGGG 1741
Db 1457 GTGACAGACCAAGAGTCTAGCACATGCAATGTTTGTCCAGATCAATTTAGGAGTTTACGGG 1516
Qy 1742 TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATTCGAT 1801
Db 1517 TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATTCGAT 1576
Qy 1802 TGTGTGCGCACTTGAATATCTTGAATTTGGATTTGGATTTCTGATCCATATATTTCACTTTCCA 1861
Db 1577 TGTGTGCGCACTTGAATATCTTGAATTTGGATTTGGATTTCTGATCCATATATTTCACTTTCCA 1636
Qy 1862 GATCATTTGGTAACTACAGGCGCTACAACTTTGAAACATCCGAGCACATACATTTGCAG 1921
Db 1637 GATCATTTGGTAACTACAGGCGCTACAACTTTGAAACATCCGAGCACATACATTTGCAG 1696
Qy 1922 CACTACCAAGTGAGATCAGTAACTCCAACTGTCTGCATACCTTCTCGTTGTATAGCACAGT 1981
Db 1697 CACTACCAAGTGAGATCAGTAACTCCAACTGTCTGCATACCTTCTCGTTGTATAGTAAAGT 1756
Qy 1982 TTCATTATGACAACTTTAGTCTAAACCAACCACTGAAGTGCATAACTAAACAATATATGCC 2041
Db 1757 TTGTTCTGACAACTTTAGTCTAAACCAACCACTGAAGTGCATAACTAAACAATATATGCC 1816
Qy 2042 TGCCTAAAGTATTCACACTTTAGTTAGTTCGCGATGATCGTGCAAAACAAATTTGCTGAAT 2101
Db 1817 TGCCTAAAGTATTCACACTTTAGTTAGTTCGCGATGATCGTGCAATAACAATTTGCTGAAT 1876
Qy 2102 TGCACATGGCCACCAAAAGTTGCTGGTCTGATTCATTCGCGTGTGAAGTATCCCAAGGAA 2161
Db 1877 TGCACATGGCCACCAAAAGTTGCTGGTATAAATCAATTCGCGTGTGAAGTATCCCAAGGAA 1936
Qy 2162 TAGGTAAGTTCGGAGACTTTCAGGTTCTTAGAGTATGTAGATATCAGGCGGACCAAGTAGTA 2221
Db 1937 TAGGTAAGTTCGGAGACTTTCAGGTTCTTAGAGTATGTAGATATCAGGCGGACCAAGTAGTA 1996
Qy 2222 GAGCAATCAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAAATTAGGTTGTGACAAACAACG 2281
Db 1997 GAGCAATCAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAAATTAGGTTGTGATGACAAATG 2056
Qy 2282 GGTGCAAAAGGAAAAATGTAAGTATCTTTATGAGGCCATTTGAGAAGCTCTCTTCCCTCC 2341

Db 2057 GCTCGACAAGGAAAAATGTAAGATACCTTTGTGCAGCCATTTGAGAAGCTCTCTTCCCTCC 2116
Qy 2342 AATCTCTCCATGTGGATGCTGTCAGGAATCTCAGATGGTGGAACTTTGAGTGCCTAGATT 2401
Db 2117 AATATCTCTATGTGAATGCTGCAGGAATCTCAGATGGTGGAACTTTGAGTGCCTAGATT 2176
Qy 2402 CTATTTTCATCTCTCTCTCCCTACTCTAGGACACCTGCTGTTGGATGGAATCTTTGAGGAGA 2461
Db 2177 CTATTTCTCTCTCTCTCTCCCTACTCTAGGACACCTGCTGTTGGATGGAATCTTTGAGGAGA 2236
Qy 2462 TGCCTAACTGATTTGAGCAGCTCACTCAGCTGAAAGAGATCTACTTTATTTAGGAGCAAAAC 2521
Db 2237 TGCCTAACTGATTTGAGCAGCTCACTCAGCTGAAAGAGATCTACTTTATTTAGGAGCAAAAC 2296
Qy 2522 TAAAGGAGGTAAACCATGCTGATCTTGGGGCACTGCCCCAACCCTCATGCTCTTTCATC 2581
Db 2297 TAAAGGAGGTAAACCATGCTGATCTTGGGGCACTTGGGGCACTTGGGGCACTTGGGGCACT 2356
Qy 2582 TTTATCGGAATGCTTACTTGGGGAGAACTAGTATTTCAAACAGGAGCATTTCCAAATC 2641
Db 2357 TTTATCGGAATGCTTACTTGGGGAGAACTAGTATTTCAAACAGGAGCATTTCCAAATC 2416
Qy 2642 TTAGAACACTTTTGGATTTATGAAATTTGGATCAGCTAAGAGAGATCAGATTTTCAGGACGCA 2701
Db 2417 TTAGAACACTTTTGGATTTATGAAATTTGGATCAGCTAAGAGAGATTTAGATTTTGGAGACGCA 2476
Qy 2702 GCTCACCCCTGTTGGAAAAAGATAGAAATAGCCAGTGCAGGTTGGAATCTGGGATTTACTG 2761
Db 2477 GCTCGCCCACTGTTGGAAAAAGATAGAAATAGATTTCTGCAGGTTGGAATCAGGGATTTATG 2536
Qy 2762 GTATCATTTCACTTTCCAAAGCTCAAGGAGATTTCAAATTTAGATAGCGAAGTAAAGTGGCTG 2821
Db 2537 GTATTTATCCACTTTCCAAAGCTCAAGGAGATTTTCACTTTGGATAGGAAAGTAAAGTGGCTG 2596
Qy 2822 GGCTTGTCTAGCTGGAGGAGAGTGAACGACACCCAAATCGCCCGCTGCTGCTAAATGT 2881
Db 2597 GGCTTGTCTAGCTGGAGGAGAGTGCACACACCCAAATCGCCCGCTGCTGCTGAAAGA 2656
Qy 2882 ACAGTGACCAAGGATATCAGACCTGGGGGCTGAAGCCGGAAGGATCTTTCTATAGAAGTGC 2941
Db 2657 GGGAGGACCGAAGTATCAGGACCTTCTTGTGACGCGGAAGGATCCCTGTTTGAAGTGG 2716
Qy 2942 AAACAGCAGATCTCTGTTTCTGATGCCGAAGA 2973
Db 2717 AAGCAACGGATCCCTCCAGAGCAGGAGGA 2748

RESULT 8
ADM72252
ID ADM72252 standard; cDNA; 2422 BP.
XX
AC ADM72252;
XX
DT 03-JUN-2004 (first entry)
XX
DE O. minuta Pi2 region fragment cDNA-21.
XX
KW Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance;
XX gene; 88.
OS Oryza minuta.
XX
FN WO2004022715-A2.
XX
PD 18-MAR-2004.
XX
PF 08-SEP-2003; 2003WO-US027913.
XX
PR 09-SEP-2002; 2002US-0409216P.
XX
PR 18-MAR-2003; 2003US-0455713P.
XX
PR 05-SEP-2003; 2003US-00656394.
XX
PA (OHIS) UNIV OHIO STATE.

KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
 KW plant breeding; transgenic plant; plant; gene; ds.
 XX
 OS Oryza minuta.
 XX
 PN US2004006798-A1.
 XX PD 08-JAN-2004.
 XX
 PF 27-JAN-2003; 2003US-00352179.
 XX
 PR 25-JAN-2002; 2002US-0352106P.
 PR 01-FEB-2002; 2002US-0353304P.
 XX
 PA (WANG/) WANG G.
 PA (LIU/) LIU G.
 XX
 PI Wang G, Liu G;
 XX
 DR WPI; 2004-121064/12.
 DR P-PSDB; ADI57174.
 XX
 PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
 PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
 PT infection.
 XX
 PS Claim 3; SEQ ID NO 90; 136pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of nucleotide
 CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
 CC blight and rice blast resistance genes). The DNA sequences may be used as
 CC markers for resistance to infection with Magnaporthe grisea in plant
 CC breeding programs. The present DNA sequence represents an NBS gene from
 CC the Oryza minuta Pi9 locus.
 XX
 SQ Sequence 3220 BP; 990 A; 616 C; 747 G; 867 T; 0 U; 0 Other;

Query Match 50.8%; Score 1574.2; DB 12; Length 3220;
 Best Local Similarity 72.8%; Pred. No. 0;
 Matches 2168; Conservative 0; Mismatches 763; Indels 46; Gaps 9;

QY 1 ATGGGGAGAGCGTCTGAGCATGCGGAGTGGTGGGAGCGCCATCAGCAAGGCC 60
 DB 1 ATGGCGGATACAGTACTCAGCATTCGAAAGTCCCTGGTGGGAGTGGTGAAGCGTT 60
 QY 61 GCCTCCGCTGCTGCCGAGCAGACAGCTCCTGCTGGGCGTGGAGAGACATCTGGTAT 120
 DB 61 GCTTCGGTGGCGCAGACAAGATGATCATGCTGCTGGGAGTGCAGAGGAGATATGGTTC 120
 QY 121 ATCAAGATGAGCTAAAAACGATGCAAGCATTCCTTAGAGCTGCTGAACTTATGAAAAAG 180
 DB 121 ATCAAGATGAGCTACAAACGATACAGCATTTTGTGTTGCTGCCGA--GCATCAAG 177
 QY 191 AAGATGAATATTAAGGTTGGGAGAGCAAAATACGTGACCTGTCTATATGACATTGAA 240
 DB 178 AAAAGCATACTATTGAAGGTTGGGAGCAGCAAGTAAGGATCTTTCCTATGACATTGAA 237
 QY 241 GATTCCTTGTATGATTTAAGTCCATATTGAAGCCAAACCTATTTGCTCAGTTGGTG 300
 DB 238 GATTCCTTGTATGATTTAAGTCTCATGTGGGAGCCAAACCTTGTGAGGAGGTTGATG 297
 QY 301 AAACCTCAGAGAAACGACCGAATGCTATCCGTATCCCAACACCTTTAAATCAAGAGTTGAA 360
 DB 298 AAGCTAAAGGATGCGCATCGGATTGCCATCAGATCCGATCTCAGGACAGAAATGGA 357
 QY 361 GAAGTGAGTAGAGAAACACAGCTACAGTTTGTAGTCAAGCCT--ATTTCCTCTGGCACA 417
 DB 358 GAAGTGAGTAGAGAAACATAGCTACAACTTAATAGAGATGACCTCACCTGACCACT 417
 QY 418 GAGATTGACATGGATTCTATGCAGACACATTCGTATCATGCTGCGCAATGTGGAT 477
 DB 418 ACTGATGAGGAATTTTATTTATGGAAGACATTCGCAACCAATAGCTTAACAACTTGAG 477

QY 478 GAGGCTGAGCTGTGGGTTTTCTGACTCCAAGAAAGCGTCTGTTGAATGATCATACC 537
 DB 478 GAAGCTGATCTGTGGTTTTCTGGACCCAAAAGAGAGTTGCTTGATCTTATAGATGTC 537
 QY 538 AATGCTAATGATGGTCCGCCCAAGGTAATCTGTGTGTGTGGATGGGTGGTTAGGCAAG 597
 DB 538 CATGCCAATGACGGACCTTCAAAAAGTTGTATGTGTGTGTGGTATGGGTGGTTAG 597
 QY 598 ACAGCTCTTTCGAGGAAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTTGC 657
 DB 598 ACTACTATTGCAAGGAATTTATGAAAGCAAGAGGACATTTGCAAGAAATTTTCTTGC 657
 QY 658 AATGCTGGATTACAGTGTCAAAATCATTTTACAGGATTGAGCTACTTAAAGATATGATA 717
 DB 658 TGTGCTTGGATTACTGTTTCAAGTCTTTGTAGGGTGAACACTACTCAAGGATTGTATG 717
 QY 718 CGCCAACTTCTTGGCCCGAGTTCTCTGATCAACTCTTTCGAAGATTTGCNAGGGAAGTGT 777
 DB 718 GTGAAACTTTTGGAGAGGAAGTACTGAAAGCGGCTGAGAGAACTCGNAGGGA--G 774
 QY 778 GTGGTGCAAGTACATCATCTTTCTGAGTACCTGTAGAAAGAGCTCAAGGAGAGAGGTAC 837
 DB 775 GTTCCACAGTAGAGGACCTCGCAGCTACTCTCAGGACAGAGTTAAATGAAGAGAGGTAC 834
 QY 838 TTTGTTGTTCTAGATGATCTATGGATTTTACATGATTGGAATTTGGATAAATGAAATGCA 897
 DB 835 TTTGTTGTTGATTAACGTGTGGAGTACAGATTTCATGGAATGGAATTAATAGTATGCC 894
 QY 898 TTTCTTAAGACAATTAAGAGCGGACGTGCAATAGTAATAACACCTCGGAATGTTGATCTT 957
 DB 895 TTCCCTGAAATAACAATAAAGGGAGCGGGTGTAGTAACAACAAGAGAGATGTTGGCTTA 954
 QY 958 GCGGAGAGTGTGCGACAGCCCTCACTGCTGTACACCTTTGATTTCTTCAGATGAACGAT 1017
 DB 955 ACTAAGGAGTGTACTTCTGAAATGCTTATCTACAGCTTTAAACCCCTAGAAATAAAGCTAT 1014
 QY 1018 GCCATAACATTTGCTACTGAGAAAAACAAATAAAATCAATGAAGACATGGAATCAATAAA 1077
 DB 1015 GCAAAAGAGTTGCTTCTACGGAAGCAAAATAAAGCAATAGGAGATATGGAAGTATATAA 1074
 QY 1078 AATATGCAAAAGATGGTTGAACGAATTTGTAATTAATGTGTGCTCTACCATTAGCAATA 1137
 DB 1075 AAGATGATGACATTTATAACTTAAATAATAAAGAGTGTGGCTATTTTACCGCTGGCTATA 1134
 QY 1138 CTTACAATAGAGCTGTGCTTTCACAACTAAAACAGGTGTGAGATGGGAGAAATTTCTATGAA 1197
 DB 1135 CTCAATAGAGGCGTGTCTTCCACCAAGAGATTAAGAGATGGGAGATCTTTTATAGT 1194
 QY 1198 CACCTTCTTCCAGAACTAGAAATAAACCCAAAGCCTTGAAGCTTTGAGGAGAAATGCTGACC 1257
 DB 1195 CAGATACCTTCCAGAGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAGGATAGTGACC 1254
 QY 1258 CTAGGTTACAAACCACTACCATCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTT 1317
 DB 1255 CTAAGTTACAACTACTTACCGTCTCATCTTAAGCAATGCTTTTGTATCTAAGCATATTT 1314
 QY 1318 CCTCAGGATTTTGAATTCAAAGGAATGCTGTAGTGTAGTGTAGTATGAGAGAGGTTT 1377
 DB 1315 CCTGAGGATTTGAAATTAATAGGAACCGTCTGGTAAATAGATGGATGGCAGAGGGTTT 1374
 QY 1378 GTTAGACAAAGGTTGGGATGACGACTAAGGATGTCCGAGAAAGTTACTTTAATGAGCTA 1437
 DB 1375 ATTAAGCTAGGACTAATATGACTATTGAGATGTTGGGAAGAGTTACTTTAAGAACTT 1434
 QY 1438 ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCAATAGCAGGAAAAAATTTAAGCTTGT 1497
 DB 1435 ATCAACCGTATGATGATTTAGCCATCAAGAGCGGTATACGAGGAGATTTTAAAGAGCTGT 1494
 QY 1498 CGAATTCATGATCATCCCGTATATCACAGTTTCAATCTCGACAGCAGGAAAAATTTTGA 1557
 DB 1495 CGAGTCCACGACATCATGCGTGATATTAACAATTTTCGATTTCTAGAGAGAAAAATTTTACA 1554
 QY 1558 TTATTACCAATGGGAGATGGCTCTGATTTAGTTTACGGAATAACACCTCGCCACATAGCATTC 1617

Db 1555 CTCTTACCCGATGGCACTGACTATGATGTAGTACATGGGAACACTCGGCACATAGAATTT 1614
Qy 1618 CATGGAGTAGTCTCTGC---AAAACCTGGATTGGATGGACATATTTCGATCATTAGCT 1674
Db 1615 CACGGGAGTAAGTATTGCTCTGAAACCAAGCTTTGGACTGGAGCATTTATACGGTCAATTA 1674
Qy 1675 ATTTTGGTGTACAGACCCCAAGAGTCTAGCATGCAAGTTCGTCCAGATCAATTCAGGAATG 1734
Db 1675 ATGTTTGGTGTAGAGTCCGTAGAACTAGAGCAATTCAGTTTGTTCATCTCAGTTGAGGATG 1734
Qy 1735 TTACGGGTCTTGGATCTTTGAAGATGTGACATCTTAAATCACTCAAAAAGATTTTCGACCGT 1794
Db 1735 TTACGGGTCTTGGATCTTAAACAGATGCAAAATTTCTATCACACAAAATGATGTGCAAC 1794
Qy 1795 ATTGCATTTGTTGGCACTTGAATACATTGAGTATT-----GGATATTGTCATC 1844
Db 1795 ATAGTGCTCTTTGGCCACTTGAATACCTTATGCAATTAAGATACAGATACCGGTTCAACCA 1854
Qy 1845 CATATATTCACTTCCAGATCCATTGGTAAACTACAGGGCCTACAAAATCTTTGAACATGCC 1904
Db 1855 TATTATTCACTTCCACATCCATAGCTAGACTGCAATGCTCTGCAGACATTTGGACTTGGG 1914
Qy 1905 GAGCACATACATTCGACGACCTACCAAGTGAGATCAGTAAACTCCAATGTCTGCACTACTCT 1964
Db 1915 TCAGAGGTACATTTCAACACTGCCAACTCAGATTACT-AACTTCGGAGTCTCCGTAGCCT 1973
Qy 1965 TCGTTGTATAGGACAGTTTCATTATGACAACTTTTAGTCTTAAACCAACCAATGAAGTGCAT 2024
Db 1974 TCGATGCAATGAAGAATATTTTCTCTCTTT-----AACAAATATTT 2018
Qy 2025 AACTAAACATATATGCTCCCTGCTTAAAGTATTCACACCTTTAGTTCGCGATGATCGTC 2084
Db 2019 AACTAAACATATATGCTCCCTGCTTAAAGTATTCACACCTTTAGTTCGCGATGATCGTC 2078
Qy 2085 AAAACAAATTTCTGAATGTCATGCGCCACCAAAAGTTGCTGCTGCAATCAATCGGTGT 2144
Db 2079 TGAACAATTTCTAAATTTGCACATGGCCACCAAAAGGCTTCGTTTCAAAATCAAAATGGTGT 2138
Qy 2145 GAAGGTACCCAAAGGAATAGT-----AAGTTGCGAGACTTCGAGGTTCTAGAGTATGTAG 2200
Db 2139 CAAGGTACCAAAAGGAATATGTAATAAAAGTTCGCTTCAAAATCAAAATGGAGTATGG 2198
Qy 2201 ATATCAGCGCACAGTAGTAGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGA 2260
Db 2199 ATATTAGAGGACTAGCAGTAGAGCAATCAAAAGAGTTGGGCGAGTTAAGCAAGCTGAGGA 2258
Qy 2261 AATTAGGTGTGACAAACAAACGGGTGCAAAAGGAGAAATGTAAGATACCTTTATCGAGCCA 2320
Db 2259 AATTATGTGTGTAACAAAGGAGTCCACAAAGGAGAAATGTGAGATACCTTATACAGCTA 2318
Qy 2321 TTGAGAGGCTCTTTCCCTCCATCTCTCCATGTGGATGCTGCAGGAACTCTCAGATGGTG 2380
Db 2319 TCCAGAAGCTGTGTTCTTACAACTCTCTCCATGTGAATGCTGTGGGATTTTTCAGGTATG 2378
Qy 2381 GAACACTTGAGTGCTAGATTCTATTTCATCTCTCTCCCTACTGAGGACACTCGTGT 2440
Db 2379 GAACACTTGAGTGATAGTTCTATTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438
Qy 2441 TGGATGGAATTTCTTGAGGAGATGCTTAACCTGGATTGAGCAGCTCACTCACCTGAGGAAGA 2500
Db 2439 TGAATGGAAGCTTTGAGGAGATGCTTAACCTGGATTGAGCAGCTCACTCACCTGATGAAGT 2498
Qy 2501 TCTACTTATTGAGGAGCAAACTAAAGGAGGTAATAACATGCTGATATCTTTGGGCACTGC 2560
Db 2499 TCAACTTATTGAGGAGCAAACTAAAGGAGGTAATAACATGCTTGGTATCTTTTCGCGGTGC 2558
Qy 2561 CCAACCTCATGCTCTCTCATCTTTATCGGAATGCTTACTTGGGAGAGCTAGTATTCA 2620
Db 2559 CCAACCTCATGCTCTCTTTATCTTCAATCCAAATGCTTACCATGGGAGAGCTAGTATTCA 2618
Qy 2621 AAACAGGAGCAATCCCAAAATCTTGAACACATTTTGGATTTGAATTCAGCTAGCTAAGAG 2680

Db 2619 AAATGGGAGCATTTCCAAAATCTTTAGAACATTTTCGATTTACAATTTGGAGCAGCTAAGAG 2678
Qy 2681 AGATCACATTTGAGGCGGCGAGCTCACCCCTGTTGGAAAAGATAGAAATAGCGGAGTGCA 2740
Db 2679 AGATTAGATTTGAGGCGGCGAGCTCAATCTTTGTTGAAAAGATAGAAATATTTCAGG---- 2734
Qy 2741 GGTTTGGAATCTGGGATTTACTGGTATCATTCACCTTCCAAAAGCTCAAGGAGATTTCCAAATTA 2800
Db 2735 GGTGGAATCAGGGATGTTGTTGATCATTCACCTTCCAAAGCTCAAGGAGATTTCACTTG 2794
Qy 2801 GATACGGAATAAGTGGCTGGCTTGGTACGTGAGGAGGAGAAAGTGAACCCACACCCAA 2860
Db 2795 GATACGGAATAAGTGGCTGGCTTGGTACGTGAGGAGGAGAAAGTGGCAGACACCCAA 2854
Qy 2861 ATGCCCCGCTGCTCTAATGTACAGTACCGAAGGTATCACGACCTCGGGGCTCGAAGCCG 2920
Db 2855 ATACCCCGCTGCTCGAATGAGGAGGAGCCGAAGTATCACGACCTTGTGTGACGCCG 2914
Qy 2921 AAGGATCTTCTATAGAAAGTGCAAACACGACAGATCCTGT 2957
Db 2915 AAGGATCCCTGTTGAAGTGGAGCAACAGATCCTGT 2951

RESULT 10
ADI57167
ID ADI57167 standard; DNA; 2940 BP.
XX
AC ADI57167;
XX
DT 22-APR-2004 (first entry)
XX
DE Oryza minuta P19 locus nucleotide binding site (NBS) gene #1.
XX
KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; gene; ds.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JAN-2003; 2003US-00352179.
XX
PR 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX
PA (WANG/) WANG G.
PA (LIUG/) LIU G.
XX
PI Wang G, Liu G;
XX
DR WPI; 2004-121064/12.
XX
DR P-PSDB; ADI57168.
PT
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.
XX
PS Claim 3; SEQ ID NO 84; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present DNA sequence represents an NBS gene from the Oryza minuta P19 locus.
XX
SQ Sequence 2940 BP; 915 A; 547 C; 717 G; 761 T; 0 U; 0 Other;

Query Match 50.4%; Score 1562.2; DB 12; Length 2940;
Best Local Similarity 71.7%; Pred. No. 0;
Matches 2092; Conservative 0; Mismatches 818; Indels 9; Gaps 3;

Db 2158 AGAGGAATTGACAAACCTAAAGAGAGTTACAGATTCTAGAAAGTCGTGGACATCAACAGAACT 2217
Qy 2215 AGTAGTAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAGAAATTAAGGTGTGACA 2274
Db 2218 AGTAGGAAGGCGATTGAGAGCTGGGGGAGCTAATTCAGTTTAAGAAATTAAGCGTGACA 2277
Qy 2275 ACAACCGGGTCGACAAAGGAAAAATGTAAGATACCTTTATGACGCAATTTGAGAAAGCTCTCT 2334
Db 2278 ACARAAGGCGCACAAATAGAGATACAGATATTTTGTGAGCGATTTGAGAAAGCTCTCT 2337
Qy 2335 TCCCTCCAATCTCTCCATGTGCGATGTCGAGAAATCTCAGATGTTGGAACACTTTGAGTGC 2394
Db 2338 TCTCTGCAATCTCTCCGTGTGATGCTGAGGGATCTCAGATACCTGGAACACTTTGAGTGC 2397
Qy 2395 CTAGATTCTATTTTCATCTCCCTCCCTCACTGAGGACACTCGTGTGGAATGGAATCTT 2454
Db 2398 CTCAATTGATGATGCTCTCCCTCCATCTTTGAGACACACTCAAGTTGAATGGATCTCTT 2457
Qy 2455 GAGGAGATGCTTAAGTGGATTGAGCAGCTCACTCACTGAAAGAGATCTACTTATTTGAGG 2514
Db 2458 GCAGATACCAAACTGTTTGGGAACCTTAAGCAGCTGGTGAAGATGTGCTTATCCAGA 2517
Qy 2515 AGCAAACTAAAGGAAGTAAACCAATGCTGATACCTTTGGGGCACTGCCCAACCTCATGTC 2574
Db 2518 TGTGTGCTTACAAGATGGTAAACTATGAGATACCTTTGGGGCACTGCCCAACCTTATGTT 2577
Qy 2575 CTTCATCTTTATCGGATGCTTACTCTTTGGGAGAGCTAGTATTTCAAACAGGAGCATTC 2634
Db 2578 CTTCGTCTTTATCGAAGCATATGCTGACGAGAAATGGCAATTCAGAAGGGGAACATTC 2637
Qy 2635 CCAATCTTAGAACACTTTTGGATTATGAATTTGATCAGCTAAGAGATCAGATTTTGA 2694
Db 2638 CCAATCTCAGGTCTTGTATTTACTTGTGAGCAACTTAGAGATTAAGATTGAG 2697
Qy 2695 GACGCGAGCTCACCCCTGTTGGAAAGATAGAAATAGCGAGTGACAGTTTGGATCTGGG 2754
Db 2698 GAGGCGACCTCGCCAAACAATGGAAGTATAGAAATTTATGGTTGAGGTTTGGAAATCAGGG 2757
Qy 2755 ATTACTGTATCATCTACCTTCCAAAGCTCAAGGATTTCCAAATTAGATCGGAAGTAA 2814
Db 2758 ATTATGGTATCAAGCACTTCCAAAGCTTTAAGATTTATTCGCTTGAATATGATGGTAA 2817
Qy 2815 GTGGCTGGGCTTGGTCACTGGAGGAGAGTGAACGACACCCAAATCGCCCGTGTCTG 2874
Db 2818 GTCGGAGCTTGTATGTCTGCAAGAGGAAGTGAATACACACCCCAATCATCTACTGAAC 2877
Qy 2875 CTAATGTACAGTACCGAAGGTATCACGACCTGGGGCT 2913
Db 2878 CAAATGGCAGGATCGAAGTCAATCATGACCTAGGAGGT 2916

RESULT 11

ADMT2238
ID ADM72238 standard; cDNA; 2982 BP.

XX AC ADM72238;

XX DT 03-JUN-2004 (first entry)

XX DE O. minuta NBS1 polypeptide encoding cDNA.

XX KW Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance; gene; ss.

XX OS Oryza minuta.

XX FH Key Location/Qualifiers
XX CDS 1..2982

FT /+tag= a

FT /product= "NBS1"

XX WO2004022715-A2.

XX 18-MAR-2004.
XX 08-SEP-2003; 2003WO-US027913.
XX 09-SEP-2002; 2002US-0409216P.
XX 18-MAR-2003; 2003US-0455713P.
XX 05-SEP-2003; 2003US-00656394.
XX (OHIS) UNIV OHIO STATE.
XX Wang G;
XX WPI; 2004-257576/24.
XX P-PSDB; ADM72239.
XX New rice Pi2-like disease resistance nucleic acid molecule that confers
XX disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.
XX Disclosure; SEQ ID NO 1; 120pp; English.
XX The invention relates to novel broad-spectrum resistance gene Pi2 and the
XX NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
XX disease resistance nucleic acid molecules are useful for enhancing
XX disease resistance in plants. The present sequence represents a cDNA
XX encoding a rice NBS1 polypeptide.
XX SQ Sequence 2982 BP; 917 A; 560 C; 733 G; 772 T; 0 U; 0 Other;
Query Match 50.1%; Score 1553.4; DB 12; Length 2982;
Best Local Similarity 71.5%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 821; Indels 9; Gaps 3;
Qy 3 GGGCGAGCGGTGCTGAGCATGGCGAGGTCCCTGGTGGGAGCGCCATCAGCAAGGCCGC 62
Db 6 GGGCGAGCGGTGCTGAGCATGGCGAGGTCCCTGGTGGGAGCGCCGTGCGGAAGGCCGC 65
Qy 63 CTCGCTGCTGCCACGAGACAGCCTCTCTCTGGGCGTCGAGAAAGACATCTGTGTAT 122
Db 66 CTCGCGCGCCGCGAGCGCACCTCTCTCTGGCATCCAGAAGGAGATCTGTGTAT 125
Qy 123 CAAAGATGAGCTAAAAACGATGCAAGCATTCCTTAGAGCTGCTGAACCTTATGAAAAAGAA 182
Db 126 CAGGACGAGCTGAAAACTATTCAAGGCACTTCTTAAGAGCTGCTGAAGTAAACAAAGAGAA 185
Qy 183 AGATGAACCTTAAAGGTTTGGCGAGCAATACGTGACCTGTGCATATGACATTGAAGA 242
Db 186 AGATGACTTGTAAAGGTATGGGAGCAAGTACGAGATCTGTGCATATACATTTGAAGA 245
Qy 243 TTCCCTTGATGAATTTAAGGTCCATATTGAAGGCCAAACCCCTATTTCGCTAGTTGGTCAA 302
Db 246 TTGCTAGACGAATTCAGGTTTCATGTTGAGAGCCAAAGCTTGGCAAAGCAACTAATGA 305
Qy 303 ACTCAGAGAACGCCACCGAATTTGCTATCCGATCCACAACTTAAATCAAGAGTTGAAGA 362
Db 306 GCTTGGTGAACGCCCATCGAATTTGCTGTACAGATTGCGAACTTAAATCAAGAAATGAAGA 365
Qy 363 AGTGAGTAGCAGGAAACACACCGCTACGTTTATGCAAGCTTATTCCTCTGG---CACAGA 419
Db 366 AGTGAGCAACAGGAATACACGCTTAATCAAGCCCAATTTCTCTATAAACACAGA 425
Qy 420 GATTGACATGATTCCTTATGCAAGAACATTCGTAATCAGTCAGCTCCGAATGTGGATGA 479
Db 426 GGATGAGGGGATTCCTACCTAGAGATGCTCGCAATCGATCAGGTAGCAACACTGACGA 485
Qy 480 GGCTGAGCTTGTGGGTTTCTGACTCCAGAAAGGCTGCTTGAATGATGATACCAA 539
Db 486 GTCAGAACTTGTGGGCTTTGCAAGACTAAAGATGAGTTGCTTAACTGATAGATGTCAA 545
Qy 540 TGCTAATGATGCTCGGCAAGGTAATCTGTGTTGGGATGGGTGGTTAGGCAAGAC 599
Db 546 TACTAATGACGGTCCAGCTAAAGTGATATGTGTGGTTGGTATGGGTGGATTAGGCAAGAC 605


```
Db 2763 TATTTGGTATCAAGCACCTTCCAGACTTAAGATTATTTCGGCTTGAATATGATGTAAGT 2822
Qy 2817 GGCTGGGCTTGGTCAGCTGGAGGGAAGTGAACGCACACCAATCGCCCGTGGCTGCT 2876
Db 2823 CGCAAGCTTTGATGTGCTGCAAGAGGAAGTGAATACACACCCCAATCATACTGAATTGCA 2882
Qy 2877 AATGTACAGTGACCGAAGGTATCAGCCTGGGG 2911
Db 2883 AATGGCAGAGATCGAAGTCATCATGACCTAGGAG 2917

RESULT 12
ADI57169
ID ADI57169 standard; DNA; 2982 BP.
XX AC
XX ADI57169;
XX DT
XX 22-APR-2004 (first entry)
XX DE
XX Oryza minuta Pi9 locus nucleotide binding site (NBS) gene #2.
XX KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
XX KW plant breeding; transgenic plant; plant; gene; ds.
XX OS
XX Oryza minuta.
XX FN US2004006788-A1.
XX PD
XX 08-JAN-2004.
XX XX
XX 27-JAN-2003; 2003US-00352179.
XX PF
XX 25-JAN-2002; 2002US-0352106P.
XX PR 01-FEB-2002; 2002US-0353304P.
XX XX
XX (WANG/) WANG G.
XX PA (LIUG/) LIU G.
XX PA
XX Wang G, Liu G;
XX FI
XX WPI; 2004-121064/12.
XX DR P-PSDB; ADI57170.
XX DR
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
XX PT infection.
XX PS Claim 3; SEQ ID NO 86; 136pp; English.
XX PS
XX CC The invention comprises the amino acid and coding sequences of nucleotide
XX CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
XX CC blight and rice blast resistance genes). The DNA sequences may be used as
XX CC markers for resistance to infection with Magnaporthe grisea in plant
XX CC breeding programs. The present DNA sequence represents an NBS gene from
XX CC the Oryza minuta Pi9 locus.
XX XX
XX SQ Sequence 2982 BP; 921 A; 545 C; 722 G; 794 T; 0 U; 0 Other;

Query Match 36.6%; Score 1133.8; DB 12; Length 2982;
Best Local Similarity 65.1%; Pred. No. 7.7e-311;
Matches 1903; Conservative 0; Mismatches 932; Indels 90; Gaps 12;

Qy 1 ATGGCGGAGACGGTGTGAGATGGCGAGGTGCTGGTGGGCGAGCGGCATCAGCAAGGCC 60
Db 1 ATGACTGAGACGGTGTGTAAGCATGGCCATGTCGCTGGTGGGAGTGGCCATCAGAGTGGCT 60
Qy 61 GCCTCCGCTGTCGCGACGACCGACTCTGCTGGTGGCGCTCGAAGACATCTGGTAT 120
Db 61 TCTTCTGCTTCAGCCAAGATGAGCATGCTGATTTGGTGTGCAAAACGAGATTGGTTC 120
Qy 121 ATCAAGATGAGCTAAAAACCATGCAAGCATTCCTTAGAGCTGCTGAACCTTATGAAAAG 180
```

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Db 121 ATAAAGATGAGCTGAAGACAAATGACAGCAATTCCTGAGGGCGGCTGAAGTAAGGAAGAT 180
Qy 181 AAAGATCAACTATTAAAGTTTGGGCAGAGCAAAATACGTGACCTGTGTATATGACATTCAA 240
Db 181 CAAGATGAACCTCGTGAAGGTGTGGGCTGAGCAAGTGAAGATCTAGCCTACGACATTGAA 240
Qy 241 GATTCCCTTGTATGAATTTAAGGTCCATAATTGAAAGCCAAACCTATTTCGTGAGTTGGTG 300
Db 241 GATTGTCTTCAGGAGTTTGTGTCCATGTTGGGCATCAAAGCCTATCAATCGAGCTGATT 300
Qy 301 AAATCAGAGAAACGCCACCGAATTTGCTATTCGTTATCCACAAACCTTAAATCAAGAGTTGAA 360
Db 301 AAGCTCTGCCACCGACACCGAATCGCTGCCAGATTCCGAATTCGGAACCTGGAACAGAGGTTGAA 360
Qy 361 GAGTGTAGTAGCAGGAACACACGCTACAGTTTACTCAAGCCTATTTCCTCTGGGCACAGAG 420
Db 361 GAAGTGAGCAATAGAAACATGCGTTACAATCTAATCAAGTCTGTTCCTATCTAGCAGTACC 420
Qy 421 ATTGACATGGATTCTTATGCAAGACATTCGTAAATCAGTCAGCTCGCAATGTGGATGAG 480
Db 421 GATGACTCCCAAGCAACATGGAATTGATTCGGTATCAGACTGCTCATATTATGTTAAATGAA 480
Qy 481 GCTGAGCTTGTGGTGTTCGACTCCAAAGAAAGGCTGCTTGAATGATCGATACCAAT 540
Db 481 TCAGAGCTTGTGGTGTTCGACTTCCCAAAAGAGAGATCCTGTGAGATTGGTATCAAGCAGT 540
Qy 541 GCTAATGATGCTCGGCCAAGGTAATCTGTGTTCTGSGAGTGGTGTAGGCAAGACA 600
Db 541 GAAATGCTG---AAGCCCAAAACAATTTGGATTGTGCGAAGAGTGGTCTTGGGAAGACT 597
Qy 601 GCTCTTTCGAGGAAGATCTTTTGAAGCGAAGACATTTAGGAAGAACTTCCTTTGCAAT 660
Db 598 ACTCTTCAAGAGAGTTTATGAAGCTCAGATG---TTAGTAGCAAGTTCCTCGTGTGCT 654
Qy 661 GCTTGGATTACAGTGTCAATCATTTTCAAGGATGAGCTACTTAAAGATATGATACGC 720
Db 655 GCTTGGATCACTGTGTCAAGATCAATTTAAATGTCAGGATTTTACTGAAGAACATGATCAAG 714
Qy 721 CAACTTCTGGCCCCAGTTCCTCGATCAACTTTGCAAGAAATTCGAGGGAAGTGTG 780
Db 715 CAATTACTAGGGGAAGACTCACTCAAGAACTCTTGGATGAACACAAG---AGTGAAT 771
Qy 781 GTGCAAGTACATCATCTTTCTGAGTACTGATAGAAGAGCTCAAGGAGAAAGAGGTACTTT 840
Db 772 GTAGAAAAGCACACCTTACAGACCACTGAACAAGGGCTTAGAGGGAGAGGTATTTT 831
Qy 841 GTTGTCTTAGATGATATGGAATTTTACATGATTTGGAATTGGATAAATGAAATTCGATTT 900
Db 832 CTTGTTCTTGATGACTTGTGGACCACACAGCATGGGATTGCATTTAAACCTACTTCTCTGG 891
Qy 901 CCTAAGAACAAATAGAAGGGCAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTGG 960
Db 892 GGAATAAAC---ATGGAAGGTAGCCGAGTTGTAGTAACAACAAGAAACAAAACCTAGCA 948
Qy 961 GAGAAGTGTGCCACAGCCTCACTGGTGTACCACCTTGATTTCTTCGACATGAACGATGCC 1020
Db 949 GGTGGTAGTTCCA---CCTCGCAGTCTACTGCTCTTAAACCTCTAGAGAAAGAGATGCT 1005
Qy 1021 ATAACTTGTCTAGAGAAAACAAATAAATAATCATGAAGACATGGAATCAATAAATAAT 1080
Db 1006 ACCAAATTTGTTTGAAGAAAGACAAAAGAGTCTGCGATGACATAGAAAAAGATCAA--- 1062
Qy 1081 ATGCAAAAGATGGTTGACGAATTTGTAATAAATGTCGTCTCTACCACTATTAGCAATCTT 1140
Db 1063 ATGAAGAATAATTTTGAAGAAAGATACTAAGAAATGTTGGAGGTCTACCCCTAGCTATAATC 1122
Qy 1141 ACAATAGAGCTGTGCTTGCAACTTAAACAGAGTGTCAAGATGGGAGAAATTTCTATGAACAC 1200
Db 1123 ACATAGGTGAGTCTCTTGAAGGGAAGATATAAAGAGTGGGAAATTTTGTATGCTCAA 1182
Qy 1201 CTTCTCTCAGAACTAGAAAATAAACCAAGCTGGAGAGCTTTTGAGAGAAATGGTGAACCTTA 1260
Db 1183 CTTCCATCAGAACTTGAAGCAATCCAATCGCTGAAACCAATCGCTGAAACCAATGGAAGAGGTGTTAACCTT 1242
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Qy 1846 ATATATTCACATTCCTCCAGATTCATTTGGTAAACTACAGGCGCTACAAACTTTGAAACATGCGG 1905
 |||||
 Db 1855 ATTTATTCACATTCCTCCAAATCCATAGCTAGATGCTGCTGCGACATTTGGACTTTGGGT 1914
 |||||
 Qy 1906 AGCACATACATTCGAGCACTACCAAGTGAGATCAGTAAACTCCAATGCTGTCATACCTTT 1965
 |||||
 Db 1915 CAGACGTACATTTCAACACTGCCAATCAGATTTACT-AACTTCGGAGTCTCCGTAGCCCTT 1973
 |||||
 Qy 1966 CGTTGTATPAGACAGATTTTCATTATGACAACTTTTAGTCTTAACACCACCAATGAAGTGCATA 2025
 |||||
 Db 1974 CGATGCATGAAAGATATTTTCTCTCTTT-----AAGAACATATTTA 2018
 |||||
 Qy 2026 ACTAACCAATATGCTGCTGCTTAAAGTATTCACACTTTAGTTAGTTCGGATGATCGTGCA 2085
 |||||
 Db 2019 ACTAACCAATATGCTGCTGCTTAAAGTATTCACACTTTAGTTAGTTCGGATGATCGTGCA 2078
 |||||
 Qy 2086 AACAATTTGCTGAATTCACATGCGCACATGCGCAACCAAGTTGCTGCTGATCAATCGGTGTG 2145
 |||||
 Db 2079 GAAACAAATTTGCTGAATTCACATGCGCACATGCGCAACCAAGTTGCTGCTGATCAATCGGTGTG 2138
 |||||
 Qy 2146 AAGTACCCAAAGGAATAGTAAAGTTGCGGACCTTGCAAG 2185
 |||||
 Db 2139 AAGTACCCAAAGGAATAGTAAAGTTGCGGACCTTGCAAG 2178
 |||||

RESULT 14

AD157179
 ID AD157179 standard; DNA; 2265 BP.

XX AD157179;

XX 22-APR-2004 (first entry)

XX Oryza minuta Pi9 locus-related DNA sequence #1.

XX nucleotide binding site; NBS; Pi9; bacterial blight; rice blast;

XX plant breeding; transgenic plant; plant; ds.

XX Oryza minuta.

XX US2004006788-A1.

XX 08-JAN-2004.

XX 27-JAN-2003; 2003US-00352179.

XX 25-JAN-2002; 2002US-0352106P.

XX 01-FEB-2002; 2002US-0353304P.

XX (WANG/) WANG G.

XX (LIU/) LIU G.

XX Wang G, Liu G;

XX WPI; 2004-121064/12.

XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.

XX Disclosure; SEQ ID NO 96; 136pp; English.

XX The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present Oryza minuta DNA sequence was used in the exemplification of the invention.

XX Sequence 2265 BP; 638 A; 471 C; 558 G; 598 T; 0 U; 0 Other;

Query Match

29.6%; Score 918.8; DB 12; Length 2265;

RESULT 15

Best Local Similarity 94.8%; Pred. No. 8.9e-250;
 Matches 961; Conservative 0; Mismatches 52; Indels 1; Gaps 1;
 Qy 2087 AACAAATTTGCTGAATTTGCACATGCGCCACCAAAAGTTGCTGCTCTGCTGAATCAATTCGGTGTGA 2146
 |||||
 Db 90 AACAAATTTGCTGAATTTGCACATGCGCCACCAAAAGTTGCTGCTCTGCTGAATCAATTCGGTGTGA 149
 |||||
 Qy 2147 AGGTACCCAAAGGAATAGTTAAGTTGGAGACTTTCGAGGTTCTAGAGTTATGTAGATATCA 2206
 |||||
 Db 150 AGGTACCCAAAGGAATAGTTAAGTTGGAGACTTTCGAGGTTCTAGAGTTATGTAGATATCA 209
 |||||
 Qy 2207 GCGCGACAGTAGTAGAGCAATCAAGAGCTGGGGCACTTAAAGCAAGTTGAGGAAATTAG 2266
 |||||
 Db 210 GCGCGACAGTAGTAGAGCAATCAAGAGCTGGGGCACTTAAAGCAAGTTGAGGAAATTAG 269
 |||||
 Qy 2267 GTGTGACAAACAAACCGGTCGACAAAGGAATAATGTAAGATACCTTTATGACGCCATTGAGA 2326
 |||||
 Db 270 GTGTGATTAACAAAGGCTCGACAAAGGAATAATGTAAGATACCTTTATGACGCCATTGAGA 329
 |||||
 Qy 2327 AGCTCTCTTCCTCCAAATCTCTCCATGFGATGTCGAGGAATCTCAGATGGTGGAAACAC 2386
 |||||
 Db 330 AGCTCTCTTCCTCCAAATCTCTCTATGTGAATGCTGCGTTATATCAGATATGAAACAC 389
 |||||
 Qy 2387 TTGAGTGCCTAGATTTCTATTTTCATCTCTCTCCCTACTGAGGACACTCGTGTGGATG 2446
 |||||
 Db 390 TTGAGTGCCTAGATTTCTATTTTCATCTCTCTCCCTACTGAGGACACTCGGGTTGAAATG 449
 |||||
 Qy 2447 GAAATCTTTGAGGAGATGCTAACTGGATTGAGCAGCTCACCTCACCTGAAGAGATCTACT 2506
 |||||
 Db 450 GAGTCTTTGAAGAGATGCTTAACCTGGATTGAGCAGCTCACCTGAGGAAGATCTACT 509
 |||||
 Qy 2507 TATTGAGGAGCAAACTAAAGGAAGGTAAACCATCTGTATATTGGGGCACTGCCCAACC 2566
 |||||
 Db 510 TATTGAGGAGCAAACTAAAGGAAGGTAAACCATCTGTATATTGGGGCACTGCCCAACC 569
 |||||
 Qy 2567 TCATGGTCTTCATCTTTTATCGGAATGCTTACCTTTGGGAGAGCTAGTATTTCAAAACAG 2626
 |||||
 Db 570 TCATGGTCTTCATCTTTTATGGAAATGCTTACCTTTGGGAGAGCTAGTATTTCAAAACAG 629
 |||||
 Qy 2627 GAGCATTTCCC-AAATCTTAGAACACTTTGGATTTTATGAATTTGGATTCAGTCAAGAGAGATC 2685
 |||||
 Db 630 GAGCATTTCCAAATCTTAGAACACTTCGTATTTACGAAATTTGGATTCAGTCAAGAGAGATG 689
 |||||
 Qy 2686 AGATTTGAGGACGCGAGCTCACCCCTGTGTGAAAGATAGAAATAGGCGAGTGCAGGTTG 2745
 |||||
 Db 690 AGATTTGAGGATGCGAGCTCACCCCTGTGTGAAAGATAGAAATCTCTTGTGCGAGGTTG 749
 |||||
 Qy 2746 GAATCTGGGATTTACTGTTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCCAAATTAGATAC 2805
 |||||
 Db 750 GAATCAGGGATTTATGGTATTCATTCACCTTCCAAAGGCTCAAGGAGATTTCACTTGAATAC 809
 |||||
 Qy 2806 GGAAGTAAAGTGGCTGGGCTTGGTCACTGGAGGAGAGGTGAACGACACCCCAATCGC 2865
 |||||
 Db 810 AAAAGTAAAGTGGCTAGGCTTGGTCACTGGAGGAGAGGTGAACACACACCCCAATCGC 869
 |||||
 Qy 2866 CCCGTGCTGCTTAATGTATCAGTGACCGAAGGTATCACGACCTGGGGGCTGAAAGCGAAGGA 2925
 |||||
 Db 870 CCCGTGCTGCGAATGGACAGTGAACGAGGATCACGACCTGGGGGCTGAAAGCGAAGGA 929
 |||||
 Qy 2926 TCTTCTATAGAGTGGCAAAACAGCAGATCTCTGTTCTGTATGCGGAAGGATCAGTCACTGTA 2985
 |||||
 Db 930 TCTTCTATAGAGTGGCAAAACAGCAGATCTCTGTTCTGTATGCGGAAGGATCAGTCACTGTA 989
 |||||
 Qy 2986 GCAGTGAAGCAACCGGATCCCTTTCCGAGCAGAGGAGAGAGCTCCGAGTCGCGAGGTG 3045
 |||||
 Db 990 GCAGTGAAGCAACCGGATCCCTTTCCGAGCAGAGGAGAGAGCTCCGAGTCGCGAGGTG 1049
 |||||
 Qy 3046 ATCAGTTGACGACGAATATGATAGCAAGAGATAGGCACAGCTCAAGCTGGCTGA 3099
 |||||
 Db 1050 ATCAGTTGACGACGAACGATAGCAAGAGATAGGCACAGCTCAAGCTGGCTGA 1103
 |||||

AD157180
ID AD157180 standard; DNA; 2351 BP.
XX
AC AD157180;
XX
DT 22-APR-2004 (first entry)
XX
XX Oryza minuta P19 locus-related DNA sequence #2.
DE
XX nucleotide binding site; NBS; P19; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; ds.
XX
XX Oryza minuta.
OS
XX US2004006788-A1.
PN
XX 08-JAN-2004.
PD
XX 27-JAN-2003; 2003US-00352179.
XX
XX 25-JAN-2002; 2002US-0352106P.
PR
XX 01-FEB-2002; 2002US-0353304P.
XX
XX (WANG/) WANG G.
PA
XX (LIU/) LIU G.
XX
XX Wang G, Liu G;
PI
XX WPI; 2004-121064/12.
DR
XX
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
XX Disclosure; SEQ ID NO 97; 136pp; English.
PS
XX
XX The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present Oryza minuta DNA sequence was used in the
CC exemplification of the invention.
XX
XX Sequence 2351 BP; 703 A; 420 C; 559 G; 651 T; 0 U; 18 Other;
SQ
Query Match 27.0%; Score 838.2; DB 12; Length 2351;
Best Local Similarity 67.8%; Pred. No. 7.6e-227;
Matches 1253; Conservative 0; Mismatches 573; Indels 21; Gaps 5;
QY 1079 ATATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGCTACCATTTAGCAATAC 1138
DB 5 AAATGAAGAATAATTTGAAAGATACATAAAGAAATGAGAGGTTCCCGCTAGCTATA 64
QY 1139 TTACAATAGGAGCTGTCTTCAACTAAACAGGTGTCAGAAATGGGAGAAATTTCTATGAAC 1198
DB 65 TCACAAATAGGTGCAGTCTTGAAGGAAGATATAAAGAGTGGGAATTTTGTATGCTC 124
QY 1199 ACCTTCTTCAGAACTAGAAATAAACCGCTGGAAGCTTTGAGGAGAATGGTGACC 1258
DB 125 AACTTCCATCAGAACTTGAAGCAATCCATCGCTGAACCAATGAAGAGGTGTAACCC 184
QY 1259 TAGGTACAACCACTACATCCCAATTTGAACCAATGCTTTTGTATCTAAGTATCTTC 1318
DB 185 TTAGTTACAATTTACTTGCATCTCATCTTAAGCCCTTGTCTGTACCTTTGCACTTTC 244
QY 1319 CTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGATGAGAGAGGGTTG 1378
DB 245 CTGAGGATTTTGAATCAAAAGGAAGCCCTAGTATACATAGATGATTCAGAGGGTTA 304
QY 1379 TTAGACCAAGGTTGGGATGACGACTAAGAGTGTGGAGAAAGTTACTTTTATGAGCTAA 1438
DB 305 TTAGAGCTAGGGGTGGAGTGGGAATTTGGGATGTGGCACAAAAGATTTTGTAGTGTGA 364

1439 TCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGACAGGAAAAAATTAAAGACTTGT 1498
365 TCAACCGAAGTATGATTCAACGATCTAGAGTGGATATAGAGGGAAAAATTAAAGAGCTGCC 424
1499 GAATTCATGATATCATCGGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTGTAT 1558
425 GAGTCCATGATATCATCGGTGATGTCATGATATCAATATCTAGGGAAGAAAAATTTTGTAT 484
1559 TATTACCAATGGGAGATGGCTCTGATTAGTTTTCAGGAAAAACACTCGCCACATATGCAATCC 1618
485 ACTTGATGGGTGATGATGGAACTAGTGTAGTGGAGGAAAAATATTCGCCCTTTAGTGCAAC 544
1619 ATGGGAGTAT---GTCCTGCAAAAACCTGGATTGGAGTATGGAGCATTTATTCGATCATTAGCTA 1675
545 ATGATACTAGCAAGTGTTCAAATATAGGCATGGATGGAGCCATGTACGGTCATTTAACTT 604
1676 TTTTGG---TGACAGACCCAGAGTCTAGCACATGCGATTTGTGTCAGATCAATTTAGAGA 1732
605 TGTTTGGCAATGAGAGACCCCAAGGGCTATCTCCTTCATTTTGTTCCTCCCAATTTGAAGA 664
1733 TGTTACGGTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACC 1792
665 TGCTAAGAGTCTGGATCTTCAAGATGTCAAATTTGGGATGACACAAAAGATATCGGAA 724
1793 GTATTGCATTTGTTGTCACCTTGAATACTTTGAGTATTTGGATATTTGTCATCCCATATAT 1852
725 AATAGGGTTGCTGGTCACTTTGAANATATGTAATATTTGGAGGGCATTTCAAGTATTTATG 784
1853 CACTTCCAGATCATTTGGTTAAACTACAGGGCTTACAAACTTTTGAAATGTCGGAGCACAT 1912
785 CACTTCTCTAGGTATAGGAAAAATTAAGAACTTTGTGCATTTTGGACATAACTGCACGTT 844
1913 ACATTGACGACTACCAAGTGAGATCAGTAACTCCCAATGTCATGTCATCTCTGTTCTGTA 1972
845 ACATTACAGAACTACCACTGAGATTAGTAATTTGAGAGTCTATGTAATTTCTCGGTTGTA 904
1973 TAGGACAGATTTCAATATGACAACTTTTGTCTAAACCCACCAATGAAGTGCATACTAAACA 2032
905 GAGGAGACCAAACTCGGGGATTTTAACTTAATATGATCTTAAGGATTTGTCTAATTTGCT 964
2033 CAATATGCTGCTTAAAGTATTCACCTTTAGTTAGTGGCGATGATCGTGGAAAAACAAA 2092
965 TCTCATGTTTGCCT---CTGCTTATGGCTGCAACCGATTTCTGATGAACGTAATAAATAA 1021
2093 TTGCTGAATTCACATGSCCAACCAAAAGTTGCTGTC-----TCAATAAATCGGTG 2143
1022 TTGCTGAGCTACACGTGGGTTGTTCAAGTCAATGCTCTCTTAAGTGGTACATATGGTG 1081
2144 TGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTTGCGAGTCTAGAGTATGTAGATA 2203
1082 TGAGGGTACCTTAGAGGAATCAAGAATTTGAAAAGGCTGCGAGTGTAGAGACAGTGGATA 1141
2204 TCAGGGGACCAAGTAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAT 2263
1142 TCAATCGAACCAAGCAAGTAAAGTCAAGTGAAGAGTTGGGAGAGCTTATCCAGCTTAAGAAA 1201
2264 TAGGTGTGACAAACAAAGGTCGACAAAGGAAAAATGTAAGTACTTTATGCGACCATTTG 2323
1202 TAAGTGTAGTAACCAAGGGTCCACCAAGGAAAAATGCAAAATCTCTGTACAGGCATTC 1261
2324 AGAAGCTCTCTTCCTCCCAATCTCTCCATGTTGGATGCTGCGAGGAATCTCAGATGGTGGAA 2383
1262 AGAAGCTAACTTCCCTCAAAACTCTCTATCTGAATGCTCATGGACCTTGGATATCGGAA 1321
2384 CACTTGATGCTTGAATTTCTATTTTCATCTCTCTCCCTTACCTGAGGACACTCTCGTGTGG 2443
1322 CACTTGAATGGCTACTATTTTCCCATCTCTCTCTCC---CTGAGGATCATCAGATTGA 1378
2444 ATGGAATCTTTGAGGAGATGCTTAAGTGTGAGTGTGAGAGCTCACTCACCTGAAGAGATCT 2503
1379 TCGGATCATGAAAGAGATGCCCACTGGTTTAGGGAGCTCAGACAGCTGGTGAAGATTC 1438
2504 ACTTATTGAGGAGCAAACTAAAGGAAGGTAAAAACCATGCTGATACTTTGGGGCACTGCCCA 2563

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 22:53:15 ; Search time 6394.15 Seconds
(without alignments)
18448.290 Million cell updates/sec

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Perfect score: 3099

Sequence: 1 atggcgagacggtgctgag.....gcacagctcaagctggtga 3099

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_ges1:*

9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1555.4	50.2	2925	9	CL964072
3	1170.6	37.8	3024	9	CL963354
4	587.6	19.0	662	9	AG210016
5	497.4	16.1	698	9	AG208890
6	431.6	13.9	810	6	CF071622
7	393	12.7	703	9	CL832740
8	361.6	11.7	737	9	CL858532
9	361.4	11.7	740	9	CL861885
10	358.4	11.6	709	6	CA147958
11	354.2	11.4	875	9	CW518670
12	352.6	11.4	663	8	AQ578469
13	350.4	11.3	709	9	CL801486
14	339.6	11.0	603	9	CL197270
15	317.6	10.2	673	8	BZ338669
16	314.2	10.1	551	9	CL197271
17	313.8	10.1	808	9	CL582275
18	312.2	10.1	738	9	AB155403
19	308.4	10.0	527	8	AQ510644
20	305.4	9.9	650	8	AQ579138
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22	301.2	9.7	727	9	CL190018
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BZ341503 ic45g08.g
BE216309 HV CEB001
AZ047631 nb50086H
AG006783 Oryza sat
AG208447 Oryza sat
CB652975 OSJNEC031
CB652258 OSJNEC01P
AG212538 Oryza sat
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BZ338670 ia97a07.g
CL196451 104_422.1
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BG101746 EM1_5.G07
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AQ163442 nbx0007A
CK168020 FGAS05249
CL175621 104_381.1
CK166588 FGAS05075

ALIGNMENTS

RESULT 1
CL964074
LOCUS
DEFINITION
CL964074 3159 bp DNA linear GSS 21-SEP-2004
Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CL964074 3159 bp DNA linear GSS 21-SEP-2004
Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
CL964074
GI:52382860
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 3159)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1. 3159
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

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Matches 2501; Conservative 0; Mismatches 473; Indels 6; Gaps 1;
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Db GAAGAGATGCTCAACCTGATTTGAGAGCTCTCGCACCTCATGAATTTCTACTTTAGG 2697
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Qy CTATGTACATGATGACCGAGTATCAGCAGCTGGGGCTGAGCGAAGGATCTTCTATA 2934
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RESULT 2
CL964072 2925 bp DNA linear GSS 21-SEP-2004
LOCUS
DEFINITION O81FCC010259 Oryza sativa Expressed Sequence Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION
VERSION CL964072
KEYWORDS CL964072.1 GI:52382856
SOURCE
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 2925)
REFERENCE
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1. 2925
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:3946"
/clone_lib="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences"

FEATURES
source

ORIGIN

Query Match 50.2%; Score 1555.4; DB 9; Length 2925;
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Matches 2087; Conservative 0; Mismatches 821; Indels 9; Gaps 3;
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Db 6 GGCAGAGCGGTGCTGAGCATGGCGAGGTCTGCTGGGCGAGCGCGCTCGGGAAGGCGCG 65
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Db 66 CTCCGCTGCTGCCAGCAGGACCGCTCTCTGCTGGGCGTCCGAGAGATCTGGTATAT 125
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Qy 123 CAAAGATGAGCTAAACAGCATGCAAGCATTCCTTAGAGCTCTGAACTTATGAAAAAGAA 182
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Db 126 CAGGAGAGCTGAAACATTTTACGGCATTTCTTAAGAGCTCTGAGTAAACAAGAGAA 185
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Qy 183 AGATGAATCTTAAAGGTTTGGGCGAGCAAAATACGTGACCTGTATATGATGAAAGA 242
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Db 186 AGATGACTTGTCTAAAGGTATGGGCGAGCAAGTACGAGATCTGTATATAACATTTGAAGA 245
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Qy 420 GATTGACATGGATTCCTATGCGAGAGACATTCGTAATCAGTCAGCTCGCATGTGGATGA 479
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Db 426 GGATGAGAGGGATTTCTTACCTAGAAAGATGCTCGCAATTCGATCAGGTAGCAACACTGACGA 485
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Qy 480 GGCTGAGCTTTGTTGGGTTTCTTGAATCAAGAAAGGCTGCTTCAAAATGATCGATACCA 539
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Qy 540 TGCTAATGATGTTCCGCGCAAGGTAATCTGTGTTGTTGGGATGGGTGGTTAGGCAAGAC 599
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Qy 600 AGCTTTTTCAGGAGAGATCTTTTGAAGCGAAGAGACATTTAGGAGAACTTTCCCTTGCA 659
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Qy 780 GGTGCAAGTATCATCATCTTTCTGAGTACCTGTATAGAGAGCTCAAGGAGAGAGGTTACTT 839
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Db	903	TCCGAAGATTAAACAAAGAGGTAGTCGCAATAATAACCAACGCGAGATGCTGGCTTAGC	962
Qy	960	GGAGAAGTGTGCCACAGCCTCACTGGTGTACCACTTGTGATTTCTTGAGATGAACGATGC	1019
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Db	1023	TATACATTTGCTACTAGCAAAAGACAAACATTAAGACTTTGAAGACATGGAAATGATGAGGA	1082
Qy	1080	TATGCAAAAGATGGTTGAACGAAATGTAAATAAATGTGGTGGTCTCAACATTTAGCAATPACT	1139
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Qy	1740	GGTCTTGGATCTTGAAGATGTGACATCTTCAATCACTCAAAAAGATTTTCGACCGTATTCG	1799
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Qy	1860	CAGATCCATTTGGTAAACTACAGGGCCTACAAACTTTGAACATGCCGAGCACATCATTTGC	1919
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DEFINITION OsIFCC009286 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL963354

VERSION CL963354.1 GI:52381436

KEYWORDS GSS.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 3024)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)

TITLE

JOURNAL

COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES
source
1. 3024
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
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Best Local Similarity 65.2%; Pred. No. 0;
Matches 1919; Conservative 0; Mismatches 964; Indels 60; Gaps 11;

Qy 1 ATGCGGAGACGGTGTGAGCATGGCAGATGGCGAGTGGCTGGCGAGCGCCATCAGCAAGGCC 60

Db 1 ATGCGGAGACGGCGCTGAGCATGGCGAGTGGCGAGTGGCGAGCGCCATCAGCGCGGCT 60

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Qy 121 ATCAAGATGAGCTAAAGACGATCGACGATTCCTTAGAGCTGCTGACTTATGAAAG 180

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Qy 181 AAAGATGAACCTATTAAAGGTTTGGGAGCAAAATACGTGACCTGTCTATGACATTGAA 240

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Db 241 GATTGTCTTGAAGAGTTTATGGTCCATGTGCGAAACCAAGCCTCTTGCAGCAATTGACA 300

Qy 301 AAATCAGAGAACCCGACCGAATGCTATCCGATCCACACCTTAATCAAGAGTTGAA 360

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Qy 361 GAAGTGAAGTACGAGAACACAGCTTACAGTTTATGTCAGGCTATTTCCTCGGACAGAG 420

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Qy 421 ATTGACATGGATTCCTATGCAAGAGACATTCGTAATCAGTCAGCTCGCAATGTGGATGAG 480

Db 421 GATGAGATCGAGTCC---ATGAGGATGTTGCGAATCATCTCTGTAGCAACATCGAGAA 477

Qy 481 GCTGAGCTTGTGGTTCCTGACTCCGAAGAAAGGCTGCTTGAATGATCGATCCCAT 540

Db 478 GCAAAGCTTGTAGCTTTGACACCCCAAAAGAGATTACTTGACAAGATAAACAATGGAT 537

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Db 538 GCCAATGATGATGACCACTGTGGGTGCTTGTGTGGTGGGAGGATTTGGGTAAAG 597

Qy 598 ACAGCTCTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAGAACTTCCTTGGC 657

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Qy 718 CGCCAACTCTTGGCCCCAGTTCTCTGGATCAACTCTTTCGAAGAATTGCAAGGGAAGTG 777

Db 718 AGCCAACTCTTAGGTC-----ATGAATCATTTGAAAGATTTGAAGGGAAGCG 765

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DEFINITION   FE1_17_D11.g1.A002 Iron-deficient seedlings Sorghum bicolor cDNA
ACCESSION    CF071622
VERSION      CF071622.1 GI:33108281
KEYWORDS     EST.
SOURCE       Sorghum bicolor (sorghum)
ORGANISM     Sorghum bicolor
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE    1 (bases 1 to 810)
AUTHORS      Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C.,
              Sun,F., Sullivan,R., Harris,K., Eastman,A. and Pratt,L.H.
              An EST database from Sorghum: iron-deficient seedlings
TITLE        Unpublished (2003)
JOURNAL
COMMENT      Other ESTs: FE1_17_D11.b1.A002
              Contact: Cordonnier-Pratt MM
              Laboratory for Genomics and Bioinformatics
              The University of Georgia, Department of Plant Biology
              Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
              Tel: 706 542 1860
              Fax: 706 583 0210
              Email: mmpratt@uga.edu
              Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
              the Human Genome Center, University of Tokyo Institute of Medical
              Science; plant material and RNA prepared at Texas A & M University;
              sequencing done in the Laboratory for Genomics and Bioinformatics;
              University of Georgia. Sequence ends have been trimmed to exclude
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                  /note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
                  library was prepared from polyA+ RNA from seedlings grown
                  hydroponically and in the absence of added iron. At 8 days
                  of age, roots and shoots were harvested and stored at -80
                  C until RNA was isolated. Double-stranded cDNA was cloned
                  unidirectionally into different DraIII sites of the
                  pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
                  3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
                  insert."

FEATURES             source
  source              1..810
    LOCATION/QUALIFIERS
      1..810
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        355 AAGCTTCGTATCGCCATCGAATTCGATATCCGATATCCGATATCCGATATCCGATATCCG
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        415 GAGGTAGCAACAGGAACACACGCTACAGCTAATTAAGCCATTTCTCTAGCAGACA
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        540 GCTGAGCTTGTGGGTTTCTGACTCCAGAAAGGCTGTTGAAATGATGATGATACCAAT
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        594 GCTAAATGATGTCGCGCAAGGTAATCTGTGTTCTGCG--ATGSGTGGTTTACGCAAGA
        598 CTTGATGATGCTCTACTAAGGTAAATATGTTGTTGCGTATGGGGTGGTTTACGCAAGA
        654 CAGCTCTTTGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGACATTTCCCTTTGCA
        658 CTACTTTGGCAAGGAGACCTACGAAAGTAGGAGGATATTTCAAGGTACTTCTCTTGTCT
        714 ATGCTGGATACAGTGTCAATCATTTCACAGGATGAGTACTTAAAGATATGATAC
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        774 GCCAACTTCTTGGCCCGAGTTCTCTGATCAACTCT 754
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RESULT 7
LOCUS    CL832740
DEFINITION OR_CBA0055J06.r OR_CBA Oryza rufipogon genomic clone OR_CBA0055J06
          3', genomic survey sequence.
ACCESSION CL832740
VERSION    CL832740.1 GI:51078350
KEYWORDS   GSS.
SOURCE     Oryza rufipogon
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           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 703)
AUTHORS    Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
           Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
           Wing,R.
           OMAP project
           Unpublished (2004)
           Contact: Rod A. Wing
           Arizona Genomics Institute
           University of Arizona
           Forbes Building Room 303, Tucson, AZ 85721-0036, USA
           Tel: 520 626 9595
           Fax: 520 621 1259
           Email: http://genome.arizona.edu
           PCR Primers
           FORWARD: TAA TAC GAC TCA CTA TAG GG
           BACKWARD: CAC TCA TTA GGC ACC CCA
           Plate: 0055 row: J column: 06
           Seq primer: CAC TCA TTA GGC ACC CCA
           Class: BAC ends.
           Location/Qualifiers
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        301 AACTCAGAGAAAGCCACCGAATTCGATATCCGATATCCACACCTTAATCAAGATTTGAA
        355 AAGCTTCGTATCGCCATCGAATTCGATATCCGATATCCGATATCCGATATCCGATATCCG
        361 GAAGTGTAGTACGAGAACACACGCTACAGTTTGTAGTCAAGCCATATTTCTCTGGCAGAG
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        654 CAGCTCTTTGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGACATTTCCCTTTGCA
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Db 478 CATAGATGCATGGAATTGGATTTCATGATATTGCTTTTCCGGAAGATTAAACAAGAGGTAG 537
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 Db 538 TCGATATAATAACAACACGAGATGCTGGCTTAGCTGGAAGGTGTACCTCTGATCACT 597
 Qy 984 GGTGTACCACCTTGATTTCTTGCAGATGAACGATGCCATAACATTTGCTACTTGAGAAAAAC 1043
 Db 598 TATTACCACCTTGAACCGTTACATATATAGATGATGCTATACACTTGCTACTAGCAAGAC 657
 Qy 1044 AAATAAAATCATGAAGACATGGAATCAATAAATAAATAATGCAAAAGATGGTTGAACGAT 1103
 Db 658 AAACATAGACTTTGAAGACATGGAATAATGATGAGGACTTGGGCAGCATAGTTACAAAATT 717
 Qy 1104 TGTAATAAATGTGCT 1119
 Db 718 GGTAAAGGGTGTGCT 733

RESULT 9
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 DEFINITION 5', genomic survey sequence.
 ACCESSION CL861885
 VERSION CL861885.1 GI:51276691
 KEYWORDS GSS.
 SOURCE Oryza rufipogon

ORGANISM Oryza rufipogon
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 740)
 Kim,H., Yu,Y., Wisotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
 Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
 Wing,R.

TITLE OMAP project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Plate: 0093 row: P column: 17
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

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 /note="Vector: pGIBAC1; Site 1: HindIII; Site 2: HindIII;
 drk treated 36 hrs before harvest"

ORIGIN
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 Best Local Similarity 70.0%; Pred. No. 3e-89;
 Matches 517; Conservative 0; Mismatches 216; Indels 6; Gaps 2;
 Qy 387 CAGTTTACTCAAGCCTATTTCCTCT---GGCACAGAGATTGCATGGATTCTTATGCAGA 443
 Db 1 CAGCTTAATCAAGCCCAATTCCTCTATAACCAACAGAGGATGAGGGGATTCCTACCTAGA 60

Qy 444 AGACATTCGTAATCAGTCAGCTCGCAATGTGGATGAGGCTGAGCTTGTGGGTTTTCTGA 503
 Db 61 AGATGCTCGCAATCGATCAGTAGCAACAACATGACGAGTCAGAACTTGTGGGCTTTCGCAA 120
 Qy 504 CTCCAAGAAAAGGCTGTTGAAATGATCGATACCAATGCTTAATGATGGTCCGGCCNAGGT 563
 Db 121 GACTAAAGATGAGTTGCTTAAACTGATAGATGTCAATACTAATGACGGTCAGCTAAAGT 180
 Qy 564 AATCTGTGTTGTTGGGATGGGTGTTAGGCAAGACAGCTCTTTTCGAGGAAGATCTTTGA 623
 Db 181 GATATGTGTGGTATGGGTGATTTAGGCAAGACTTACCTTCGAAGGAGGCATATGA 240
 Qy 624 AAGCGAAGAGACATTAGGAAGAACTTCCCTTGCATGCTTTGGATTACAGTGTCACAATC 683
 Db 241 AAACAAGGAAACACAT---GAAGAACTTCTCGTGTGTGTTGGATCACTGTGTCTCAGTC 297
 Qy 684 ATTTACAGGATTCAGCTACTTTAAAGATATGATAGCGCAACTTTTGGCCCCCACTCTCT 743
 Db 298 ATTTGACAGGAAGAAAATTTCTGAAACAAATGATCAGGCAACTTCTGGGTGCTGATTCATT 357
 Qy 744 GGATCAACTCTTTCGAAGAAATTGCAAGGAAGGTGGTGCAGGTATCATCATCTTTCTGA 803
 Db 358 AGACAAACTCTTGAAGAAGATTTAGTGAGAGTTGCTCTGTGCAAGTCCAGCATCTCGCTGA 417
 Qy 804 GTACCTGATAGAAGCTCAAGGAGAGAGTACTTTGTTGTTCTTAGATGATCATATGAT 863
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 Qy 864 TTTACATGATGGAAATGGATTAATGAAATGCAATTTCTTAAGAACATATAGAAGGGCAG 923
 Db 478 CATAGATGCATGGAAATTTGGATTTCATGATATTGCTTTTCCGAAGATTAAACAACAGAGGTAG 537
 Qy 924 TCGAATAGTAATAACCACTCGGAATGTTGATCTTTCGCGAGAAGTGTGCCACAGGCTCACT 983
 Db 538 TCGATATAATAACAACAGAGATGCTGGCTTAGCTGGAAGGTGATCTCTGATCACT 597
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 Db 598 TATTTACCACCTTGAACCGTTACATATAGATGATGTATACACTTGTCTACTAGCAAGAC 657
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 Db 658 AAACATAAGACTTTGAAGACATGGAATAATGATGAGGACTTGGGCAGCATTAATACAAAAAT 717
 Qy 1104 TGTAATAAATGTGCTGCT 1122
 Db 718 TGGTAAAGGGTGTGCT 736

RESULT 10
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LOCUS SCEZR21015C04.g RZ1 Saccharum officinarum cdna clone SCEZR21015C04
 DEFINITION 5', mRNA sequence.

ACCESSION CL147958
 VERSION CL147958.1 GI:35048518
 KEYWORDS EST.
 SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.

REFERENCE 1 (bases 1 to 709)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
 The libraries that made SUCEST
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 COMMENT Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089

Email: parruda@unicamp.br
 Clone distribution: Clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>
 Plate: 015 row: C column: 04
 Seq primer: T7 Promoter Primer.
 Location/Qualifiers
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 /notes="Organ: Shoot-root transition zone from young plants
 (large insert library); Vector: pSport1; Site_1: SalI;
 Site_2: NotI; An unidirectional cDNA library generated
 from (Shoot-root transition zone from young plants (large
 insert library)). cDNA was prepared from polyA+ mRNA
 using SuperScript Plasmid System Kit (Invitrogen). The
 double-strand cDNAs were fractionated in a sapharose
 CI-2B 40cm-columns and fragments sizing between 0.8 and
 1.5 Kb were directionally cloned into the vector. Details
 of each source of RNA and library construction can be
 obtained at <http://sucet.lad.ic.unicamp.br/public>"

FEATURES
SOURCE

Obtained at <http://779dce6e8c1bad1e10:uncamp@bf/pubml>

ORIGIN	Query Match Best Local Similarity Matches	11.6%; 69.9%; 498;	Score Pred. No. Mismatches	358.4; 2.1e-86; 211;	DB 6; Length Indels	709; 3; Gaps
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Qy	2243	AGTTTAAGCAAGCTCAGGANAATTAGTGTGACAACAACCGGTGCACAAAAGGAATAAATGTA	2302			
Db	61	AGCTGACCCGATYAAGANAACACTACCCTGGNACNAACGGGGCTTCCAAGANAATGTA	120			
Qy	2303	AGATACTTTTATGACCATTTAGAGAGCTCTCTTCCCCTCAATCTCTCACTGTGGATGCTG	2362			
Db	121	AGATACCTTTGTGATCCATTAGAGAAGCTCTCTCCCTTCATCTCTCACCTGTAGGGCCG	180			
Qy	2363	CAGGAATCTCAGATGGTGGAACACTGAGTGCCTAGATCTCTATTTTCATCTCCCTCCCC	2422			
Db	181	GCAACACCAGATAAAG---ACTTGGATGGTTAA'TTCTTCTCTCCCTCCTCCCC	237			
Qy	2423	TACTGAGGACACTCGTGTGGATGGAAT'CTTGTAGGAGATGCCCTAACTGGATTGAGCAGC	2482			
Db	238	ACCTGAGGAGCCTCAGCTTGTA CGGATATATAGGAGAGATGACCGACTGGTTCAGGAATC	297			
Qy	2483	TCACTCACTGAAGAAGATCTACTATTATGAGGAGCAAACTAAGAGAGGTAAACCAATGC	2542			
Db	298	TTACACAGCTGGTGAAGATTTTCCCTTAATCTGTAGCCAGCTAAAGGAAGATATAAACCATGG	357			
Qy	2543	TGATACTTGGGGCACTGCCAACCTCATGTGCTCTTCATCTTTATCGGAATGCTTACCTTG	2602			
Db	358	AGATACTTGGGAACTGCCAANAACCTCATGCTCTCTTCAGTTTATCCCACTGTCATACCTTG	417			
Qy	2603	GGGAGAAGCTAGTATTCAAAA CAGGAGCATTTCCAAATCTTTPAGAACACTTTGGATTTATG	2662			
Db	418	GGGAGAAATTAGTGT'TTAGAACCAAGAGGATTTCTTGAACTTCAGGACACTTGGATTTGGG	477			
Qy	2663	AATTTGGATCAGCTAAGAGAGATCAGATTTTGGAGCGGAGCTCACCCCTGTTGGAAAAAGA	2722			
Db	478	GAACGNA CGACCGAAAAGAGATTATATTTTGGAGGGGCA CAGGCCCTCAGATGGAAACGA	537			
Qy	2723	TAGAAATAGGGCAGTGCAGGTTTGGAACTCTGGGATTTACTTGGTATCATTTCACTTCCAAAGC	2782			
Db	538	TAGAAATCAGGGCGTGCATTTTGAAGTCAGGGATTTATGGCATCAGGACCTTCCAGGC	597			
Qy	2783	TCAAGGAGATTTCCAATTAGATACGGAAAGTAAAGTGGCTGGGCTTGGTCACTGGAGGGAG	2842			

Db 598 TCAAGGTGATTTCACTCTGCTATGTAATCTAAGGTGGCGAGGCTTAGTATGCTTGGAGAGG 657
 Qy 2843 AAGTGAACGCACACCCAAATCGCCCGTGTCTTAATGTACATGACCGAAG 2894
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 Db 658 AAGTGAACGCACACCCCAATCATCTGTCTCTGGGCTGGTACATGACCGAAG 709
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RESULT 11
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 LOCUS Ba0025003.r OP_Ba Oryza punctata genomic clone OP_Ba0025003
 DEFINITION 3*_genomic survey sequence.
 ACCESSION CW518670
 VERSION CW518670.1 GI:53992892
 KEYWORDS GSS.
 SOURCE Oryza punctata
 ORGANISM Oryza punctata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 875)
 AUTHORS SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D.,
 Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
 Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
 TITLE OMAP Project - Purdue University
 JOURNAL Unpublished (2004)
 COMMENT Contact: Scott A. Jackson
 Jackson Laboratory
 Purdue University
 915 W. State St., West Lafayette, IN 47907, USA
 TEL: 7654963621
 FAX: 7654967255
 Email: sjackson@purdue.edu
 Basecalling by phred version 0.020425.c. This sequence was derived
 from the raw sequence read by clipping with Lucy version 1.19s.
 Bases 119-993 of the raw sequence (length 1389) were retained after
 clipping.
 PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Insert length: 161000 Std Error: 0.00
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 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.
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 Best Local Similarity 65.4%; Pred. No. 3.3e-87;
 Matches 567; Conservative 0; Mismatches 293; Indels 7; Gaps 3;
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 Db 121 TAAGGAAGATCTTTGAAAGTAAAGAGACATTCGAATAATATTTTACACATCGTGTGGA 180
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QY 1532 CAATCTCGAGACAGGAATAATTTTGTATTATTATTAACCAATGGAGATGGCTCTGATTTAGTTC 1591
DB 110 CGATTCTAGAGAGGAAAATTTTGTATTCTTACCTAGGGGCACTGACTATGAAGCAGTAC 51
QY 1592 AGGAAAAACACTCGGCACATAGCATTTCCATGGGAGATGTCCTGC 1635
DB 50 AGGGGAACACTCGGCACATAGCATTTTCAGGGGANGTAAGTATTC 7

RESULT 13
CL801486
LOCUS CL801486 709 bp DNA linear GSS 06-AUG-2004
DEFINITION OR_CBa0013H04.f OR_CBa Oryza rufipogon genomic clone OR_CBa0013H04
5', genomic survey sequence.
ACCESSION CL801486
VERSION CL801486.1 GI:51027447
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 709)
AUTHORS Kim,H., Yu,Y., Wlasotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
TITLE OMAP project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0013 row: H column: 04
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
FEATURES
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location/Qualifiers
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/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII;
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ORIGIN
Query Match 11.3%; Score 350.4; DB 9; Length 709;
Best Local Similarity 70.2%; Pred. No. 3.6e-86;
Matches 500; Conservative 0; Mismatches 206; Indels 6; Gaps 2;
QY 387 CAGTTTAGTCAAGCCTATTTCCTCT- -GGCAGAGAGATTGACATGGATTCCTATGCAGA 443
DB 1 CAGCTTAATCAAGCCCATTTCTCTATAACACAGAGGATGAGGGGATTCCTACCTAGA 60
QY 444 AGACATTCGTAATCAGTCAGCTCGCAATGTGTGATGAGGCTGAGCTGTGGGTTTCTGA 503
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QY 504 CTCCAAGAAAAGGCTGCTTGAATATCGATACCAATGCTATGATGTCGCGGCAAGGT 563
DB 121 GACTAAAGATGAGTTGCTTTAACTGATAGATGTCATTAATGACGCTCCAGCTAAGT 180
QY 564 AATCTGTGTTGTGGGATGGGTGTTTAGGCAAGACAGCTCTTTTCGAGGAAGATCTTTGA 623

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DB 181 GATATGTGTGTTGTTATGTTGGTGGATTAGGCAAGACTACCCCTTGCAAGGAAGGCATATGA 240
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DB 241 AAACAAGGAACACAT- -GAAGAACTTCTGTTGTTGCTTGGATCACTGTGTCAGTC 297
QY 684 ATTTACACAGGATTCAGCTACTTAAAGATATATAGCCAACTTTCTGGCCCCAGTTCTCT 743
DB 298 ATTTGACAGGAAGAAATTTCTGAACAATGATCAGGCAACTTCTGGGTGCTGATTCAAT 357
QY 744 GGATCACTCTTGCAGGAATTTCAAGGGAAGGTGGTGGTCAAGTACATCATCTTTCTGA 803
DB 358 AGACAAATCTTTGAAGAATTTAGTGAAGATTGCTGTCGAAGTCCAGCATCTCGCTGA 417
QY 804 GTACTCTGATAGAAGAGCTCAAGGAGAGAGAGTACTTTTGTCTTCTAGATGATCTATGGAT 863
DB 418 TCACCTTGGTTGAAGGCTTAAGGAGAGAAAGTACTTTTGTCTTGTGATGACCTATGAC 477
QY 864 TTTACATGATTGGAATTTGGATAAATGAATTTGCAATTTCTTAAGAACATAAGAAGGGCAG 923
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QY 924 TCGAATAGTATTAACCACTCGGAATTTGATCTTGGCGGAGAAGTGTGCCACAGCCCTCACT 983
DB 538 TCGCATATAATAACAACAGAGATGCTGGCTTACCTGGAAGGTGTACCTCTGAATCACT 597
QY 984 GGTGTACCACCTTCGATTTCTTTCAGATGAAGAGTGCCTAATACATTTGCTACTGAGAAAAAC 1043
DB 598 TATTTACCACCTTGAACCGTTACATATAGATGATGCTATACACTTGTCTACTAGCAAAAGC 657
QY 1044 AAATAAAATCATGAAGACATGGAATCAAAATATAAAATATGCAAAAGATGGTT 1095
DB 658 AACATAAGACTTTTGAGACATGGAATAATGATGAGGACTTGGGCAGCATAGTT 709

RESULT 14
CL197270
LOCUS CL197270 603 bp DNA linear GSS 06-JAN-2004
DEFINITION 104_424_10943635_114_32333_078 Sorghum methylation-filtered library
(Li5ID:104) Sorghum bicolor genomic clone 10943635, genomic survey
sequence.
ACCESSION CL197270
VERSION CL197270.1 GI:40709793
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 603)
AUTHORS Budiman,M.A., Flick,E., Jones,J., Nunberg,A., Citek,R.W.,
Robbins,D., Rohlfing,T., Bradford,K., Fries,J., McMenamy,J.,
Trani,L., Isak,A., Zimmerman,C., Iakey,N. and Bedell,J.A.
GeneThresher methylation filtered genomic sequences from Sorghum
bicolor
Unpublished (2004)
JOURNAL Contact: Bedell JA
COMMENT Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 424 row: c column: 19
Seq primer: M13/pUC Forward
Class: shotgun
High quality sequence stop: 603.
FEATURES
source
location/Qualifiers
1..603
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATX623"
/db_xref="taxon:4558"

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Job time : 6399.15 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 22:56:15 ; Search time 337.705 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	81.6	2.6	5113	4	US-09-336-946B-3
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37	40.6	1.3	1036	3	US-09-004-838-3	Sequence 3, Appli
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39	39.8	1.3	832	4	US-09-621-976-2813	Sequence 2813, Ap
c 40	39	1.3	832	4	US-09-621-976-2813	Sequence 2813, Ap
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ALIGNMENTS

RESULT 1
US-09-330-330-2
; Sequence 2, Application US/09330330
; Patent No. 6274789
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; APPLICANT: Iwamoto, Masao
; APPLICANT: Katayose, Yuichi
; APPLICANT: Sasaki, Takuji
; APPLICANT: Wang, Zi-Xuan
; APPLICANT: Yamanouchi, Utako
; APPLICANT: Ishimaru, Lisa
; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,330
; FILING DATE: 11-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 10-181455
; FILING DATE: 12-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/032001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 82...3696
US-09-330-330-2

QY 1186 AATCTATGAACCTTCCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTGAGG 1245
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QY 1540 AGACAGGAATTTTGTATTTATTACCAATGGAGATGCTCTGATTTAGTTTCAGGAAAC 1599
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QY 7567 ATTGCTATCTTGTATAGTAGCACTGGAAGGAGATAGAGTGAATTCGAGGGCATA 7626
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QY 1720 GATCAATTTGAGGATTTACGGGCTTGGATCTTGAAGTGAATCTTAACTCACTCAA 1779
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Db |||||
QY 7747 CATCACCTTGATCAGATTTGGAAGCTTAATCACCTAAATTTCTTCTACGAGGATGC 7806
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QY 1840 TCATCCATATATTCATTTCCAGATCCATTTGGTAAACTACAGGGCTACAACTTTGAAC 1899
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QY 7807 TATCGTATTTGATCTACTGCCAGATTTACTGGCAACCTGAGGCACTCCAGATGCTAGAC 7866
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QY 1960 ACTCTTCGT 1968
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QY 7927 TACATTCAT 7935
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RESULT 3
US-09-336-946B-3
; Sequence 3, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: E. I. du Pont de Nemours and Company
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336.946B
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 68
; LENGTH: 5222

; SEQ ID NO 3
; LENGTH: 5113
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-336-946B-3

Query Match 2.6%; Score 81.6; DB 4; Length 5113;
Best Local Similarity 46.7%; Pred. No. 3.1e-14;
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

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QY 3604 TCATCAATTCATAGAAAATAAAGTCATGGAAGAAAGTTGCAGGAACTATTTTGTATGAAC 3663
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QY 1436 TAATCAACCGAAGTATGATTCACAGCATCAAGAGTGGGATAGCAGGAAAATTAAGACTT 1495
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QY 3664 TTGTTGTTAGGGCTGCTGTCACACAGTAGATTTAACTGCAAAAATGAGGTATTTGTCTAT 3723
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; Sequence 68, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336.946B
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 68
; LENGTH: 5222

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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-936-946B-68

Query Match      2.6%; Score 81.6; DB 4; Length 5222;
Best Local Similarity 46.7%; Pred. No. 3.2e-14;
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

Qy 908 ACAATAGAGGGGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTCGCGAGAGT 967
Db 3438 ATAATAATAGTTGAGTAGAATACTAATAACAACAGAAATTTGAACCTTTGGCAT 3497
Qy 968 GTGCCACAGCCTCACTGGTGPAACACCTTTGATTTCTTCAGATGAACGATGCCATAACAT 1027
Db 3498 GCTGTGATATACTCAGAGCACAATTAATAGATTGATCCACTGGGTGATGATGCTCAA 3557
Qy 1028 TGCTACTGAGAAAAACAATAAAAAATCATGAGACATGGATCAATAAAAAATATGCAAA 1087
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Db 3678 CCAGACATTTTAAAGCCAGCTGTTAGNTGGATGCGCAATGGNAATCACATACAAAAAT 3737
Qy 1203 -----TCCTTCAGAACTAGAAATAAACCCAGCCTGGAGCTTTGAGGAGAAATGGTGA 1255
Db 3738 CATTGACTACTTCCAAATTTGAAGAAAAATCTACTTTGCAGGGGATGAGGCAAGTACTCA 3797
Qy 1256 CCCTAGGTTACACCACTACCATCCCATTTTGAACCAATGCTTTTGTATCTAAGTATCT 1315
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Qy 1316 TTCCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTGGATGAGATAGCAGAGGTT 1375
Db 3858 ACAAGAGGACTACATAATAGGAAGGCCAACTTGGTGAGGCAATGGATGCTGAAGTT 3917
Qy 1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAAGAAAGTTTACTTTAATGAGC 1435
Db 3918 TCATCAATTCATAGAAAAATAAGTCATGGAAGAAAGTTGCAAGGAACTATTTTGTATGAAC 3977
Qy 1436 TAATCAACCGAAGTATGATTCACAGATCAAGATGGGATGAGGCAAAAAATTAAGACTT 1495
Db 3978 TTGTTGAGGGGCTGCTCCAAACAGTAGATGTTAACTGCAAAAAATGAGGTATTTGTCAT 4037
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US-09-936-170-57
; Sequence 57, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: BB1385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 5222
; TYPE: DNA
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; ORGANISM: Oryza sativa
US-09-993-170-57

Query Match      2.6%; Score 81.6; DB 4; Length 5222;
Best Local Similarity 46.7%; Pred. No. 3.2e-14;
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

Qy 908 ACAATAGAGGGGAGTCGAATAGTAATAACCACTCGGAATGTTGATCTTCGCGAGAGT 967
Db 3438 ATAATAATAGTTGAGTAGAATACTAATAACAACAGAAATTTGAACCTTTGGCAT 3497
Qy 968 GTGCCACAGCCTCACTGGTGPAACACCTTTGATTTCTTCAGATGAACGATGCCATAACAT 1027
Db 3498 GCTGTGATATACTCAGAGCACAATTAATAGATTGATCCACTGGGTGATGATGCTCAA 3557
Qy 1028 TGCTACTGAGAAAAACAATAAAAAATCATGAGACATGGATCAATAAAAAATATGCAAA 1087
Db 3558 GTCAATTTGTTTTTCAGTGGAGTTGTTGGCCAAGGAATGAATTTCTCTGGACATCTTACTG 3617
Qy 1088 AGATGGTTGAACGAATTTGTAATAAATGTTGTCCTACCAATTAGCAATCTTACAATAG 1147
Db 3618 AAGTTTCTCATGACATGATAAAAAAATGTTGGTCTTGGCCACTAGCAATAACTATAACAG 3677
Qy 1148 GAGCTGTGCTTGCAACTAAACAGGTGTGAGAAATGGGAGAAATTTCTATGAACACCT----- 1202
Db 3678 CCAGACATTTTAAAGCCAGCTGTTAGNTGGATGCGCAATGGNAATCACATACAAAAAT 3737
Qy 1203 -----TCCTTCAGAACTAGAAATAAACCCAGCCTGGAGCTTTGAGGAGAAATGGTGA 1255
Db 3738 CATTGACTACTTCCAAATTTGAAGAAAAATCTACTTTGCAGGGGATGAGGCAAGTACTCA 3797
Qy 1256 CCCTAGGTTACACCACTACCATCCCATTTTGAACCAATGCTTTTGTATCTAAGTATCT 1315
Db 3798 ACCTTATTTACATAAATCTTCCCTCATTTGTTTGAAGCAATGCTGTTATACCTTAGCATCT 3857
Qy 1316 TTCCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTGGATGAGATAGCAGAGGTT 1375
Db 3858 ACAAGAGGACTACATAATAGGAAGGCCAACTTGGTGAGGCAATGGATGCTGAAGTT 3917
Qy 1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAAGAAAGTTTACTTTAATGAGC 1435
Db 3918 TCATCAATTCATAGAAAAATAAGTCATGGAAGAAAGTTGCAAGGAACTATTTTGTATGAAC 3977
Qy 1436 TAATCAACCGAAGTATGATTCACAGATCAAGATGGGATGAGGCAAAAAATTAAGACTT 1495
Db 3978 TTGTTGAGGGGCTGCTCCAAACAGTAGATGTTAACTGCAAAAAATGAGGTATTTGTCAT 4037
Qy 1496 GTCGAATTCATGATATCATCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTT 1553
Db 4038 GTGTAGTGCCACCATGTTAATAATTTTCATCAGGTGTAACTCAATAGAGGAGAAATTT 4095
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RESULT 6
US-09-993-170-60
; Sequence 60, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: BB1385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 60
; LENGTH: 5696
; TYPE: DNA
; ORGANISM: Artificial Sequence
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Query Match	2.6%	Score 81.6;	DB 4;	Length 5757;
Best Local Similarity	46.7%;	Pred. No. 3.4e-14;		
Matches 307;	Conservative 0;	Mismatches 339;	Indels 12;	Gaps 1;
Qy	908	ACAATAGAGGGCAGTCGAATAGTATATACCACTCGGAATGTTGATCTTGGCGAGAAGT	967	
Db	3731	ATAATAATGTTGCGAGTAGAATACTAATAACACAGAAATTTGAACCTGTGTAGCTTTGGCAT	3790	
Qy	968	GTGCCACAGCCTCACTGGTGTACCACCTTCGATTTCTTGCGAGTGAACGATGCCATAACAT	1027	
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Qy	1256	CCCTAGGTTACAACCACTACCATCCCATTTGAAACCATGCTTTTCTATCTAAGTATCT	1315	
Db	4091	ACCTTATTTACAAATCTTCTCCTCATTTGTTTGAAGCATGTCTGTTATACCTTTAGCATCT	4150	
Qy	1316	TTCTGTAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGT	1375	
Db	4151	ACAAAGAGGACTACATAATTAGGAAGGCCAACTTTGGTGGAGCAATGATGCGTGAAGGTT	4210	
Qy	1376	TTGTTAGACCAAGGTTGGGATGACGATAAGGATGTTCGAGAAAGTTACTTTAATGAGC	1435	
Db	4211	TCATCAATCCATAGAAAAATAAGTCATGGAAGAAGTTGCAAGGAACTATTTTGATGAAC	4270	
Qy	1436	TAATCAACCGAATATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTT	1495	
Db	4271	TTGTTGTGAGGGCCTGGTCCAACACAGTAGATGTTAATCTGCCAAAAATGAGGTATTGTCTAT	4330	
Qy	1496	GTGGAATTCATGATPATCATCCGTGATATCACAGTTTCAAATCTCGAGACACGAAAAATTT	1553	
Db	4331	GTGTAGTGCACCAATGGTATTTAAATTTCAATCAGGTGTAACTCAATAGAGAGAAATTT	4388	

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RESULT 9
US-09-360-186-4
; Sequence 4, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2718)
US-09-360-186-4

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Query Match	2.0%;	Score 62.6;	DB 3;	Length 2718;
Best Local Similarity	47.2%;	Pred. No. 2.3e-08;		
Matches 265;	Conservative	0;	Mismatches 284;	Indels 12; Gaps 2;

Qy	821	TC	AAGGAGAGAGAGGTACTTTGTTGTTCTAGATGATCTATCGAATTTTACATGATGCGAAAT	880
Db	755	TA	AGAGAAGAGGTACTTAAATTTGCTTGGATGATATCTGGAGTCTGGAAGTCTGGGATG	814
Qy	881	GG	ATAATGAAATTCGATTTCTTAAGAACAAATAAGAGGCGAGTTCGAATAGTAATAACCA	940
Db	815	GC	GTGA---GACGATGCTTTCCAACATCGAAGACAAATCGAGGAGTCGAATACTGTTGACTA	871
Qy	941	CT	CGGAATGTTGATCTTGGGAGAGGTGTGCCACGCCCTCACTGGTGTACCACTTTGATT	1000
Db	872	CC	GTAAATGATGAAGTAGCTTTATATGCTGTGTTAGAGAAATTTCTTTCCGGATGAGCT	931
Qy	1001	TC	TTCGAGATGAACGATGCCATAAATGCTACTGAGAAAAACAAATAAAAAATCATGAAG	1060
Db	932	TC	ATGATCAAGATGAGATTTGGAGTCTTTCAAAAGTCAGCATTTTCAAGTGA-----	986
Qy	1061	AC	ATGGAATCAAAATAAAATATGCAAAAGATGGTTCGAACGAATTTGTAATAATATGGTTC	1120
Db	987	----	AGCATTTACCATATGAGTTCGAGACTGTTTGGAAAGCAAAATCGCAGATGAATGTCACG	1042
Qy	1121	GT	CTACCATTAGCAATACTTTACAATAGGAGCTGTGCTTGCACATAAACACAGGTGTCAGAAT	1180
Db	1043	GG	TACCACCTAACTATTGTCGTGTTTCGAGGGCTTCTCAAATCTCAAAGGACAAATAGAAAG	1102
Qy	1181	GG	GAGAAATCTATGAACACCTTCCTTCAGAACTAGAAATAAACCCAGCGTGGAGCTT	1240
Db	1103	AT	TGGAAAACTGTTTGTCAAGATGTCAAGTCATTCGTCAAAATGATCCTGTATGAACGAT	1162
Qy	1241	TG	AGGAGAAATGGTGACCCTAGGTTTACAACACCCTACCATCCCACTTTTGAACACCATGCTTTT	1300
Db	1163	GT	TCAGTGTGCTGGTTCAGTTTACGATCACTTGCACAGCGATCTAAAAACATGCTTTC	1222
Qy	1301	TG	TATCTAAGTATCTTTTCTGAGGATTTTGAATAACAAAGGAATCGTCTAGTAGGTAGAT	1360
Db	1223	TG	CATTTCCGAAATTTTTCAGAAAGACAGTGATATTCGAGTGAGAAATTTGATGAGATCAT	1282
Qy	1361	GG	ATAGCAGAAGGTTTGTTGA	1381
Db	1283	GG	ATGGCTGAGGGTTCCTGA	1303

RESULT 10
US-09-864-680A-4
; Sequence 4, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B2 REGISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-864-680A-4

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RESULT 10
US-09-864-680A-4
: Sequence 4, Application US/09864680A
: Patent No. 6762285
: GENERAL INFORMATION:
: APPLICANT: Staskawicz, Brian J
: APPLICANT: Dahlbeck, Douglas
: APPLICANT: Tai, Thomas H
: TITLE OF INVENTION: Bc2 RESISTANCE GENE
: FILE REFERENCE: 42250/234021 (5830-4A)
: CURRENT APPLICATION NUMBER: US/097864,680A
: CURRENT FILING DATE: 2001-05-24
: PRIOR APPLICATION NUMBER: US 09/360,186
: PRIOR FILING DATE: 1999-07-23
: PRIOR APPLICATION NUMBER: US 60/093,957
: PRIOR FILING DATE: 1998-07-23
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 2718
: TYPE: DNA
: ORGANISM: Capsicum annuum
US-09-864-680A-4

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Query Match	2.0%	Score 62.6;	DB 4;	Length 2718;
Best Local Similarity	47.2%;	Pred. No. 2.3e-08;		
Matches 265; Conservative	0;	Mismatches 284;	Indels 12;	Gaps 2;

QY 821 TCAAGGAGAGAGGACTTTGTTCTTAGATGATCTATGATTTTACATGATTTGGAATT 880
DB 755 TAAAGAGAGAGAGGACTTAATTTGTTCTTGGATGATATCTGGAGTTGTGAAGTTGGGATG 814
QY 881 GGATAAATGMAATTCATTTCTTAAGAACAAATAAGAGGGCAGTCGAATAGTAATAACCA 940
DB 815 GCGTGA---GACGATGCTTTCCACTGAGACNATGCGAGGAGTCGAATACTGTTGACTA 871
QY 941 CTCGGAATGTTGATCTTCGGGAGAAAGTGTGCCACAGCCTCACTGGGTACCACCTTGATT 1000
DB 872 CCGGTAATGATGAAGTAGCTTGTATGCTGGGTAGAGAAATTTTCTTTGCGGATGAGCT 931
QY 1001 TCTTCAGATGACATGCCATAACATTTGCTACTGAGAAAACAATAAATCATGAAG 1060
DB 932 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAAGTGCAGCATTTTCAAGTGA----- 986
QY 1061 ACATGGAATCAAAATAAATAATGCAAAAGATGTTGAAAGCAATTTGTAATAAATGTTGTC 1120
DB 987 ----AGCATACCATAATGAGTTCGAGACTGTTGGAAGCAATTCGAGATGAATGTCAG 1042
QY 1121 GTCTACCAATAGCAATCTTACAATPAGGAGTGTGCTTGCACACTAAACAGGTTGCAGAA 1180
DB 1043 GTTACCACTAATATTTGCTGGGTGTCAGGCTTCTCAAAATCTAAAGGCAATAGAAG 1102
QY 1181 GGGAGAAATCTATGAAACACCTTCTTCAGAACTAGAAATAAACCAGCCTGGAAGCTT 1240
DB 1103 ATTGAAAACCTGTTGCTTAAAGATGTCAAAGTCAATTCGTCAAAAATGATCCTGATGAAC 1162
QY 1241 TGAGGAGAAATGTTGACCTAGCTTACACCACTACCATCCATTTGAAACCATGCTTTT 1300
DB 1163 GTTACGTTGCTTGGGTTGAGTTAGCATCTTGCAAGCGATCTAAACAATGATCTGATGATCAT 1282
QY 1301 TGTATCTAAGTATCTTTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1360
DB 1223 TGCAATTCGGAATTTTCCAGAGACAGTATATTCAGTGAAGAAATTTGATGATCAT 1282
QY 1361 GGATAGCAGAGGGTTTGTGA 1381
DB 1283 GGATGGCTGAGGGGTTCTCTGA 1303

RESULT 11

US-09-360-186-2
; Sequence 2, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
US-09-360-186-2

Query Match 2.0%; Score 62.6; DB 3; Length 3099;
Best Local Similarity 47.2%; Pred. No. 2.6e-08;
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;

QY 821 TCAAGGAGAGAGGACTTTGTTCTTAGATGATCTATGATTTTACATGATTTGGAATT 880
DB 847 TAAAGAGAGAGGACTTAATTTGTTCTTGGATGATATCTGGAGTTGTGAAGTTGGGATG 906
QY 881 GGATAAATGMAATTCATTTCTTAAGAACAAATAAGAGGGCAGTCGAATAGTAATAACCA 940

DB 907 GCGTGA---GACGATGCTTTCCAACTGAAGACAAATGCAGGGAGTCGAATACTGTTGACTA 963
QY 941 CTCGGAATGTTGATCTTCGGGAGAAAGTGTGCCACAGCCTCACTGGGTACCACCTTGATT 1000
DB 964 CCGTAAATGATGAAGTAGCTTGTATGCTGGGTAGAGAAATTTTCTTTGCGGATGAGCT 1023
QY 1001 TCTTCAGATGAAAGATGCCATAACATTTGCTACTGAGAAAACAATAAATCATGAAG 1060
DB 1024 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAAGTGCAGCATTTTCAAGTGA----- 1078
QY 1061 ACATGGAATCAAAATAAATAATGCAAAAGATGTTGAAAGCAATTTGTAATAAATGTTGTC 1120
DB 1079 ----AGCATACCATAATGAGTTCGAGACTGTTGGAAGCAATTCGAGATGAATGTCAG 1134
QY 1121 GTCTACCAATAGCAATCTTACAATPAGGAGTGTGCTTGCACACTAAACAGGTTGCAGAA 1180
DB 1135 GTTACCACTAATATTTGCTGGGTGTCAGGCTTCTCAAAATCTAAAGGCAATAGAAG 1194
QY 1181 GGGAGAAATCTATGAAACACCTTCTTCAGAACTAGAAATAAACCAGCCTGGAAGCTT 1240
DB 1195 ATTGAAAACCTGTTGCTTAAAGATGTCAAAGTCAATTCGTCAAAAATGATCCTGATGAAC 1254
QY 1241 TGAGGAGAAATGTTGACCTAGCTTACACCACTACCATCCATTTGAAACCATGCTTTT 1300
DB 1255 GTTACGTTGCTTGGGTTGAGTTAGCATCTTGCAAGCGATCTAAACAATGATCTGATGATCAT 1314
QY 1301 TGTATCTAAGTATCTTTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1360
DB 1315 TGCAATTCGGAATTTTCCAGAGACAGTATATTCAGTGAAGAAATTTGATGATCAT 1374
QY 1361 GGATAGCAGAGGGTTTGTGA 1381
DB 1375 GGATGGCTGAGGGGTTCTCTGA 1395

RESULT 12

US-09-864-680A-2
; Sequence 2, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B2 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
; OTHER INFORMATION:
US-09-864-680A-2

Query Match 2.0%; Score 62.6; DB 4; Length 3099;
Best Local Similarity 47.2%; Pred. No. 2.6e-08;
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;

QY 821 TCAAGGAGAGAGGACTTTGTTCTTAGATGATCTATGATTTTACATGATTTGGAATT 880
DB 847 TAAAGAGAGAGGACTTAATTTGTTCTTGGATGATATCTGGAGTTGTGAAGTTGGGATG 906
QY 881 GGATAAATGMAATTCATTTCTTAAGAACAAATAAGAGGGCAGTCGAATAGTAATAACCA 940


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Db 907 GCCTGA---GACGATGCTTTCCAACTGAAGACAATGCAGGGAGTCGAATACCTGTTGACTA 963
Qy 941 CTCGGATGTTGATCTTCGGGAGAGTGTGCCACAGCCTCACTGGTGACCACTTGATT 1000
Db 964 CCCGTAATAGTGAAGTAGCTTTGTTATGCTGTGTAGAGAAATTTTCTTTGCGGATGAGCT 1023
Qy 1001 TCTTGCAGATGAACGATGCCATAACATTTGCTACTGAGAAAAACAATAAAAAATCATGAAG 1060
Db 1024 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGACTTTTCAAGTGA----- 1078
Qy 1061 ACATGGATCAAAATAAAAATATGCAAAAGATGGTTGAACGAATGTAAATAAATGTGCTC 1120
Db 1079 ----AGCATTACCATAATGAGTTCGAGTCTTTGGAAGCAAAATCGCAGATGAATGTCAAG 1134
Qy 1121 GTCTACCAATAGCAATACCTTACATAGAGCTGTGCTTGCACACTAACACAGGTGTCAGAT 1180
Db 1135 GGTTACCATAACTATTGTGCTGGTTGCGAGGCTTCTCAAAATCTAAAAAGGCAATAGAAG 1194
Qy 1181 GGGAGAAATCTATGAACACCTTCCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTT 1240
Db 1195 ATTGAAAACTGTGCTTAAGATGCAAGTCAATGCTGCTCAAAATGATCCTGATGAACGAT 1254
Qy 1241 TGAGGAGAAATGGTGAACCTTAGCTTACAAACCACTACCAATCCCATTTGAAACCATGCTTTT 1300
Db 1255 GTTCACGTGTCTTGGGTGAGTTAGGATCACTTGACAAGCGATCTAAAAACATGTCTTC 1314
Qy 1301 TGTATCTAAGTATCTTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1360
Db 1315 TGCATTTCCGAAATTTTTCAGAAAGCAGTGATATTCCAGTGAAGAAATTTGATGATCAT 1374
Qy 1361 GGATAGCAGAAGGTTTCTGTTA 1381
Db 1375 GGATGGCTGAGGGGTTCTCTGA 1395
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RESULT 13
US-09-360-186-1
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staekawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-360-186-1
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Query Match 2.0%; Score 62.6; DB 3; Length 31491;
Best Local Similarity 47.2%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;

Qy 821 TCAAGGAGAAAGAGGTACTTTGTTGTTCTAGATGATCTATGATTTTACATGATTGGAATT 880
Db 2234 TAAAGAGAAAGAGGTACTTAATTTGTTGGATGATATCTCGAGTTGTGAAGTGGGATG 2293
Qy 881 GGATAAATGAAATGCAATTTCTTAAGAAACAATAAGAGGGCAGTCGAATAGTAATAACCA 940
Db 2294 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCAGGGAGTCGAATACCTGTTGACTA 2350
Qy 941 CTCGGATGTTGATCTTCGGGAGAGTGTGCCACAGCCTCACTGGTGACCACTTGATT 1000
Db 2351 CCCGTAATAGTGAAGTAGCTTTGTTATGCTGTGTAGAGAAATTTTCTTTGCGGATGAGCT 2410
Qy 1001 TCTTGCAGATGAACGATGCCATAACATTTGCTACTGAGAAAAACAATAAAAAATCATGAAG 1060
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Db 2411 TCATGGATCAAGATGACAGTTGGAGTCTTTTCAAAAGTGCAGCATTTTCAAGTGA----- 2465
Qy 1061 ACATGGATCAAAATAAAAATATGCAAAAGATGGTTGAACGAATGTAAATAAATGTGCTC 1120
Db 2466 ----AGCATTACCATAATGAGTTCGAGACTGTTGGAAGCAAAATCGCAGATGAATGTCAAG 2521
Qy 1121 GTCTACCAATAGCAATACCTTACAAATAGGAGCTGTGCTTGCACACTAAACAGGTGTCAGAT 1180
Db 2522 GGTTACCATACTAATTTGTTGCTGGTTGCGAGGCTTCTCAAAATCTAAAAAGGACATAGAAG 2581
Qy 1181 GGGAGAAATTTCTATGAACACCTTCTTTCAGAACTAGAAAAATAAACCCAGCCTGGAAGCTT 1240
Db 2582 ATTGAAAACTGTGTTGCTTAAAGATGTCGAAGTCAATTCGTCACAAAATGATCTCTGATGAACGAT 2641
Qy 1241 TGAGGAGAAATGGTGAACCTTAGCTTACAAACCACTACCAATCCCATTTGAAACCATGCTTTT 1300
Db 2642 GTTCACGTGTCTTGGGTTGAGTTACGATCACTTGCACAGCGATCTAAAAACATGTCTTC 2701
Qy 1301 TGTATCTAAGTATCTTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1360
Db 2702 TGCATTTCCGAAATTTTTCAGAAAGCAGTGATATTCCAGTGAAGAAATTTGATGAGATCAT 2761
Qy 1361 GGATAGCAGAAGGTTTGTGTTA 1381
Db 2762 GGATGGCTGAGGGGTTCTCTGA 2782
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RESULT 14
US-09-864-680A-1
; Sequence 1, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staekawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B2 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-864-680A-1
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Query Match 2.0%; Score 62.6; DB 4; Length 31491;
Best Local Similarity 47.2%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;

Qy 821 TCAAGGAGAAAGAGGTACTTTGTTGTTCTAGATGATCTATGATTTTACATGATTGGAATT 880
Db 2234 TAAAGAGAAAGAGGTACTTAATTTGTTGGATGATATCTCGAGTTGTGAAGTGGGATG 2293
Qy 881 GGATAAATGAAATGCAATTTCTTAAGAAACAATAAGAGGGCAGTCGAATAGTAATAACCA 940
Db 2294 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCAGGGAGTCGAATACCTGTTGACTA 2350
Qy 941 CTCGGATGTTGATCTTCGGGAGAGTGTGCCACAGCCTCACTGGTGACCACTTGATT 1000
Db 2351 CCCGTAATAGTGAAGTAGCTTTGTTATGCTGTGTAGAGAAATTTTCTTTGCGGATGAGCT 2410
Qy 1001 TCTTGCAGATGAACGATGCCATAACATTTGCTACTGAGAAAAACAATAAAAAATCATGAAG 1060
Db 2411 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGCATTTTCAAGTGA----- 2465
Qy 1061 ACATGGATCAAAATAAAAATAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTGCTC 1120
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Db 2466 ----AGCAATACCATAGTTCGAGACTGTTGGAAAGCAATCGCATGAATGTCACG 2521
Qy 1121 GTCTACCAATAGCAATACCTTCAATAGGAGCTGTGCTTGCACCACTAAACAGGTGTCAGAA 1180
Db 2522 GGTACCACTAACTATTGCTGGTGGTTCAGGGCTTCTCAAAATCTAAAGGACAATAGAAG 2581
Qy 1181 GGGAGAAATCTATGCAACACCTTCTCCAGAACTAGAAATAAACCAAGCCTGGAGCTT 1240
Db 2582 ATTGAAACATGTTGCTAAAGATGTCAAGTCAATGTCACAAATGATCCTGATGAACGAT 2641
Qy 1241 TGAGGAGAATGCTGACCCCTAGCTTACAAACCACTACCACTCCCATTTGAAACCACTGCTTTT 1300
Db 2642 GTTCAGGTGCTTGGGTGAGTTACGATCACTTGACAAGCGATCTAAACATGTCCTTC 2701
Qy 1301 TGTATCTAAGTATCTTCTCGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1360
Db 2702 TGCATTTCCGAAATTTTCCAGAGACAGTATATCCAGTGAAGAAATTTGATGAGATCAT 2761
Qy 1361 GGATAGCAGAAGGTTTGTGTTA 1381
Db 2762 GGATGGCTGAGGGGTTCTGTA 2782

RESULT 15

US-08-947-823-2
; Sequence 2, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kaloshian, Isouhi
; APPLICANT: Yaghoobi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Milligan, Stephen
; TITLE OF INVENTION: Procedures and Materials for Conferring
; TITLE OF INVENTION: Pest Resistance in Plants
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 85..3852
; OTHER INFORMATION: /note= "Copy 1 cdna for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
US-08-947-823-2
Query Match 1.9%; Score 57.4; DB 3; Length 3997;
Best Local Similarity 51.4%; Pred. No. 1.5e-06;
Matches 161; Conservative 0; Mismatches 146; Indels 6; Gaps 1;
Qy 1241 TGAGGAGAATGGTGACCCCTAGGTTTACAAACCACTACCACTCCCATTTGAAACCACTGCTTTT 1300
Db 2342 TGATGAAGTTATAGAATTAAAGTTATGACCATTTTACCAATCACCCTCAAGCCATGCTTGC 2401
Qy 1301 TGTATCTAAGTATCTTCTCGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1360
Db 2402 TGTATTTGCAAGTTTTCGGAAGGACACTTCATTGACAACTCTATGAGTTGAATGTTTATT 2461
Qy 1361 GGATAGCAGAAGGTTTGTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGAGAGAAA 1420
Db 2462 TCGGTGCTGAAGGATTTGTGGGAAAGACGGAGATGAACAGATATGGAAGAGTGGTGAAGA 2521
Qy 1421 GTTACTTTAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAG 1480
Db 2522 TTTATATGGATGATTTAAATTTACAGTAGCTTGGTAAATTTGTTTCAATGAG-----ATAG 2575
Qy 1481 GAAAAAATTAAGACTTGTGCAATTCATGATATCATCCGTTGATATCACAGTTTCAATCTCGA 1540
Db 2576 GTTATGCACTGAATTTCCAAATTCATGATCTTGTGCGATGACTTTTGTGTTGATAAAGCAA 2635
Qy 1541 GACAGGAAAAATTT 1553
Db 2636 GAAAGGAAAAATTT 2648
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Job time : 343.705 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2005, 07:09:17 ; Search time 1092.99 Seconds
(without alignments)
16729.796 Million cell updates/sec

Title: US-10-656-394A-7
Perfect score: 3099
Sequence: 1 atggcgagagcgtgctgag.....gcacagctcaagctggctga 3099

Scoring table: IDENTITY NUC
Gap 10'0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3099	100.0	3099	18	US-10-656-394A-7
2	2951.6	95.2	9090	18	US-10-656-394A-13
3	2916.2	94.1	3096	17	US-10-352-179-88
4	2910.2	93.9	3099	18	US-10-656-394A-3
5	2910.2	93.9	3674	18	US-10-656-394A-16
6	2850.2	92.0	3276	17	US-10-352-179-92
7	2820.4	91.0	76272	17	US-10-352-179-83
8	2565.2	82.8	4596	18	US-10-437-963-37316
9	2393.6	77.2	2997	18	US-10-656-394A-11
10	1882	60.7	2982	18	US-10-437-963-2483
11	1621	52.3	2422	18	US-10-656-394A-15
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					Sequence 13, Appl
					Sequence 88, Appl
					Sequence 3, Appli
					Sequence 16, Appl
					Sequence 92, Appl
					Sequence 83, Appl
					Sequence 37316, A
					Sequence 11, Appl
					Sequence 2483, Ap
					Sequence 15, Appl

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13 1562.2 50.4 2940 17 US-10-352-179-84 Sequence 84, Appl
14 1557 50.2 2925 18 US-10-437-963-41016 Sequence 41016, A
15 1553.4 50.1 2982 18 US-10-656-394A-1 Sequence 1, Appli
16 1170.6 37.8 3024 18 US-10-437-963-7778 Sequence 7778, Ap
17 1143.2 36.9 3492 18 US-10-437-963-49433 Sequence 49433, A
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ALIGNMENTS

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; Sequence 7, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; TITLE OF INVENTION: broad-spectrum resistance gene Pi2
; FILE REFERENCE: 035718/252082
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(3099)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 99090
; TYPE: DNA
; ORGANISM: Oryza minuta
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Db	77933	CAGAGATTGACATGGATTCCTATGCAGAACATTCGTAAATCAGTCAGCTCGCAATGTGG	77992
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Qy	836	ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGAAATTG	895
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Qy	896	CATTTCCTTAAGAACAAATAAGAAAGGCGAGTCCGAATAGTAATAACCACTCGGAATCTTGATC	955
Db	78413	CATTTCCTTAAGAACAAATAAGAAAGGCGAGTCCGAATAGTAATAACCACTCGGAATCTTGATC	78472
Qy	956	TTGCGGAGAGTGTGCCACAGCCTCACTGGTGTACCACTTGTGATTTCTTGAGATGAACG	1015
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Qy	1016	ATGCCATAACATTTGCTACTCAGAAAACAAATAAAATCATGAGACATGGAATCAATA	1075
Db	78533	ATGCCATAACATTTGCTACTCAGAAAACAAATAAAATCATGAGACATGGAATCAATA	78592

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Qy	1436	TAATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTT	1495
Db	78953	TAATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTT	79012
Qy	1496	GTGGAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTG	1555
Db	79013	GTGGAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTG	79072
Qy	1556	TATTTATPACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAACACTCGCCACATAGCAT	1615
Db	79073	TATTTATPACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAACACTCGCCACATAGCAT	79132
Qy	1616	TCCAATGGGAGTATGTCCTCGAAAACTGGATTTGGATTTGGAGCATTTATCGATCATTTAGCTA	1675
Db	79133	TCCAATGGGAGTATGTCCTCGAAAACTGGATTTGGATTTGGAGCATTTATCGATCATTTAGCTA	79192
Qy	1676	TTTTTGTGTGACAGCCACAGAGTCTAGCAGATGCGAGTTTGTCCAGATCAATTTGAGGATGT	1735
Db	79193	TTTTTGTGTGACAGCCACAGAGTCTAGCAGATGCGAGTTTGTCCAGATCAATTTGAGGATGT	79252
Qy	1736	TACGGGTCTTTGGATCTTGAAGATGTCACATCTCTTAATCACTCAAAAAAGATTTTCGACCGTA	1795
Db	79253	TACGGGTCTTTGGATCTTGAAGATGTCACATCTCTTAATCACTCAAAAAAGATTTTCGACCGTA	79312
Qy	1796	TTGCATTTGTTGTGCCACTTTGAAAATCTCTGAGTATTTGGATATTTCGTATCATCATATTCAC	1855
Db	79313	TTGCATTTGTTGTGCCACTTTGAAAATCTCTGAGTATTTGGATATTTCGTATCATCATATTCAC	79372
Qy	1856	TTCCGAGATCCATTTGGTAAACTACAGGGCCTACAACTTTTGAAACATGCGGAGCACATACA	1915
Db	79373	TTCCGAGATCCATTTGGTAAACTACAGGGCCTACAACTTTTGAAACATGCGGAGCACATACA	79432
Qy	1916	TTGCAGACCTACCAAGTGAGATCAGTAAATCTCCAATGCTCGCATACTCTTCGTCTGTATAG	1975
Db	79433	TTGCAGACCTACCAAGTGAGATCAGTAAATCTCCAATGCTCGCATACTCTTCGTCTGTATAG	79492
Qy	1976	GACAGTTTCATTTATGACAACTTTTAGTCTAAAAACCAACCAATGAAGTGCATAATCAACACAA	2035
Db	79493	GACAGTTTCATTTATGACAACTTTTAGTCTAAAAACCAACCAATGAAGTGCATAATCAACACAA	79552
Qy	2036	TATGCTTCGCTTAAAGTATTCACACCTTTTAGTTAGTTCGGATGATCGTGCAAAAACAATTTG	2095
Db	79553	TATGCTTCGCTTAAAGTATTCACACCTTTTAGTTAGTTCGGATGATCGTGCAAAAACAATTTG	79612
Qy	2096	CTGAATTCGATGCGGCCACCAAAAGTTGCTGGTCTGAAATCAATCCGTGTGAAGGTACCCA	2155
Db	79613	CTGAATTCGATGCGGCCACCAAAAGTTGCTGGTCTGAAATCAATCCGTGTGAAGGTACCCA	79672
Qy	2156	AAGGAATPAGGTAAGTTTCGAGACTTCGACAGGTTCTTAGAGTATGTTAGATATTCAGCGCGGACCA	2215

[illegible]

RESULT 3

US-10-352-179-88

US-10-352-179-88
: Sequence 88, Application US/10352179

Sequence 88, Application US/1006788A1
Publication No. US20040096788A1

; Publication No: US20
: GENERAL INFORMATION:

APPLICANT: Wang. Guo-liang

APPLICANT: wang, Guo-Li
APPLICANT: Liu, Guifu

APPLICANT: LIL, GUIGU
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Plants

; TITLE OF INVENTION: PROCEDURE
; FILE REFERENCE: 22727/04108

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; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3096)
; OTHER INFORMATION:
; US-10-352-179-88

Query Match      94.1%; Score 2916.2; DB 17; Length 3096;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2975; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATGCGGAGACGGTGCTGAGCATGCGAGGTGCTGCTGGTGGGAGCGCCATCAGCAAGGCC 60
DB 1 ATGCGGAGACGGTGCTGAGCATGCGAGGTGCTGCTGGTGGGAGCGCCATCAGCAAGGCC 60

QY 61 GCCTCCGCTGCTGCCGAGCAGACCAGCCTCCTGCTGGGCGTCGAGAAAGACATCTGGTAT 120
DB 61 GCCTCCGCTGCTGCCAATGAGACGAGCCTCCTGCTCGGCGTCGAGAAAGACATCTGGTAT 120

QY 121 ATCAAGATGAGCTAAAAACGATGCAAGCATTCCTTAGAGCTGCTGGAATATGAAAAAG 180
DB 121 ATCAAGATGAGCTAAAAACGATGCAAGCATTCCTTAGAGCTGCTGGAATATGAAAAAG 180

QY 181 AAAGATGAACATTTAAAGGTTTGGGAGAGCAAAATACGTGACCTGTCTATATGACATTGAA 240
DB 181 AAAGATGAACATTTAAAGGTTTGGGAGAGCAAAATACGTGACCTGTCTATATGACATTGAA 240

QY 241 GATTCCTTTGATGAATTTAAGTTCATATGAAAGCAGCAACCTATTTTCGTGAGTTGGTG 300
DB 241 GATTCCTTTGATGAATTTAAGTTCATATGAAAGCAGCAACCTATTTTCGTGAGTTGGTG 300

QY 301 AAACCTCAGAGAACGCCACCGAATTCGTATCCGATCCACAACTTAAATCAAGAGTTGAA 360
DB 301 AAACCTCAGAGAACGCCACCGAATTCGTATCCGATCCACAACTTAAATCAAGAGTTGAA 360

QY 361 GAAGTGAGTAGCAGAAACACGCTACAGTTTGTAGTCAAGCCCTATTTCTCTGGCAGAG 420
DB 361 GAAGTGAGTAGCAGAAACACGCTACAGTTTGTAGTCAAGCCCTATTTCTCTGGCAGAG 420

QY 421 ATTGACATGGATTTCCTATGCGAGAGACATTCGTATATCAGTCAGCTCGCAATGTGGATGAG 480
DB 421 GATGACATGGATTTCCTATGCGAGAGACATTCGTATATCAGTCAGCTCGCAATGTGGATGAA 480

QY 481 GCTGAGCTTTGTTGGTCTTCTGACTCCAGAAAGGCTGCTTGAATCATGATCCCAAT 540
DB 481 GCTGAGCTTTGTTGGTCTTCTGACTCCAGAAAGGCTGCTTGAATCATGATCCCAAT 540

QY 541 GCTAATGATGTGTCGCGCCCAAGGTAATCTGTGTTGTTGGGATGGGTGTTTAGGCAAGACA 600
DB 541 GCTAATGATGTGTCGCGCCCAAGGTAATCTGTGTTGTTGGGATGGGTGTTTAGGCAAGACA 600

QY 601 GCTCTTTCGAGAGAGATCTTTGAAAGCGAAGACATTTAGAGAACTTCCCTTGCAT 660
DB 601 GCTCTTTCGAGAGAGATCTTTGAAAGCGAAGACATTTAGAGAACTTCCCTTGCAT 660

QY 661 GCTTGGATTACAGTGTCAATCATTTTACAGGATTTAGGCTACTTAAAGATATGATACGC 720
DB 661 GCTTGGATTACAGTGTCAATCATTTTACAGGATTTAGGCTACTTAAAGATATGATACGC 720

QY 721 CAACTTCTTGGCCCCAGTTCTCTGGATCAACTCTTTCGAGAAATTCGAAGGGAAGTGGTG 780
DB 721 CAACTTCTTGGCCCCAGTTCTCTGGATCAACTCTTTCGAGAAATTCGAAGGGAAGTGGTG 780

QY 781 GTGCAAGTACATCATCTTTCTGAGTACCTGTGATGAGAGCTCAAGGAGAGAGGTACTTTT 840
DB 781 GTGCAAGTACATCATCTTTCTGAGTACCTGTGATGAGAGCTCAAGGAGAGAGGTACTTTT 840
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Db 1861 AGATCCATTGGTAAACTACAGGGCTACAAACTTTGAAACATGCTGAGAACATACATTGCA 1920
Qy 1921 GCATCTACCAAGTGAATCAGTAACTCCAAATGCTCGCATACTCTTCGTTGTATAGGACAG 1980
Db 1921 GCATCTACCAAGTGAATCAGTAACTCCAAATGCTCGCATACTCTTCGTTGTATAGGACAG 1980
Qy 1981 TTTCAATTATGACAACTTTAGTCTAAACACCCCAATGAAGTGCATAAATCAACAAATATGC 2040
Db 1981 TTTGTTTATGACAACTTTAGTCTAAACACCCCAATGAAGTGCATAAATCAACAAATATGC 2040
Qy 2041 CTGCCTAAAGTATTCACACCTTTAGTCTAAACACCCCAATGAAGTGCATAAATCAACAAATATGC 2100
Db 2041 CTGCCTAAAGTATTCACACCTTTAGTCTAAACACCCCAATGAAGTGCATAAATCAACAAATATGC 2100
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Db 2101 TTGCACATGGCCACCAAAAGTTGCTGCTCAATCAATCGGTGGAAGGTACCCCAAGGA 2160
Qy 2161 ATAGGTAAGTTGCGAGACTTGCAGGTTCTAGATATGTAGATATCAGCGGACCAAGTAGT 2220
Db 2161 ATAGGTAAGTTGCGAGACTTGCAGGTTCTAGATATGTAGATATCAGCGGACCAAGTAGT 2220
Qy 2221 AGAGCAATCAAAAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTAGGTGTGACAAAC 2280
Db 2221 AGAGCAATCAAAAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTAGGTGTGACAAAC 2280
Qy 2281 GGGTCGACAAAGGAAATGTAAGATCTTTATGACGCAATGAGAGCTCTTCCCTC 2340
Db 2281 GGGTCGACAAAGGAAATGTAAGATCTTTATGACGCAATGAGAGCTCTTCCCTC 2340
Qy 2341 CAATCTCTCCATGTGGATGCTGCGAGGATCTCAGATGTGGAAACACTTTGAGTGCCTAGAT 2400
Db 2341 CAATCTCTATGTGATGCTGCGTATTATCAGATATTGAAACACTTTGAGTGCCTAGAT 2400
Qy 2401 TCTATTTCACTCTCTCCCTACTAGGACACTGCTGTTGGATGGAATCTTTGAGGAG 2460
Db 2401 TCTATTTCACTCTCTCCCTACTAGGACACTGCTGTTGGATGGAATCTTTGAGGAG 2460
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Db 2461 ATGCTTAACCTGATGAGCAGCTCACTCACCTGAGAGAGATCTACTTTATGAGGAGCAAA 2520
Qy 2521 CTAAAGGAAGTAAACCATCTGATCTTTGGGCACTGCCCAACCTCATGCTCTTTCAT 2580
Db 2521 CTAAAGGAAGTAAACCATCTGATCTTTGGGCACTTGCCCAACCTCATGCTCTTTCAT 2580
Qy 2581 CTTTATCGGAATGCTTACCTTTGGGAGAGCTAGTATTCAAACCGGAGCAATCCCAAT 2640
Db 2581 CTTTATCGGAATGCTTACCTTTGGGAGAGCTAGTATTCAAACCGGAGCAATCCCAAT 2640
Qy 2641 CTTAGAACACTTTGGAATTTAGATTCAGCTCAGCTAAGAGAGATCAGATTTGAGGAGCGC 2700
Db 2641 CTTAGAACACTTTGGAATTTAGATTCAGCTCAGCTAAGAGAGATCAGATTTGAGGAGCGC 2700
Qy 2701 AGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGTTGGGAATCTGGGAATTA 2760
Db 2701 AGCTCACCCCTGTTGGAAAGATAGAAATCTTCTGCTGCGAGTTGGGAATCAGGGAATTA 2760
Qy 2761 GGTATCATATCACTTCCAAAGCTCAAGAGATTCCTTATGATGAGGAGTAAAGTGGCT 2820
Db 2761 GGTATCATATCACTTCCAAAGCTCAAGAGATTCCTTATGATGAGGAGTAAAGTGGCT 2820
Qy 2821 GGGCTTGGTCACTGAGGAGGAGTGAACCAACCAATCCCGGCTGCTCTAATG 2880
Db 2821 GGGCTTGGTCACTGAGGAGGAGTGAACCAACCAATCCCGGCTGCTCTAATG 2880
Qy 2881 TACAGTACCCAAAGGTATCAGCACTGGGGCTCAAGCCCAAGGATCTTCTATAGAAAGTG 2940
Db 2881 GACAGTACCCAAAGGTATCAGCACTGGGGCTCAAGCCCAAGGATCTTCTATAGAAAGTG 2940
Qy 2941 CAAACAGCAGATCTCTGTTCTGATGCCGAAGGATCAGTCACTGTAGCAGTGGAAAGCAACG 3000
Db 2941 CAAACAGCAGATCTCTGTTCTGATGCCGAAGGATCAGTCACTGTAGCAGTGGAAAGCAACG 3000

Qy 3001 GATCCCCCTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCACTGTTGACGACG 3060
Db 3001 GATCCCCCTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCACTGTTGACGACG 3060
Qy 3061 AATGATAGCGAAG 3073
Db 3061 AATGATAGCGAAG 3073

RESULT 4

US-10-656-394A-3
; Sequence 3, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: broad-spectrum resistance gene P12
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3099)
US-10-656-394A-3

Query Match 93.9%; Score 2910.2; DB 18; Length 3099;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 1 ATGCGGAGACGGTGTGAGCATGGCGAGGTGCTGGTGGCGAGCGCCATCAGCAAGGCC 60
Db 1 ATGCGGAGACGGTGTGAGCATGGCGAGGTGCTGGTGGCGAGCGCCATCAGCAAGGCC 60
Qy 61 GCCTCGCTGCTGCGACGAGACGAGCTCTGCTGGGCGTCGAGAAAGCATCTGGTAT 120
Db 61 GCCTCGCTGCTGCGACGAGACGAGCTCTGCTGGGCGTCGAGAAAGCATCTGGTAT 120
Qy 121 ATCAAGATGAGCTAAAGGTTTGGGCGAGCAATACGTGACCTGTGATGACATTGAA 240
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Qy 181 AAAGATGAACCTATTAAAGGTTTGGGCGAGCAATACGTGACCTGTGATGACATTGAA 240
Db 181 AAAGATGAACCTATTAAAGGTTTGGGCGAGCAATACGTGACCTGTGATGACATTGAA 240
Qy 241 GATTCCTTGAATGAATTAAGGTCCATATTGAAAGCCAAACCCCTATTTCGTGAGTTGGTG 300
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Qy 301 AAAGTGAAGAAAGCGGCGAGGAGTTCGATCCGATCCAGCTTAAATCAAGAGTTGAA 360
Db 301 AAAGTGAAGAAAGCGGCGAGGAGTTCGATCCGATCCAGCTTAAATCAAGAGTTGAA 360
Qy 361 GAAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 361 GAAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 421 ATTGAATGAATTCCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 421 ATTGAATGAATTCCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy 481 GCTGAGCTTCTGGGTTTCTGAGTCCAGAAAGGCTGCTGAAATGATGATACCAAT 540
Db 481 GCTGAGCTTCTGGGTTTCTGAGTCCAGAAAGGCTGCTGAAATGATGATACCAAT 540
Qy 541 GCTAATGATGGTCCGGCCAAAGGTAATCTGTGTTGTTGGGATGGGTGTTTAGGCAAGACA 600

Db 541 GCTAATGATGGTCCGGCCCAAGGTAATCTGTGTGTTGGGATGGGTGGTTTAGGCAAGACA 600
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Db 601 GCTCTTTTCGAGGAAGATCTTTGAAAGCGAAGAAGACATTAGGAAGAACTTCCCTTGGCAAT 660
Qy 661 GCTTGGATACAGGTGTCACAATCATCTTTCACAGGATGAGCTACTTAAAGATATGATACGC 720
Db 661 GCTTGGATACAGGTGTCACAATCATCTTTCACAGGATGAGCTACTTAAAGATATGATACGC 720
Qy 721 CAACCTTCTGGCCCGAGTCTCTGATCAACTCTTTCGAAGAACTTTCGAAGGGAAGGTGGT 780
Db 721 CAACCTTCTGGTCCCGAGTCTCTGATCAACTCTTTCGATGAATTCGAAGGGAAGGTGGT 780
Qy 781 GTGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGGAAGAGGTACTTT 840
Db 781 GTGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGGAAGAGGTACTTT 840
Qy 841 GTTGTCTAGATGATCTAATGATTTTACATGATTTGGAAATTCGATAAATGAAATTCATTT 900
Db 841 GTTGTCTAGATGATCTAATGATTTTACATGATTTGGAAATTCGATAAATGAAATTCATTT 900
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Db 901 CCTAAGAACATTAAGAGGCGAGTCGATAGTAAATTAACCACTCGGAAATGTTGATCTAGCG 960
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Qy 1081 ATGCATAAGATGTTGAACGAATTTGTAATTAATTAATGTTGTCCTCTACCAATAGCAATACTT 1140
Db 1081 ATGCAAAAGATGGTTGAACGAATTTGTAATTAATTAATGTTGTCCTCTACCAATAGCAATACTT 1140
Qy 1141 ACAATAGAGCTGTCTTGCACCTAAACAGGTGTGAGAAATCGAGAAATTTCTATGAACAC 1200
Db 1141 ACAATAGAGCTGTCTTGCACCTAAACAGGTGTGAGAAATTTCTATGAACAA 1200
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Db 1201 CTTCTCTTCAGAACTAGAAATTAACCCAGCTGGAAGCTTTGAGGAGAAATCGTCAACCTA 1260
Qy 1261 GGTTCACACCACTACCAATCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCT 1320
Db 1261 GGTTCACAAACCACTACCAATCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCT 1320
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Qy 1381 AGACCAAGGTTGGGTAGCAGCACTAAGGATGTCCGAGAAAGTTACTTTAATGAGCTAATC 1440
Db 1381 AGACCAAGGTTGGGTAGCAGCACTAAGGATGTCCGAGAAAGTTACTTTAATGAGCTAATC 1440
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Db 1501 ATTCATGATATCATCCGATATCAACAGTTTCAATCTCGACACAGGAAAAATTTTGTATTA 1560
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Qy 1681 GGTGACAGACCAAGAGTCTAGACATGCGAGTTGTCCAGATCAATTTAGGATGTTACGG 1740
Db 1681 GGTGACAGACCAAGAGTCTAGACATGCGAGTTGTCCAGATCAATTTAGGATGTTACGG 1740
Qy 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACGGTATTGCA 1800
Db 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACGGTATTGCA 1800
Qy 1801 TTGTTGTGCCACTTTGAAATACTTTCAGTATTGGATATTGCTCATCATATATTCACCTCCC 1860
Db 1801 TTGTTGTGCCACTTTGAAATACTTTCAGTATTGGATATTGCTCATCATATATTCACCTCCC 1860
Qy 1861 AGATCCATTTGGTAAACTACAGGGCTTACAACTTTTGAACATGCGGAGCACATACATTGCA 1920
Db 1861 AGATCCATTTGGTAAACTACAGGGCTTACAGACTTTTGAACATGTCACGACACATACATTGCA 1920
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Db 1921 GCATCTACCAAGTGAATCAGTAAACTCCAATGTCTGCTGATCTCTTCTGTTGATAGGACAG 1980
Qy 1981 TTTCAATATGACAACTTTTAGTCTAAACCCACCCTAATGAAGTGCATAAACAACAATATGC 2040
Db 1981 CTTGAAATTTGACAACTTTTAGTCTAAATCACCCTAATGAAGTGCATAAACAACAATATGC 2040
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Db 2281 GGGTCGACAAAGGAAAAATGTAGATATCTTTATGCGACCATTTGAGAGCTCTCTTCCCTC 2340
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Qy 2401 TCTATTTTCATCT 2460
Db 2401 TCTATTTTCATCT 2460
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Db 2461 ATGCTTAACTGGATTGAGCAGCTCACTCAGCTGGAAGAGATCTCAACTTTATGAGTATGAAA 2520
Qy 2521 CTAAAGGAGGTAACCATGCTGATCTTTGGGGCACTGCCCCAACCTCATGCTCTTCTCAT 2580
Db 2521 CTAAAGGAGGTAACCATGCTGATCTTTGGGGCACTGCCCCAACCTCATGCTCTTCTCTCT 2580
Qy 2581 CTTTATCGGAATGCTTACCTTTGGGGGAGAGCTAGTATTTCAAAACAGGAGCAATTCCTCAAT 2640
Db 2581 CTTTATCATATTTCTTATCTTTGGGAGAGAGCTAGTATTTCAAAACGGGAGCAATTCCTCAAT 2640
Qy 2641 CTTAGAACACTTTTGGATTTTATGAAATTTGATCAGCTAAGAGAGATCAGATTTTGGAGCGGC 2700
Db 2641 CTTAGAACACTTTTGTGATTTTCAATTTGGAACAGCTAAGAGAGATCAGATTTTGGAGCGGC 2700
Qy 2701 AGCTCACCCCTGTGGAAAAAGATAGAAATAGGCGAGTGCAGGTTGGATCTGCGGATTAAT 2760
Db 2701 AGCTCACCCAGTTGGAAAAAGATAGAAATCTCTTGTCTGCAGGTTGGAATCAGGAGTATTT 2760

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Qy 2761 GGTATCATTTACCTTCCAAAGCTCAAGGAGATTCCTCAATTAGATACGGAGTAAAGTGGCT 2820
Db |||||||
Qy 2761 GGTATCATTTACCTTCCAAAGCTCAAGGAGATTCCTCAATTAGATACAAAGTAAAGTGGCT 2820
Db |||||||
Qy 2821 GGGCTTGGTACGCTGGAGGAGAGTGAACCCACACCCCAATCGCCCGTCTCTCTAATG 2880
Db |||||||
Qy 2821 AGGCTTGGTACGCTGAAGGAGAGTGAACACACACCCCAATCGCCCGTCTCTCGAATG 2880
Db |||||||
Qy 2881 TACAGTACCGAAGGTATCAGACCTTGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTG 2940
Db |||||||
Qy 2881 GACAGTACCGAAGGATCAGACCTTGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTG 2940
Db |||||||
Qy 2941 CAACAGCAGATCTGTTCTTGATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAACG 3000
Db |||||||
Qy 3001 GATCCCTTCCGAGCAGGAGAGAGCTCGCAGTGCAGAGTGCACGTTGACGACG 3060
Db |||||||
Qy 3061 AATGATAGCAAGAGATAGGACAGCTCAAGCTGGCTGA 3099
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Qy 3061 AATGATAGCAAGAGATAGGACAGCTCAAGCTGGCTGA 3099
Db |||||||
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RESULT 5

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US-10-656-394A-16
; Sequence 16, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; TITLE OF INVENTION: Broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656.394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 3674
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-656-394A-16
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Query Match 93.9%; Score 2910.2; DB 18; Length 3674;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
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Qy 1 ATGGCGGAGACGGTCTGAGCATGCGAGGTGCGTGGTGGCGAGCGCCATCAGCAAGGCC 60
Db |||||||
Qy 9 ATGGCGGAGACGGTCTGAGCATGCGAGGTGCGTGGTGGCGAGCGCCATCAGCAAGGCC 68
Db |||||||
Qy 61 GCCTCCGCTGCTGCCGACGAGACCGCTCTGCTGGCGTGCAGAAAGACATCTGGTAT 120
Db |||||||
Qy 69 GCCTCTGCGCTGCCAATGAGACGAGCTCTGCTGGCGTGCAGAAAGACATCTGGTAT 128
Db |||||||
Qy 121 ATCAAAAGATAGCTTAAACCAAGTGAAGCATCTCTAGAGCTGCTGAACCTTATGAAAAG 180
Db |||||||
Qy 129 ATCAAAAGATAGCTTAAACCAAGTGAAGCATCTCTAGAGCTGCTGAAGCTTATGAAAAG 188
Db |||||||
Qy 181 AAGATGAACTATTAAAGGTTTGGCGAGCAATACCTGCTCATATGACATTGAA 240
Db |||||||
Qy 189 AAGATGAACTATTAAAGGTTTGGCGAGCAATACCTGCTCATATGACATTGAA 248
Db |||||||
Qy 241 GATTCCTTGTATGAATTTAAGGTCCATAATTGAAAGCCAAACCTTATTCGTCAGTTGGTG 300
Db |||||||
Qy 249 GATTCCTTGTATGAATTTAAGGTCCATAATTGAAAGCCAAACCTTATTCGTCAGTTGGTG 308
Db |||||||
Qy 301 AAATCAGAGAAACCGCACCGAATTCGTCATCGGTATCCCAACCTTAAATCAAGAGTTGAA 360
Db |||||||
Qy 309 AAATCAGAGCGCACCGGATCGCTATCGGTATCCCAACCTTAAATCAAGAGTTGAA 368
Db |||||||
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Qy 361 GAAGTGAGTAGCAGGAACACACGCTACAGTTTACTCAAGCCTATTTCTCTGGCACAGAG 420
Db |||||||
Qy 369 GAAGTGAGTAGCAGGAACACACGCTACAAATTTAGTCAGCCCTATTTCTCTCGGCACAGAG 428
Db |||||||
Qy 421 ATTGACATGATTTCTATGCGAAGACATTCGTTAATCAGTCAGCTCGCAATGTGGATGAG 480
Db |||||||
Qy 429 GATGACATGATTTCTATGCGAAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAA 488
Db |||||||
Qy 481 GCTGAGCTTGTGGTCTTCTGACTCCAAAGAAAGGCTGCTTGAATAATGATCGATACCAAT 540
Db |||||||
Qy 489 GCTGAGCTTGTGGTCTTCTGACTCCAAAGAAAGGCTGCTTGAATAATGATCGATACCAAT 548
Db |||||||
Qy 541 GCTAATGATGCTCGGCAAGGTAATCTGTGTTGTTGGGATGGGTGTTTAGGCAAGACA 600
Db |||||||
Qy 549 GCTAATGATGCTCGGCAAGGTAATCTGTGTTGTTGGGATGGGTGTTTAGGCAAGACA 608
Db |||||||
Qy 601 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 660
Db |||||||
Qy 609 GCTCTTTCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCAT 668
Db |||||||
Qy 661 GCTTGGATACAGTGTCAATCAATTTACAGGATTCAGCTTAAAGATATGATACGC 720
Db |||||||
Qy 669 GCTTGGATACAGTGTCAATCAATTTACAGGATTCAGCTTAAAGATATGATACGC 728
Db |||||||
Qy 721 CAACCTTCTGGCCCGCAGTCTCTGAGTCAACTCTTCAAGAAATTCGAAGGAAAGTGGTG 780
Db |||||||
Qy 729 CAACCTTCTGGTCCCGCAGTCTCTGAGTCAACTCTTGCATGAATTCGAAGGAAAGTGGTG 788
Db |||||||
Qy 781 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGAGTACTTT 840
Db |||||||
Qy 789 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGAGTACTTT 848
Db |||||||
Qy 841 GTTGTCTTACATGATCTATGATTTTACATGATTTGGAATTCGATTAATGAAATTCATTT 900
Db |||||||
Qy 849 GTTGTCTTACATGATCTATGATTTTACATGATTTGGAATTCGATTAATGAAATTCATTT 908
Db |||||||
Qy 901 CCTAAGAACCAATAGAAGGCGAGTGAATTAACCACTCGGAATGTTGTGATCTTTGCG 960
Db |||||||
Qy 909 CCTAAGAACCAATAGAAGGCGAGTGAATTAACCACTCGGAATGTTGTGATCTTTGCG 968
Db |||||||
Qy 961 GAGAAGTGTGCCACAGCTCACTGGTGTACACCTTGATTTCTTGGAGATGAACGATGCC 1020
Db |||||||
Qy 969 GAGAAGTGTGCCACAGCTCACTGGTGTACACCTTGATTTCTTGGAGATGAACGATGCC 1028
Db |||||||
Qy 1021 ATACATTTGCTTACTGAGAAACCAATATAAATCATGAAGACATGGAATCAATATAAAT 1080
Db |||||||
Qy 1029 ATTTCTTGTCTACTGAGAAACCAATATAAATCATGAAGACATGGAATCAATATAAAT 1088
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Qy 1081 ATGCAAAAGATGGTTGAACGAAATTTGAAATTAATTTGTTGCTGCTTACCATTAGCAATCTT 1140
Db |||||||
Qy 1089 ATGCAAAAGATGGTTGAACGAAATTTGAAATTAATTTGTTGCTGCTTACCATTAGCAATCTT 1148
Db |||||||
Qy 1141 ACAATAGAGCTGTGCTTGCACCTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACAC 1200
Db |||||||
Qy 1149 ACAATAGAGCTGTGCTTGCACCTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACAA 1208
Db |||||||
Qy 1201 CTTCCTTTCAGAACTAGAAATAAACCCAGCTGGAAGCTTTGAGGAGAAATGGTGACCCCTA 1260
Db |||||||
Qy 1209 CTTCCTTTCAGAACTAGAAATAAACCCAGCTGGAAGCTTTGAGGAGAAATGGTGACCCCTA 1268
Db |||||||
Qy 1261 GGTTACCAACCACTTACCATTCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCT 1320
Db |||||||
Qy 1269 GGTTACCAACCACTTACCATTCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCT 1328
Db |||||||
Qy 1321 GAGATTTTGAATTCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAAGGTTTGT 1380
Db |||||||
Qy 1329 GAGATTTTGAATTCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAAGGTTTGT 1388
Db |||||||
Qy 1381 AGACCAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTACTTTTAAATGAGCTAATC 1440
Db |||||||
Qy 1389 AGACCAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTACTTTTAAATGAGCTAATC 1448
Db |||||||
Qy 1441 AACCAGATGATGATTCACCGATCAAGAGTGGGCATAGCAGGAAAAATTTAAGACTTGTGCA 1500
Db |||||||
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[illegible]

Db	1434	CCTAGGTTACAA	CCACCTACCATCCCATCTGAAAA	CCATGCTTTTGTGTATCTTAAGTATCAT	CTT	1499
Qy	1317	TCCTGAGGATTTT	GAAATCAAAAAGGAATCGTCTAGTAGGTAGAT	TGATAGCAAGAGGTT	1376	
Db	1494	TCCTGAGGATTTT	GAAATCAAAAAGGAATCGTCTGGTAGGTAGAT	TGATAGCAAGAGGTT	1553	
Qy	1377	TGTTAGACCAAAGGTT	GGGATGACGACTAAGGATGTGCGAGAAAGTT	TACTTTTAATGAGCT	1436	
Db	1554	TGTTAGACCGCAGGTT	GGGATGACGACTAAGGATGTGCGAGAAAGTT	TACTTTTAATGAGCT	1613	
Qy	1437	AATCAACCGAAGTATG	ATTCACAGATCMAGAGTGGCATAGCAGGAAAAATTA	AGAAGCTTG	1496	
Db	1614	AATCAGCCGAAATGAT	GAATCAACGATCAAGAGTGGGCATATCAGGAAAAATTA	AGAAGCTTG	1673	
Qy	1497	TCGAATTCATGATAT	CATCCGTGATATCACAGTTTCAATCTCGACACAGAAAAATTTT	CTGT	1556	
Db	1674	TCGATCCATGATAT	CATCCGTGATATCACAGTTTCAATCTCGACACAGAAAAATTTT	CTGT	1733	
Qy	1557	ATTATTAACCAATGGG	AGATGGCTCTGATTTAGTTTCAAGGAAAAACA	CTCGCAACATAGCAT	1616	
Db	1734	ATTGTTACCAATGGG	AGATGGCTCTGATTTAGTTTCAAGGAAAAACA	CTCGCAACATAGCAT	1793	
Qy	1617	CCATGGGAGTATG	CTCTGCGAAAACTGGATTGGATTCGAGCATTA	TTCGATCATTTAGCTAT	1676	
Db	1794	CCATGGGAGTATG	CTCTGCGAAAAACAGATTTGGATTCGAGCATTA	TTCGATCATTTAGCTAT	1853	
Qy	1677	TTTTGGTGACAGAC	CCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTC	GAGGATGTT	1736	
Db	1854	TTTTGGTGACAGAC	CCCAAGAGTCTAGCACATGCAGTTTGTCCAGATCAATTC	GAGGATGTT	1913	
Qy	1737	ACGGGCTCTGGAT	CTTTGAAGATGTGACATTTCTTAATCACTCAAAAA	AGATTTTCCGACGGTAT	1796	
Db	1914	ACGGGCTCTGGAT	CTTTGAAGATGTGACATTTCTTAATCACTCAAAAA	AGATTTTCCGACGGTAT	1973	
Qy	1797	TGCATTTGTTGTG	CCACTTGAATACTTTGAGTATTTGGAATTTGGAATTT	TGATATTTCACTATATTTCACT	1856	
Db	1974	TGCATTTGTTGTG	CCACTTGAATACTTTGAGTATTTGGAATTTGGAATTT	TGATATTTCACTATATTTCACT	2033	
Qy	1857	TCCCAGATCCATTT	GGTAAACTACAGGGCTTACAAA	CTTTTGAACTGCCGAGACACATACAT	1916	
Db	2034	TCCCAGATCCATTT	GGTAAACTACAGGGCTTACAAA	CTTTTGAACTGCCGAGACACATACAT	2093	
Qy	1917	TGCAGCACTACCA	AGTGAGATCAGTAAACTCTGCAATCTCTGCTGTTG	TATAGG	1976	
Db	2094	TGCAGCACTACCA	AGTGAGATCAGTAAACTCTGCAATCTCTGCTGTTG	TATAGG	2153	
Qy	1977	ACAGTTTCATAT	TGACAACTTTTAGTCTTAAACCAACCACTAA	CGAGTGAATTAACACAT	2036	
Db	2154	AAAGTTTGTTTAT	GCACAACTTTTAGTCTTAAACCAACCACTAA	CGAGTGAATTAACACAT	2213	
Qy	2037	ATGCCCTGCC	TAAAGTATTCACACTTTAGTTAGTTCGCGATGAT	TCGTCGAAAAACAATTCG	2096	
Db	2214	ATGCCCTGCC	TAAAGTATTCACACTTTAGTTAGTTCGCGATGAT	TCGTCGAAAAACAATTCG	2273	
Qy	2097	TGAATTCACAT	GGCCACCAAAAAGTTGCTGGTCTGAAATCAATCGG	TGTGAAGTACCCAA	2156	
Db	2274	TGAATTCACAT	GGCCACCAAAAAGTTGCTGGTCTGAAATCAATCGG	TGTGAAGTACCCAA	2333	
Qy	2157	AGGAATAGGTAA	GTTGCGAGCTTGCAGGTTCTAGAGTATGTAGATAT	CAGCGCGACCAAG	2216	
Db	2334	AGGAATAGGTAA	GTTGCGAGCTTGCAGGTTCTAGAGTATGTAGATAT	CAGCGCGACCAAG	2393	
Qy	2217	TAGTAGAGCAAT	CAAAAGAGCTGGGCGAGTTTAACGAAGCTGAGGAAAT	TAGGTGTGACAAC	2276	
Db	2394	TAGTAGAGCAAT	CAAAAGAGCTGGGCGAGTTTAACGAAGCTGAGGAAAT	TAGGTGTGACAAC	2453	
Qy	2277	AAA	CGGGTCGACAAAGGAAAAATGTAAGATPACTTTTAT	TGCAGGCCATTTGAGAAGCTCTCTTTC	2336	
Db	2454	AAA	CGGGTCGACAAAGGAAAAATGTAAGATPACTTTTAT	TGCAGGCCATTTGAGAAGCTCTCTTTC	2513	
Qy	2337	CCTC	CAATCTCTCAGATGTGAGTCTCGAGGAATCTCAGAT	TGTGGAACACTTGAGTGCCT	2396	
Db	2514	CCTC	CAATCTCTCAGATGTGAGTCTCGAGGAATCTCAGAT	TGTGGAACACTTGAGTGCCT	2573	

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Qy 2397 AGATTCTATTTCATCTCTCTCTCCCTACTGAGGACACTCGTGTGGATGGAAATCTTTGA 2456
Db 2574 AGATTCTATTTCATCTCTCTCTCCCTACTGAGGACACTCGGTGTGAATGGAAGTCTTTGA 2633
Qy 2457 GGAGATGCTTAACATGATTTGAGAGCTCACTCACTGGAAGAGATCTACTATTATTGAGGAG 2516
Db 2634 AGAGATGCTTAACATGATTTGAGAGCTCACTCACTGGAAGAGATCTACTATTATTGAGGAG 2693
Qy 2517 CAAATAAGGAAGGTAAACCATCTGCTGATCTTTGGGGCACTGCCCACCTCATCTGGTCTCT 2576
Db 2694 CAAATAAGGAAGGTAAACCATCTGCTGATCTTTGGGGCACTTTGCCAACCTCATCTGGTCTCT 2753
Qy 2577 TCATCTTTATCGGAATGCTTACCTTGGGGAGAGCTAGTATTCAAACAGGAGCAATTTCC 2636
Db 2754 TTATCTTTATTGGAATGCTTACCTTGGGGAGAGCTAGTATTCAAACGGGAGCAATTTCC 2813
Qy 2637 AAATCTTAGAACACTTTGGATTATGAAATTCGATCAGCTAAGAGAGATCAGATTGAGGA 2696
Db 2814 AAATCTTAGAACACTTTGATTTAGAAATTCGATCAGCTAAGAGAGATGAGATTGAGGA 2873
Qy 2697 CGGAGCTCACCCCTGTTGGAAAGATAGAAATAGGCGAGTGCAGGTTGGAAATCTGGGAT 2756
Db 2874 TGGCAGCTCACCCCTGTTGGAAAGATAGAAATCTCTTCTGCGAGTTGGAAATCAGGGAT 2933
Qy 2757 TACTGGTATCAATTCACCTTCAAAGCTCAAGAGATTCCAAATTAGATACGGAAATGAAGT 2816
Db 2934 TATTGGTATCAATTCACCTTCAAAGCTCAAGAGATTTCACTTGAATACAAAGTAAAGT 2993
Qy 2817 GGCTGGGCTTCGTGAGCTGGAGGAGAGTCAACCGCACCCCAATCGCCCGTCTGCT 2876
Db 2994 GGCTAGGCTTCGTGAGCTGGAGGAGAGTGAACACACACCCCAATCGCCCGTCTGCTGCG 3053
Qy 2877 AATGTACAGTCAACCGAAGGTATCAAGCTCGGGGCTGAAGCCGAAGGATCTTCTATAGA 2936
Db 3054 AATGACAGTCAACCGAAGGATCAGACCTCGGGGCTGAAGCCGAAGGATCTTCTATAGA 3113
Qy 2937 AGTCAAACAGAGATCTCTGTTCTGATGCGGAAGGATCAGTCACTGTAGCAGTGGGAAGC 2996
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Qy 2997 AACGGATCCCTCCCGAGAGGAGGAGAGCTCCGAGTCCGAGTGCAGTGCATGCTTGAC 3056
Db 3174 AACGGATCCCTCCCGAGAGGAGGAGAGCTCCGAGTCCGAGTGCAGTGCATGCTTGAC 3233
Qy 3057 GACGAATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTGA 3099
Db 3234 GACGAATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTGA 3276
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RESULT 7

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US-10-352-179-83
; Sequence 83, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR FILING DATE: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 76272
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-83
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Query Match 91.0%; Score 2820.4; DB 17; Length 76272;
Best Local Similarity 97.1%; Pred. No. 0;

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Matches 2872; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
Qy 116 GGTAATCAAAGATGAGCTAAAAACGATGCAAGCAATTCCTTAGAGCTGCTGAACCTTATGA 175
Db 62061 GGTATATCAAAGATGAGCTAAAAACGATGCAAGCAATTCCTTAGAGCTGCTGAACCTTATGA 62120
Qy 176 AAAAGAAAGATGAATTAAGGTTTGGGAGAGCAAAATACGTGACCTGTCTATGACA 235
Db 62121 AAAAGAAAGATGAATTAAGGTTTGGGAGAGCAAAATACGTGACCTGTCTATGACA 62180
Qy 236 TTGAAGATTCCTTTGATGAAATTTAAGGTCCATATTGAAAGCCAAACCTCTTTCTGTCAGT 295
Db 62181 TTGAAGATTCCTTTGATGAAATTTAAGGTCCATATTGAAAGCCAAACCTCTTTCTGTCAGT 62240
Qy 296 TGGTGAACCTCAGAGAACGCCACCGAATTCGTATCCGTATCCACAACCTTAAATCAAGAG 355
Db 62241 TGGTGAACCTCAGAGAACGCCACCGAATTCGTATCCGTATCCACAACCTTAAATCAAGAG 62300
Qy 356 TTGAAGAAAGTGAAGTAGCAGGNAACACGCTACAGTTTAGTCAAGCCTATTTCTCTCTGGCA 415
Db 62301 TTGAAGAAAGTGAAGTAGCAGGNAACACGCTACAGTTTAGTCAAGCCTATTTCTCTCTGGCA 62360
Qy 416 CAGAGATTGACATCGAATTCCTATGCAAGAGACATTCGTAAATCAGTCAAGTCCGAATGCG 475
Db 62361 CAGAGATTGACATCGAATTCCTATGCAAGAGACATTCGTAAATCAGTCAAGTCCGAATGCG 62420
Qy 476 ATGAGGCTGAGCTTTGTTGGGTTTTCGACTCCAAAGAAAAGGCTGCTTTGAAATGATCGATA 535
Db 62421 ATGAGGCTGAGCTTTGTTGGGTTTTCGACTCCAAAGAAAAGGCTGCTTTGAAATGATCGATA 62480
Qy 536 CCAATGCTAATGATGGTCCGGCCAAAGGTAATCTGTGTTGTTGGATGGTGGTGGTTAGGCA 595
Db 62481 CCAATGCTAATGATGGTCCGGCCAAAGGTAATCTGTGTTGTTGGATGGTGGTGGTTAGGCA 62540
Qy 596 AGACAGCTCTTTTCAGGAAAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTT 655
Db 62541 AGACAGCTCTTTTCAGGAAAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTT 62600
Qy 656 GCAATGCTTGGATTACAGTGTCACAATCATTTTCAAGGATTTGAGCTACTTTAAAGATATGA 715
Db 62601 GCAATGCTTGGATTACAGTGTCACAATCATTTTCAAGGATTTGAGCTACTTTAAAGATATGA 62660
Qy 716 TAGCCCAACTTTTGGCCCCAGTTCTCTGGATCAACTCTTTCGAAGAAATTCGAAGGGAAGG 775
Db 62661 TAGCCCAACTTTTAGGTCCCAATTTCTCTGAAACAACTCTTTCGAAGAAATTCGAAGGGAAGG 62720
Qy 776 TGGTGTGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGT 835
Db 62721 TGGTGTGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGT 62780
Qy 836 ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAAATTTGGATAAATGAAATTTG 895
Db 62781 ACTTTGTTTATTCTAGATGATCTATGGATTTTACATGATTTGGAAATTTGGATAAATGAAATTTG 62840
Qy 896 CATTTCCTAAGAACAAATAAGAGGAGTCCGAATAGTAATAACCACTCGGAATGTTGATC 955
Db 62841 CATTTCCTAAGAACAAATAAGAGGAGTCCGAATAGTAATAACCACTCGGAATGTTGATC 62900
Qy 956 TTGGGAGAGAGTGTGCCACAGCCCTCACTGCTGTACCACTGATTTCTTCGAGATGAACG 1015
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Qy 1016 ATGCCATAACATTTGCTACTCAGAAAAACAAATAAAAAATCATGAAGACATGGAATCAAAATA 1075
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Qy 1076 AAAATATGCAAAAAGATGGTTGAACGAATTTGTAATAAAATGTGTCGTCTACCATTAGCAA 1135
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Qy 1136 TACTTACAATAGGAGCTGTCTTGGCAACTAAACAGGTGTCAAGATGGGAGAAATTTCTATG 1195
Db 63081 TACTTACAATAGGAGCTGTCTTGGCAACTAAACAGGTGTCAAGATGGGAGAAATTTCTATG 63140
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Qy 1196 AACACCTTCCCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTGAGGAGAATGGTGA 1255
Db 63141 AACAGCTTCCCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTGAGGAGAATGGTGA 63200
Qy 1256 CCCTAGGTTACACACCCTACCATCCCACTTTGAAACCATGCTTTTGTGATCTAAAGTATCT 1315
Db 63201 CCCTAGGTTACACACCCTACCATCCCACTTTGAAACCATGCTTTTGTGATCTAAAGTATCT 63260
Qy 1316 TTCCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGAGTAGCAGAAAGGT 1375
Db 63261 TTCCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGAGTAGCAGAAAGGT 63320
Qy 1376 TTGTTAGACCAAAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGC 1435
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Qy 1496 GTCGAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTG 1555
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Db 63561 TCCATGGGAGTATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTTTCGATCATTAGCTA 63620
Qy 1676 TTTTGTGTGACAGACCCGAAGTCTAGCACATGACAGTTTGTGCCAGATCAATTTAGGATGT 1735
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Qy 1736 TACGGTCTTGGATTTGAGATGTGACATTTCTAAATCACTCAAAAGATTTCCACCGTA 1795
Db 63681 TACGGTCTTGGATTTGAGATGTGACATTTCTAAATCACTCAAAAGATTTCCACCGTA 63740
Qy 1796 TTGCATTTGTTGGCACTTGAATACCTTGAGTATTTGGATTTGGTATTCATATTTTCAAC 1855
Db 63741 TTGCATTTGTTGGCACTTGAATACCTTGAGTATTTGGATTTGGTATTCATATTTTCAAC 63800
Qy 1856 TTCCAGATCCATTTGGTAAACTACAGGSCCTACAAAATTGGAACATGCGGAGCACATACA 1915
Db 63801 TTCCAGATCCATTTGGTAAACTACAGGSCCTACAAAATTGGAACATGCTGAGAACATACA 63860
Qy 1916 TTGCAGCACTACCAAGTGAGATCAGTAACTCCAACTGCTGCATACCTTTCGTTGTATAG 1975
Db 63861 TTGCAGCACTACCAAGTGAGATCAGTAACTCCAACTGCTGCATACCTTTCGTTGTATAG 63920
Qy 1976 GACAGTTTCATATGACAACTTTAGTCTAAACCAACCCAACTGAAGTGCATACCTAACACAA 2035
Db 63921 GAAAGTTTGTATGACAACTTTAGTCTAAACCAACCCAACTGAAGTGCATACCTAACACAA 63980
Qy 2036 TATGCTGCTCCTAAAGTATTCACACTTTAGTTAGTGGGATGATCGTGCAAAAAAATAATTTG 2095
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Qy 2096 CTGAATTTGCACATGGCCACCAAAAGTTGCTGGTCTGGAATCAATCGGTGTGAAGTACCCA 2155
Db 64041 CTGAATTTGCACATGGCCACCAAAAGTTGCTGGTCTGGAATCAATCGGTGTGAAGTACCCA 64100
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Qy 2216 GTAGTAGGCAATCAAAAGAGCTGGGGCAGTTTAAGCAAGCTGAGGAAATTAGGTGTGACAA 2275
Db 64161 GTAGTAGGCAATCAAAAGAGCTGGGGCAGCTTAAGCAAGCTTGAAGGAAATTAGGTGTGATAA 64220

Qy 2276 CAAACGGGTGCAACAAAGAAAAATTAAGATACTTTATGAGCCATTGAGAAGCTCTCTT 2335
Db 64221 CAAAGGCTCGACAAAGAAAATTAAGATACTTTATGAGCCATTGAGAAGCTCTCTT 64280
Qy 2336 CCCTCCAATCTCTCATGTGGATGCTGCAGGAATCTCAGATGTTGGAAACACTTGAGTGCC 2395
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Qy 2396 TAGATTTCTATTTTCATCTCTCTCCCTACTGAGGACACTGCTGTTGCGATGGAATTTCTTG 2455
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Qy 2456 AGGAGATGCTTAACCTGGAATTCAGCAGCTCACTCACTCTGAAGAAGATCTACTTATTGAGGA 2515
Db 64401 AAGGATGCTTAACCTGGAATTCAGCAGCTCACTCACTCTGAAGAAGATCTACTTATTGAGGA 64460
Qy 2516 GCAAACTAAAGGAAGTAAACCAATGCTGATATCTTTGGGGCACTGCCCCAACCCTCATGTGTC 2575
Db 64461 GCAAACTAAAGGAAGTAAACCAATGCTGATATCTTTGGGGCACTGCCCCAACCCTCATGTGTC 64520
Qy 2576 TTTATCTTTTATTTGGAATGCTTACCTTTGGGGAGAGCTAGTATTTCAAAACCGGAGCATTTCC 2635
Db 64521 TTTATCTTTTATTTGGAATGCTTACCTTTGGGGAGAGCTAGTATTTCAAAACCGGAGCATTTCC 64580
Qy 2636 CAAATCTTAGAACACTTTTGGATTTATGAATTTGGATCAGCTAAGAGAGATCAGATTTTGAGG 2695
Db 64581 CAAATCTTAGAACACTTTTGGATTTATGAATTTGGATCAGCTAAGAGAGATCAGATTTTGAGG 64640
Qy 2696 ACAGCAGCTCACCCCTTTTGGAAAAAGATAGAAATAGCGGAGTGACAGTTTGGAAATCTCGGA 2755
Db 64641 ATGCGAGCTCACCCCTTTTGGAAAAAGATAGAAATCTCTTGTGCGAGGTTTGGAAATCAGGGA 64700
Qy 2756 TTTACTGTATCATTTCACTTTCCAAAGCTCAAGGAGTTCCAAATTTAGATACGGAAGTAAAG 2815
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Qy 2816 TGGCTGGGCTTGGTTCAGCTCGAGGGAGAGTGAACGACACACCCAAATCGCCCGCTGCTGC 2875
Db 64761 TGGCTAGGCTTGGTTCAGCTCGAGGGAGAGTGAACACACACCCAAATCGCCCGCTGCTGC 64820
Qy 2876 TAAATGTAAGTACCGAAGGTATACGACCTTGGGGCTGAAGCGCAAGGATCTTCTATAG 2935
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Qy 2936 AAGTGCACACAGCAGATCTCTTCCATGATCCGAAGGATCAGTCACTGTACGAGTGAAG 2995
Db 64881 AAGTGCACACAGCAGATCTCTTCCATGATCCGAAGGATCAGTCACTGTACGAGTGAAG 64940
Qy 2996 CAAAGGATCCCTTTCCCGAGCAGGAGGAGAGCTCGCAGTCCGAGTGCATCAGTTGA 3055
Db 64941 CAAAGGATCCCTTTCCCGAGCAGGAGGAGAGCTCGCAGTCCGAGTGCATCAGTTGA 65000
Qy 3056 CGACGAATGATAGCAAG 3073
Db 65001 CGACGAATGATAGTGCAG 65018

RESULT 8

US-10-437-963-37316
; Sequence 37316, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5321)B

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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 37316
; LENGTH: 4596
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1
US-10-437-963-37316

Query Match      82.8%; Score 2565.2; DB 18; Length 4596;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 2604; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

Qy 422 TTGACATGGATTCTCTATGCGAAGACATTCGTAATCAGTCAGCTCGCAATGTGGATGAGG 481
Db 29 TAGCAATAGATTCTATGCGAAGACATTCGCAATCAATCAGCTCGAAATGTGATGAG 88

Qy 482 CTGAGCTTTGGGTTTCTGACTCCCAAGAAAGGCTGCTTGAATGATGATACCAATG 541
Db 89 CTGAGCTTTGGGTTTCTGACTCCCAAGAAAGGCTGCTTGAATGATGATACCAATG 148

Qy 542 CTAATGATGGTCCGCGCAAGGTAATCTGTGTGTTGGGATGGGTGTTAGGCGAAGACAG 601
Db 149 CTAATGATGGTCCGCGCAAGGTAATCTGTGTGTTGGGATGGGTGTTAGGCGAAGACAG 208

Qy 602 CTCCTTTGCGAAGAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTTGCAATG 661
Db 209 CTCCTTTGCGAAGAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTTGCAATG 268

Qy 662 CTTGGATTACAGTGTCAACATCTTTCAAGATGAGTACTTTAAAGATATGATACGCC 721
Db 269 CTTGGATTACAGTGTCAACATCTTTCAAGATGAGTACTTTAAAGATATGATACGCC 328

Qy 722 AACTTCTTGGCCCCAGTTCTCTGATCNACTCTTTCGCAAGAAATTCGAAGGAGGTGGTGG 781
Db 329 AACTTCTTGGCCCCAGTTCTCTGATCNACTCTTTCGCAAGAAATTCGAAGGAGGTGGTGG 388

Qy 782 TGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTACTTTTG 841
Db 389 TGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTACTTTTG 448

Qy 842 TTGTTCTAGATGATCTATGGATTTTACATGATTCGGAATTCGGAATTCGGAATTCGATTC 901
Db 449 TTGTTCTAGATGATCTATGGATTTTACATGATTCGGAATTCGGAATTCGGAATTCGATTC 508

Qy 902 CTAAAGACATTAAGAGGGCAGTGAATAGTAAATTAACCACTCGGAATGTGATCTTGGGG 961
Db 509 CTAAAGACATTAAGAGGGCAGTGAATAGTAAATTAACCACTCGGAATGTGATCTTGGGG 568

Qy 962 AGAAGTGTGCCACAGCTCTACTGGTGTACCACTTTGATTTCTTCAGATGAACGATGCCA 1021
Db 569 AGAAGTGTGCCACAGCTCTACTGGTGTACCACTTTGATTTCTTCAGATGAACGATGCCA 628

Qy 1022 TAACATTTCTACTGAGAAAAAATAAATAAATAATCAATGAAGACATGGAATTCGAATTAATA 1081
Db 629 TAACATTTCTACTGAGAAAAAATAAATAAATAATCATGAAGACATGGAATTCGAATTAATA 688

Qy 1082 TGCAAAAGATGGTTGAACGAATTTGTAATAATGTGTGCTGTCTACCAATTAAGCAATCTTA 1141
Db 689 TGCAAAAGATGGTTGAACGAATTTGTAATAATGTGTGCTGTCTACCAATTAAGCAATCTTA 748

Qy 1142 CAATAGGAGCTGTCTTTCGAACATAAAGGTGTGCAATGGGAGAAATTTCTATGAACACC 1201
Db 749 CAATAGGAGCTGTCTTTCGAACATAAAGGTGTGCAATGGGAGAAATTTCTATGAACACC 808

Qy 1202 TTCCTTCAGAACTAGAAATAAACCAAGCCTGGAAGCTTTGAGGAGAAATGGTGACCCCTAG 1261
Db 809 TTCCTTCAGAACTAGAAATAAACCAAGCCTGGAAGCTTTGAGGAGAAATGGTGACCCCTAG 868

Qy 1262 GTTACAACCCCTACCAATCCCAATTTGAAACAATGCTTTTGTATCTAAGTATCTTTCTCTG 1321
Db 1321 GTTACAACCCCTACCAATCCCAATTTGAAACAATGCTTTTGTATCTAAGTATCTTTCTCTG
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Db 869 GTTACAACCCCTACCAATCCCAATCTGAAACCAATGCTTTTGTATCTAAGTATCTTTCTCTG 928
Qy 1322 AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA 1381
Db 929 AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA 988
Qy 1382 GACCAAAAGGTTGGGATGACGACTAAGGATGTGCGAGAAAGTTACTTTAATGAGCTAATCA 1441
Db 989 GACCAAAAGGTTGGGATGACGACTAAGGATGTGCGAGAAAGTTACTTTAATGAGCTAATCA 1048
Qy 1442 ACCGAAGTATGATTCAACGATCAAGAGTGGCATAGCAGGAAATAATTAAGACTTTGTCGAA 1501
Db 1049 ACCGAAGTATGATTCAACGATCAAGAGTGGCATAGCAGGAAATAATTAAGACTTTGTCGAA 1108
Qy 1502 TTCAATGATATCATCCGTTGATATCAAGTTTCAATCTTCGAGACAGGAAATTTTGTATTTAT 1561
Db 1109 TTCAATGATATCATCCGTTGATATCAAGTTTCAATCTTCGAGACAGGAAATTTTGTATTTGT 1168
Qy 1562 TACCAATGGGAGATGGCTCTGATTTAGTTACGAGAAACACCTCGCCACATAGCATTCATG 1621
Db 1169 TACCAATGGGAGATGGCTCTGATTTAGTTACGAGAAACACCTCGCCACATAGCATTCATG 1228
Qy 1622 GGAGTATGCTCTGCAAAACTGGATTGGATTGGAGCATTTATTCGATCATTTAGCTATTTTGT 1681
Db 1229 GGAGTATGCTCTGCAAAACTGGATTGGATTGGAGCATTTATTCGATCATTTAGCTATTTTGT 1288
Qy 1682 GTGACAGACCCAAAGAGTCTAGCACATCAGTTTGTCCAGATCAATTTGAGGATGTTACGGG 1741
Db 1289 GTGACAGACCCAAAGAGTCTAGCACATCAGTTTGTCCAGATCAATTTGAGGATGTTACGGG 1348
Qy 1742 TCTTGGATCTTGAAGATGTGACATCTTAAATCACTCAAAAGATTTTGACCGTATTTGCAT 1801
Db 1349 TCTTGGATCTTGAAGATGTGACATCTTAAATCACTCAAAAGATTTTGACCGTATTTGCAT 1408
Qy 1802 TGTGTGCCACTTGAATATCTTGAGTATTCGATATTCGATATTCGATATTCGATATTTTGT 1861
Db 1409 TGTGTGCCACTTGAATATCTTGAGTATTCGATATTCGATATTCGATATTCGATATTTTGT 1468
Qy 1862 GATCCATTTGGTAAACTACAGGGCTTACAACTTTTGAACATGCGCCGAGACATACATTTGCGAG 1921
Db 1469 GATCCATTTGGTAAACTACAGGGCTTACAACTTTTGAACATGCGCCGAGACATACATTTGCGAG 1528
Qy 1922 CACTACCAAGTGAAGTCAAGTAACTCCAATGTCTGCACTACTCTTCGTTGTATAGGACAGT 1981
Db 1529 CACTACCAAGTGAAGTCAAGTAACTCCAATGTCTGCACTACTCTTCGTTGTATAGGACAGT 1588
Qy 1982 TTCATTTATGACAACTTTAGTCTAAACCCCAACCAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2041
Db 1589 TTCATTTATGACAACTTTAGTCTAAACCCCAACCAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1648
Qy 2042 TGCCTAAAGTATTCACACCTTTTAGTTAGTGGCGATGATCGTGCAAAAACAAATTTGCTGAAT 2101
Db 1649 TGCCTAAAGTATTCACACCTTTTAGTTAGTGGCGATGATCGTGCAAAAACAAATTTGCTGAAT 1708
Qy 2102 TGCAATATGGCCACCAAAAGTTGCTGCTGAATCAATCGGTGTGAAGTACCCAAAGGAA 2161
Db 1709 TGCAATATGGCCACCAAAAGTTGCTGCTGAATCAATCGGTGTGAAGTACCCAAAGGAA 1768
Qy 2162 TAGGTAGTTGCGAGACTTGCAGGTTCTAGGATGATGATATCAGCGGACCAAGTAGTA 2221
Db 1769 TAGGTAGTTGCGAGACTTGCAGGTTCTAGGATGATGATATCAGCGGACCAAGTAGTA 1828
Qy 2222 GAGCAATCAAAAGAGTGGGGCAGTTAAGCAAGCTGAGGAAATTAAGTGTGCAACAAACG 2281
Db 1829 GAGCAATCAAAAGAGTGGGGCAGTTAAGCAAGCTGAGGAAATTAAGTGTGCAACAAACG 1888
Qy 2282 GGTGCAAAAGGAAAAATGTAAGATATCTTTATGCGCAATGAGAAAGCTCTTTCCCTCC 2341
Db 1889 GGTGCAAAAGGAAAAATGTAAGATATCTTTATGCGCAATGAGAAAGCTCTTTCCCTCC 1948
Qy 2342 AATCTCTCCTATGCTGATGCTGCGAGGAATCTCAG---ATGCTGGAACTAGTGGCTAG 2398
Db 1949 AATCTCTCCTATGCTGATGCTGCTGTTATTTCTCAGGTATTTATTTGGAACACTTTGAGTGCCTAG 2008
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QY 2399 ATTCTATTTTCATCTCCTCCTCCCTACTGAGGACACTCGTGTGGATCGAATCTTGAGG 2458
D 2009 ATTCTATTTTCATCTCCTCCTCCCTACTGAGGACACTCAGGTGGAATGGAAGTCTTGAAG 2068
QY 2459 AGATGCTTAACCTGATGAGCAGTCTACTACCTGGAAGAGATCTATTTATGAGGAGCA 2518
D 2069 AGATGCTTAACCTGATGAGCAGTCTACTACCTGGAAGAGTTCGACTTACGGAGGAGTA 2128
QY 2519 AACTTAAGGAGGTAAACCACTGATCTACTTGGGCACTGCCCAACTCATGTCCTTC 2578
D 2129 AACTTAAGGAGGTAAACCACTGATCTACTTGGGCACTGCCCAACTCATGTCCTTC 2188
QY 2579 ATCTTTATCGAATGCTTACCTTGGGAGAGCTAGTATTTCAAAACAGGAGCATTCCTCAA 2638
D 2189 ATCTTTATCGAATGCTTACCTTGGGAGAGCTAGTATTTCAAAACAGGAGCATTCCTCAA 2248
QY 2639 ATCTTAGAACACTTTGGATTTATGAATTTGATCAGCTAAGAGAGATCAGATTTGAGGACG 2698
D 2249 ATCTTAGAACACTTTGGATTTATGAATTTGATCAGCTAAGAGAGATCAGATTTGAGGACG 2308
QY 2699 GCAGCTCACCCCTGTTGGAAAGATAGAAATAGCGAGTGCAGTTGGATCTGGGATTA 2758
D 2309 GCAGCTCACCCCTGTTGGAAAGATAGAAATAGCGAGTGCAGTTGGATCTGGGATTA 2368
QY 2759 CTGGTATCATTCACCTTCCAAAGCTCAAGGAGATTTCCAAATTAGATACGGAAGTAAAGTGG 2818
D 2369 TTGGTATCATTCACCTTCCAAAGCTCAAGGAGATTTCCAAATTAGATACGGAAGTAAAGTGG 2428
QY 2819 CTGGGCTTGGTCAGCTGAGGAGAGAGTGAACGACACCCAAATGCCCCGCTGCTGTAA 2878
D 2429 CTGGGCTTGGTCAGCTGAGGAGAGAGTGAACACACACCCAAATGCCCCGCTGCTGTAA 2488
QY 2879 TGTACAGTACCGAAGGTATCACACCTGCGGGCTGAAGCGAGGATCTTCTATAGAG 2938
D 2489 TGTACAGTACCGAAGGTATCACACCTGCGGGCTGAAGCGAGGATCTTCTATAGAG 2548
QY 2939 TGCAAAACAGCAGATCTCTGTTCTGATGCCGAAGGATCAGTCACTGTAGCAGTGAAGCAA 2998
D 2549 TGCAAAACAGCAGATCTCTGTTCTGATGCCGAAGGATCAGTCACTGTAGCAGTGAAGCAA 2608
QY 2999 CGGATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTGCAGGTGATCAGTGTGACGA 3058
D 2609 CGGATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTGCAGGTGATCAGTGTGACGA 2668
QY 3059 CGAATGATAG 3068
D 2669 CGAATGATAG 2678
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RESULT 9

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US-10-656-394A-11
; Sequence 11, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; TITLE OF INVENTION: broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656.394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2997)
US-10-656-394A-11
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Query Match 77.2%; Score 2393.6; DB 18; Length 2997;

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Best Local Similarity 96.1%; Pred. No. 0;
Matches 2453; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 422 TTGACATGGAATTCCTATGCAGAGACATTCGTATATAGTCAGCTCGCAATGTGTGATGAGG 481
D 197 TAGCAATAGATTCCTATGCAGAGACATTCGCAATCAATCAGCTCGAAATGTGTGATGAG 256
QY 482 CTGAGCTTGTGGGTCTTCTGACTCCAAAGAAAGGCTGCTTGAATGATGATACCAATG 541
D 257 CTGAGCTTGTGGGTCTTCTGACTCCAAAGAAAGGCTGCTTGAATGATGATACCAATG 316
QY 542 CTAATGATGTCGGGCCAAGGTAAATCTGTGTTGTGGATGGGTGGTTTAGGCAAGACAG 601
D 317 CTAATGATGTCGGGCCAAGGTAAATCTGTGTTGTGGATGGGTGGTTTAGGCAAGACAG 376
QY 602 CTCTTTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCTCTTGCATG 661
D 377 CTCTTTTCGAGGAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCTCTTGCATG 436
QY 662 CTTGGATTACAGTGTCACAATCAATTTCAAGGATTTGAGCTACTTAAAGATATATAGGCC 721
D 437 CTTGGATTACAGTGTCACAATCAATTTCAAGGATTTGAGCTACTTAAAGATATATAGGCC 496
QY 722 AACTTCTTGGCCCCAGTTCTCTGATCAACTCTTTGCAAGAAATTTGCAAGGAGAGTGGTG 781
D 497 AACTTCTTGGCCCCAGTTCTCTGATCAACTCTTTGCAAGAAATTTGCAAGGAGAGTGGTG 556
QY 782 TGCAGATACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGGATCTTTTG 841
D 557 TGCAGATACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGGATCTTTTG 616
QY 842 TTGTTCTTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGATAAAATTTGCATTTTC 901
D 617 TTGTTCTTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGATAAAATTTGCATTTTC 676
QY 902 CTAAGAAACAATAAGAGGCGAGTCAATATACACCTCGGAATTTGTGATCTTGGGG 961
D 677 CTAAGAAACAATAAGAGGCGAGTCAATATACACCTCGGAATTTGTGATCTTGGGG 736
QY 962 AGAAGTGTGCACAGCCCTACTGCTGTPACCACTTTGATTTCTTCAGATGAACGATGCCA 1021
D 737 AGAAGTGTGCACAGCCCTACTGCTGTPACCACTTTGATTTCTTCAGATGAACGATGCCA 796
QY 1022 TAACATTTGCTACTGAGAAAAACAAATAAAATCATGAAAGACATGGAATCAAAATAAAATA 1081
D 797 TAACATTTGCTACTGAGAAAAACAAATAAAATCATGAAAGACATGGAATCAAAATAAAATA 856
QY 1082 TGCAAAAAGATGGTTGAACGAATTTGTAAATAAATGTGTCGTCTACCATTTAGCAATACTTA 1141
D 857 TGCAAAAAGATGGTTGAACGAATTTGTAAATAAATGTGTCGTCTACCATTTAGCAATACTTA 916
QY 1142 CAATAGGAGCTGTGCTTGCACACTAAACAGGTGTGCAGAAATGGGAGAAATTTCTATCAACACC 1201
D 917 CAATAGGAGCTGTGCTTGCACACTAAACAGGTGTGCAGAAATGGGAGAAATTTCTATGAACACC 976
QY 1202 TTCCTTCAGAACTAGAAAAATAAACCAAGCCCTGGAAGCTTTTGGAGGAATGGTGACCCCTAG 1261
D 977 TTCCTTCAGAACTAGAAAAATAAACCAAGCCCTGGAAGCTTTTGGAGGAATGGTGACCCCTAG 1036
QY 1262 GTTACAAACCACTTACCATCCCATTTTGAACAACATGCTTTTGTATCTAAGTATCTTCTCTG 1321
D 1037 GTTACAAACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTCTCTG 1096
QY 1322 AGGATTTTGAATCAAAAGGAATCGTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTGTTA 1381
D 1097 AGGATTTTGAATCAAAAGGAATCGTCTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTGTTA 1156
QY 1382 GACCAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTACTTTTAATGAGCTAAATCA 1441
D 1157 GACCAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTACTTTTAATGAGCTAAATCA 1216
QY 1442 ACCGAAGTATGATTTCAACGATCAAGAGTGGGATAGCAGGAAATTTAAGACTTGTGAA 1501
D 1501
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Db 1217 ACCGAATGATGTTCAACGATCAAGATGGGCGATAGCAGGAAAATTAAGACTTGTGCGAA 1276
Qy 1502 TTATCGAATGCTTTACCTTGGGAGAGCTAGTATTCAAACAAGAGCATTTCCCAATC 2641
Db 1277 TTATCGAATGCTTTACCTTGGGAGAGCTAGTATTCAAACAAGAGCATTTCCCAATC 2416
Qy 1562 TACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAACACTCGCCACATAGCATTCCTATG 2701
Db 1337 TACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAACACTCGCCACATAGCATTCCTATG 2476
Qy 1622 GGAGTATGCTCTGCAAAAACCTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTTGG 2761
Db 1397 GGAGTATGCTCTGCAAAAACCTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTTGG 2536
Qy 1682 GTGACAGACCCAAAGAGCTTACACATGCAAGTTTGTCCAGATCAATTTGAGGATGTTTACGGG 2821
Db 1457 GTGACAGACCCAAAGAGCTTACACATGCAAGTTTGTCCAGATCAATTTGAGGATGTTTACGGG 2596
Qy 1742 TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCACCGTATTGCAAT 2881
Db 1517 TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCACCGTATTGCAAT 2656
Qy 1802 TGTGTGCGCACTTGAATTTAGTATTTGATATTTGATATTTGATATTTGATATTTGATATTTG 2941
Db 1577 TGTGTGCGCACTTGAATTTAGTATTTGATATTTGATATTTGATATTTGATATTTGATATTTG 2716
Qy 1862 GATCCATTTGGTAAACTACAGGCGCTTACAAACCTTTGAACTCCGAGCACATACATTTGCGAG 2973
Db 1637 GATCCATTTGGTAAACTACAGGCGCTTACAAACCTTTGAACTCCGAGCACATACATTTGCGAG 2748
Qy 1922 CACTACCAAGTGAGATCAGTAACTTCCAAATGTCTGCATATCTCTCGTTGTTATAGACAGT 2973
Db 1697 CACTACCAAGTGAGATCAGTAACTTCCAAATGTCTGCATATCTCTCGTTGTTATAGAAAGT 2748
Qy 1982 TTCAATTATGACAACTTTTGTAGTCTTAACCAACCAATGAAGTGCATTAACCAACAATATGCC 2041
Db 1757 TTGTTCGTGACAACTTTTGTAGTCTTAACCAACCAATGAAGTGCATTAACCAACAATATGCC 1816
Qy 2042 TGCCTAAAGTATTCACACTTTTGTAGTCTGCATATCTGCATATCTCTCGTTGTTATAGTGAAT 2101
Db 1817 TGCCTAAAGTATTCACACTTTTGTAGTCTGCATATCTGCATATCTCTCGTTGTTATAGTGAAT 1876
Qy 2102 TGCACATGGCCACCAAAAGTTGCTGCTGTAATCAATCGGTGTAGAGTACCCAAAGGAA 2161
Db 1877 TGCACATGGCCACCAAAAGTTGCTGCTGTAATCAATCGGTGTAGAGTACCCAAAGGAA 1936
Qy 2162 TAGGTAACTTCGAGACTTTCAGAGTTCTAGAGTATGTAGATATCAGGCGGACCAAGTAGTA 2221
Db 1937 TAGGTAACTTCGAGACTTTCAGAGTTCTAGAGTATGTAGATATCAGGCGGACCAAGTAGTA 1996
Qy 2222 GAGCAATCAAAAGAGCTGGGGGAGTTTAAAGCAAGCTGAGGAAATTAGGTGTGACAAACG 2281
Db 1997 GAGCAATCAAAAGAGCTGGGGGAGTTTAAAGCAAGCTGAGGAAATTAGGTGTGACAAATG 2056
Qy 2282 GGTGCAAAAGGAAAAATGTAAGATACATTTATGAGGCCATTTGAGAGCTCTCTTCCCTCC 2341
Db 2057 GCTCGCAAAAGGAAAAATGTAAGATACATTTTGTGAGCCATTTGAGAGCTCTCTTCCCTCC 2116
Qy 2342 AATCTCTCCATGTCGATGCTCAGGAACTCAGATGGTGGAACTTGGATGCTAGATTT 2401
Db 2117 AATATCTCTATGTAAGTCTCAGGAACTCAGATGGTGGAACTTGGATGCTAGATTT 2176
Qy 2402 CTATTTTCACTCTCTCCCTACTGAGGACACTCTGTTGGATGGAATTTCTGAGGAGA 2461
Db 2177 CTATTTTCTCTCTCTCCCTACTGAGGACACTCTGTTGGATGGAATTTCTGAGGAGA 2236
Qy 2462 TGCCTAACTGATTTAGAGCTCACTCACTGAAAGAGATCTATTATGAGGAGCAAAAC 2521
Db 2237 TGCCTAACTGATTTAGAGCTCACTCACTGAAAGAGATCTATTATGAGGAGCAAAAC 2296
Qy 2522 TAAAGGAGGTAAACCACTGCTGATCTTTGGGCACTGCCCAACCTCATGCTCTCTCATC 2581
Db 2297 TAAAGGAGGTAAACCACTGCTGATCTTTGGGCACTTTGCCCAACCTCATGCTCTCTCATC 2356
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Qy 2582 TTTATCGAATGCTTTACCTTGGGAGAGCTAGTATTCAAACAAGAGCATTTCCCAATC 2641
Db 2357 TTTATCGAATGCTTTACCTTGGGAGAGCTAGTATTCAAACAAGAGCATTTCCCAATC 2416
Qy 2642 TTAGAACACTTTTGATTTATGAAATTTGGATCAGCTAAGAGAGATCAGATTTTGGAGCGGCA 2701
Db 2417 TTAGAACACTTTTGATTTATGAAATTTGGATCAGCTAAGAGAGATTTAGATTTTGGAGCGGCA 2476
Qy 2702 GCTCACCCCTCTTGGAAAAAGATAGAAATAGCGGAGTGCAGGTGGAATCTGGGATTACTG 2761
Db 2477 GCTGCGCCAGTTTGGAAAAAGATAGAAATCAGATTTCTGCAGGTTGGATCAGGATTTTG 2536
Qy 2762 GTATCATTTCACTTTCCAAAGCTCAAGGAGATTTCCAAATTTAGATACGGAAGTAAAGTGGCTG 2821
Db 2537 GTATTTATCCACTTTCCAAAGGCTCAAGGAGATTTCACTTTGGATACGAAAGTAAAGTGGCTG 2596
Qy 2822 GGCTTGTGCTAGCTGGAGGAGAGTGAACGACACACCCCAATCGCCCGTCTGCTAATGT 2881
Db 2597 GGCTTGTGCTAGCTGGAGGAGAGTGCACACACCCCAATCACCCCGTCTGCTGCAAGA 2656
Qy 2882 ACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGCGGAAGGATCTTCTATAGAGTGC 2941
Db 2657 GGGAGGACCGAAGTATCACGACCTTGTGTGACGCGGAAGATCCCTGTTGAAGTGG 2716
Qy 2942 AACACAGCAGATCTCTTCTGATCCCGAAGCA 2973
Db 2717 AAGCAACGATCCCTCCAGAGCAGGAGGCA 2748
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RESULT 10

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US-10-437-963-2483
; Sequence 2483, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Ross, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 2483
; LENGTH: 2982
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102251C.1
US-10-437-963-2483
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Query Match 60.7%; Score 1882; DB 18; Length 2982;
Best Local Similarity 78.9%; Pred. No. 0;
Matches 2352; Conservative 0; Mismatches 445; Indels 183; Gaps 2;
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Qy 1 ATGCGGAGACGGTGTGAGCATGCGAGGTTCGCTGGTGGCAGCGCCATCAGCAAGGCC 60
Db 178 ATGCGGAGACGGTGTGAGCATGCGAGGTTCGCTGGTGGCAGTGCATCAGCAAGGCC 237
Qy 61 GCCTCCCGCTGTCGCGAGCAGCACAGCTCTCTGCTGGCGTTCGAGAAAGACATCTGTAT 120
Db 238 ACCTCTCGGCGGCCCATGAGCGGAGCTCTCTACTCGCGCTCCAGAAAGACATCTGTAT 297
Qy 121 ATCAAGATGAGCTTAAACGATGCAAGCATTCCTTAGAGCTGCTGAACCTTATGAAAG 180
Db 298 ATCAAGATGAGCTTAAACGATGCAAGCATTCCTTAGAGCTGCTGAAGTATGAAAG 357
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Db 2341 TCCCTGCAATCTCTCCGTGTGATGCTGAGGGGTCTCAGGAAATGGAACACTTAAATGT 2400
Qy 2395 CTAGATTTCTATTTCTATCTCTCCCTCCCTACTGAGGACACTCGTGTGGATGGAATCTT 2454
Db 2401 CTAGATTTCTATTTCTATCTCTCTCTGTTACTTAAAGACACTCAAGTGTGTATGGAGATCTT 2460
Qy 2455 GAGGAGATGCTTAAGTATGAGAGCTCTACTCACTTGAAGAGATCTTACTTATGAGG 2514
Db 2461 GAAGAGATGCCCAACTGATTTGAGCAGCTCTGCGACCTCATGAAGTTTCTACTTATAGGG 2520
Qy 2515 AGCAAACTAAAGGAGGTAAACCAATGCTGATCTTGGGGCACTGCCCAACTCATGTGC 2574
Db 2521 AGTAACTAAAGGAGGAAACCAATGCTGATCTTGGGGCACTGCCCAACTCATGTGC 2580
Qy 2575 CTTCATCTTTATCGGAATGCTTACCTCGGGAGAGCTAGTATTTCAAAACAGGAGCATTC 2634
Db 2581 CTTTGTCTTTCACTTGTATGCTTACCTCGGGGAGATCTAGTATTCAGAAACAGGAGCATTC 2640
Qy 2635 CCAATCTTAGNACACTTTGGATTTATGAATTTGATCAGCTAAGAGAGATCAGATTTGAG 2694
Db 2641 CAAAGCTCGAGGACACTTTGTGTTGACAAAGCTGGATCAGCTAAGAGAGATTTAGGTTTGAG 2700
Qy 2695 GACGCACTCACCCCTCTTGGAAAGATAGAAATAGCGAGTGCGAGTTTGGAAATCTGGG 2754
Db 2701 AACGACAGCTGCCCTTATTTGGAAAGATAGAAATCCGATCTGAGGTTTGGAAATAGGG 2760
Qy 2755 ATTACTGATATCTTACCTTCCAAAGCTCAAGGAGATTTCAATTTAGATACGGAAGTAAA 2814
Db 2761 ATTATGGTATCTCTAACCTTATGAGGCTAAGGAAATTAACATTTGGATCAGAGTTAAA 2820
Qy 2815 GTGCTGGCTTGTGCTGAGCTGGAGGAGAGTGAACGACACCCAAATTCGCCCTGGCTG 2874
Db 2821 GTTGGTTATCTTGTGTCAGTTGGAAAGAGAGTGTGGCACACCCAAATTCGCCCTGGCTA 2880
Qy 2875 CTAATGTACAGTACCGAAGTATCACGACCTGGGGCTGAAGCGAGGATCTTCTATA 2934
Db 2881 CGTATGGAGGAGACCGAAGTGTACGACCTGAGAGGATGGCAAGGATCAGCTGTA 2940
Qy 2935 GAATGCAAAACAGCAGATCTTGTCTCTGATGCCGAAGGAT 2974
Db 2941 GAAATGGAAGCAACGGAGCCCTCCCTGAGCCCGAGAGCT 2980

RESULT 11
US-10-656-394A-15
; Sequence 15, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: broad-spectrum resistance gene Pi2
; CURRENT APPLICATION NUMBER: US/10/656.394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2422
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2014, 2043, 2099, 2114, 2154, 2172, 2178, 2199, 2205, 2236,
; LOCATION: 2268, 2299, 2333, 2337, 2339, 2356
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-15

Query Match 52.3%; Score 1621; DB 18; Length 2422;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1479 AGGAAAAATTAAAGCTTGTGCAATTCATGATATCATCGTGATATCAGTTTCAATCTC 1538
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Db 1 AGGAAAAATTAAAGCTTGTGCAATTCATGATATCATCGTGATATCAGATTTCAATCTC 60
Qy 1539 GAGACAGAAAAATTTTGTATTTATTAACCAATGCGAGATGGCTCTGATTTAGTTTCAAGAAAA 1598
Db 61 GAGACAGAAAAATTTTGTATTTATTAACCAATGCGAGATGGCTCTGATTTAGTTTCAAGAAAA 120
Qy 1599 CACTCGGCACATAGCATTTCCATGGGAGTATGTCCTGCAAAAACCTGGAATTTGGAGCAT 1658
Db 121 CACTCGGCACATAGCATTTCCATGGGAGTATGTCCTGCAAAAACCTGGAATTTGGAGCAT 180
Qy 1659 TATTTCGATCTTACCTATTTTGGTGACAGACCCCAAGAGTCTAGCACATGCGATTTGTC 1718
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Qy 1719 AGATCAATTTGAGGATGTTTACGGGTCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCA 1778
Db 241 AGATCAATTTGAGGATGTTTACGGGTCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCA 300
Qy 1779 AAAAGATTTGACCCGATTTGCAATTTGTCGCACTTGAATACTTGAAGTATTTGATATTC 1838
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Qy 1839 GTCATCCATATATTAACCTTCCAGATCCATTTGGTAAACTACAGGCGCTTACAACTTTGAA 1898
Db 361 GTCATCCATATATTAACCTTCCAGATCCATTTGGTAAACTACAGGCGCTTACAACTTTGAA 420
Qy 1899 CATGCCGAGCACATACATTTGAGCATCTAACAGTGAGATCAGTAAACTCCCAATGCTTCA 1958
Db 421 CATGCCGAGCACATACATTTGAGCATCTAACAGTGAGATCAGTAAACTCCCAATGCTTCA 480
Qy 1959 TACTCTTCTGTTATAGGACAGTTTCAATTTATGACAACTTTTATGCTTAAACCCCAATGAA 2018
Db 481 TACTCTTCTGTTATAGGACAGTTTCAATTTATGACAACTTTTATGCTTAAACCCCAATGAA 540
Qy 2019 GTGCATTAACCAACATATGCTTCTGCTTAAAGTATTTACACCTTTAGTTAGTCTCGGATGA 2078
Db 541 GTGCATTAACCAACATATGCTTCTGCTTAAAGTATTTACACCTTTAGTTAGTCTCGGATGA 600
Qy 2079 TCGTGCAAAACCAATTTGCTGAAATTCACATGGCCACCAAAAGTTGCTGGTCTGATCAAT 2138
Db 601 TCGTGCAAAACCAATTTGCTGAAATTCACATGGCCACCAAAAGTTGCTGGTCTGATCAAT 660
Qy 2139 CGGTGTGAAGGTACCCAAAGGAATAGTAAAGTTCGAGACTTTCAGGTCTTCTAGATATGT 2198
Db 661 CGGTGTGAAGGTACCCAAAGGAATAGTAAAGTTCGAGACTTTCAGGTCTTCTAGATATGT 720
Qy 2199 AGATATCAGCGGACCACTAGTAGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAG 2258
Db 721 AGATATCAGCGGACCACTAGTAGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAG 780
Qy 2259 GAAATTAGGTGTGACAAACAAACCGGTTCGACAAAGGAATAAGTAAAGTACTTTATGACGC 2318
Db 781 GAAATTAGGTGTGACAAACAAACCGGTTCGACAAAGGAATAAGTAAAGTACTTTATGACGC 840
Qy 2319 CATTGAGAAGCTCTCTTCCCTCCCAATCTCTCCATGTCGATGTCGAGGAATCTCAGATGG 2378
Db 841 CATTGAGAAGCTCTCTTCCCTCCCAATCTCTCCATGTCGATGTCGAGGAATCTCAGATGG 900
Qy 2379 TGGAACTTTGAGTGCCTAGATTTCTATTTATCTCTCTCCCTTCTCTGAGGACACTCGT 2438
Db 901 TGGAACTTTGAGTGCCTAGATTTCTATTTCTATCTCTCTCTCTCTGAGGACACTCGT 960
Qy 2439 GTTGGATGGAATTTCTTGGAGGAGATGCTTAACTGATTTGAGCAGCTCACTACCTGGAAGAA 2498
Db 961 GTTGGATGGAATTTCTTGGAGGAGATGCTTAACTGATTTGAGCAGCTCACTACCTGGAAGAA 1020
Qy 2499 GATCTACTTTATGAGGAGCAAACTTAAAGGAAGGTAAACCATGCTGATCTTGGGGCACT 2558
Db 1021 GATCTACTTTATGAGGAGCAAACTTAAAGGAAGGTAAACCATGCTGATCTTGGGGCACT 1080
Qy 2559 GCCCAACCTCATGGTCTTCTCATCTTTATCGGAATGCTTTACCTTGGGGAGAGCTAGTATT 2618
Db 1081 GCCCAACCTCATGGTCTTCTCATCTTTATCGGAATGCTTTACCTTGGGGAGAGCTAGTATT 1140

QY 2619 CAAACAGGAGCATTTCCCAATCTTAGAACACTTTGGATTTATGAATTTGGATCAGCTAAG 2678
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QY 2679 AGAGATCAGATTTTGGAGCGGAGCTCACCCCTGTGTGAAAAGATAGAAAATAGGCGAGTG 2738
DB 1201 AGAGATCAGATTTTGGAGCGGAGCTCACCCCTGTGTGAAAAGATAGAAAATAGGCGAGTG 1260
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DB 1321 TAGATACGAAGTAAAGTGGCTGGGCTGTGTGAGTGGAGGAGAGTGAACGACACCC 1380
QY 2859 AAATCGCCCGCTGTCTGCTTAATGTACAGTGACCGAAGGTATCACGACCTGGGGCTGAAGC 2918
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DB 1561 GCAGGTGATCAGTTGACGACGAATGATAGCGAAGAGATAGCGAGATAGCGACGCTCAAGCTGGCTG 1620
QY 3099 A 3099
DB 1621 A 1621

RESULT 12
US-10-352-179-90
; Sequence 90, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 3220
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-90

Query Match 50.8%; Score 1574.2; DB 17; Length 3220;
Best Local Similarity 72.8%; Pred. No. 0;
Matches 2168; Conservative 0; Mismatches 763; Indels 46; Gaps 9;

QY 1 ATGCGGAGACGGTGCTGAGCATGGCGAGGTGCGTGTGGGAGCGGCATCAGCAAGGCC 60
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DB 61 GCTTCGGTTCGCGCAGACAAGATGATCATGCTGCTGGGAGTGCAGAGGAGATATGGTTC 120
QY 121 ATCAAGATAGCTAAACACGATGCAAGCATTTCTTAGAGCTGCTGAACTTATGAANAAG 180

DB 121 ATCAAGATAGCTACAAACGATATCAAGCAATTTTGTATGCTGCGCAA--GCATCAAAG 177
QY 181 AAAGATGAATATTAAAGGTTTGGGCGAGACAAATAGTGCCTGTATATGACATTGAA 240
DB 178 AAAGCATACTATTGAAGGTTTGGGTGCGACGAAGTAAGGGATCTTCTATGACATTGAA 237
QY 241 GATTCCCTTGATGAATTTAAAGGTCATATTGAAAGCCAAACCCATTATTTCGTCACTGGTG 300
DB 238 GATTCCCTTGATGAATTTACAGTTTCATGTGGCGAGCCAAACTTGTGCGGCGAGTTGATG 297
QY 301 AAATCAGAGAAACGCCACCGAATTTGCTATCCGATATCCACACCTTAAATCAAGAGTTGAA 360
DB 298 AAGCTAAAGGATCGCCATCGGATTCGCAATCCAGATCCGCAATCTCAGGACAAAGAAATGAA 357
QY 361 GAGTGTAGTACGAGACACACGCTACAGTTTATGCTCAAGCT---ATTTCCTCTGGCACA 417
DB 358 GAAGTAAGCACTAGGAACATACGCTACAACCTTATAGAGAAATGACCTCACCTGCAACA 417
QY 418 GAGATTCACATGGATTCCTATGCAGAAAGACATTCGTAAATCAGTCAGCTCGCAATGTGGAT 477
DB 418 ACTGATGAGAGGAATTTATTTATGGAAGACATTCGCAACCAATAAGCTAACACATTTAG 477
QY 478 GAGCTCAGCTGTGGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATAATGATCGATACC 537
DB 478 GAAGCTGATCTTGTGGGTTTCTGAGACCCAAAGAGAGATTCCTTGATCTTATAGATGTC 537
QY 538 AATGCTAATGATGTCGCGCCAGGTAACTCTGTGTTCTTGGGATGGGTGTTTAGGCAAG 597
DB 538 CATGCCAATGACGACCTACAAAGATTTGATATGTTGTCGTGCGTATGGGTGGTTCGGGTAA 597
QY 598 ACAGCTCTTTCGAGAAAGATCTTTGAAAGCGAAAGACATTTAGGAAAGAACTTCCCTTGC 657
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QY 778 GTGGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAAGGATAC 837
DB 775 GTTCCACAGGTAGACGACCTCGCCAGCTACTCTAGGACAGAGTTAAATGAAAGAGGTAC 834
QY 838 TTTGTTGTTCTAGATGATCTATGATTTTACATGATTTGGAATTTGGAATAATGAAATGCA 897
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QY 898 TTTCTTAAGAACATTAAGAGGCGAGTCGAATAGTAAATTAACCTCGGAATGTTGATCTT 957
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DB 955 ACTAAGGAGGTACTTCTGAAATGCTTATCTACAGCTTAAACCCCTAGAAATTAACAT 1014
QY 1018 GCCATAACATTTGCTAGAGAAAAACAAATAAATCATGAAAGACATGGAATCAAAATAAA 1077
DB 1015 GCAAAAGAGTTGCTTCTACGGAAGCAATAAAGCAATAGGAGATATGGAAGATGATAAA 1074
QY 1078 AATATGCAAAAGATGTTGAACGAATTTGTAATAAATGTTGCTCTCTACCATTTAGCAATA 1137
DB 1075 AAGATGAGTGACATTAACCTAAATAATTAAGAAAGTGTGGCTATTTACCCTGCTGATA 1134
QY 1138 CTTCAATAGGAGCTGTGCTTTGCAACTAAACAGAGTGTGAGAAATGGGAGAAATTTCTATGAA 1197
DB 1135 CTCAATAGGAGCGTGTCTTCCACCAGAGATAAGAGAGTGGGAAACCTTTTATAGT 1194
QY 1198 CACCTTCCTCAGAACTAGAAATAAACCAGAGCTGGAAGCTTTGAGAGAGATGGTGACC 1257
DB 1195 CAGATACCTTCAGAGCTTGAGAGCAACCCAAACCTTGAAGCAATGGAAGGATAGTGACC 1254

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Qy 1258 CTAGGTTTCAACACCTTACCATCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTT 1317
D 1255 CTAAGTTTCAACACTACTTACCGTCTCATCTTAAGCAATGCTTTTGTATCTAAGCATATTT 1314
Qy 1318 CCTGAGGATTTTGAATCABAAGGAATCGTCTAGTGTAGTACATGATAGCAGNAGGGTTT 1377
D 1315 CCTGAGGATTTTGAATTAATAGGAACCGTCTGGTAATATAGATGATGCGCAGAGGGTTT 1374
Qy 1378 GTTAGACCAAAAGGTTGGGATGACGACTAAGGATGTCCGAGAAAGTTACTTTAAATGAGCTA 1437
D 1375 ATTAAGCTAGGACTAATATGACTATTGAAGATGTGGGAAAGTTACTTTTAAGAACTT 1434
Qy 1438 ATCAACCGAATGTATGATTAACAGATCAAGAGTGGGCATAGCAGAAATAATTAAGACTTGT 1497
D 1435 ATCAACCGTAGCATGATTCAGCCATCAAGACGGGTATACGAGGAGATTTTAAAGAGCTGT 1494
Qy 1498 CGAATTCATGATATCATCCGTTGATATCACAGTTTCAATCTCGACACAGGAAATTTTGT 1557
D 1495 CGAGTCCACGACATCATGCGTGTATTAACAATTTTCGATTTCTAGAGAAAGAAATTTTCACA 1554
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D 1555 CTCTTACCCGATGGCACTGACTATGATGATACATGCGACATAGAAATTT 1614
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Qy 1675 ATTTTGGTGACAGACCCAGAGTCTAGCACATGCACTTTGTCAGATCAATTTGAGGATG 1734
D 1675 ATGTTTGGTGAGAGGTCGTTAGAACATAGAGCATTTGATTTTCTCATCTCAGTTGAGGATG 1734
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Qy 1795 ATTCGATTTGTTGCCACTTGAATATCTTTGATGATTT-----GGATATTCGTCAATC 1844
D 1795 ATAGTGCTCTTTGGCCACTTGAATATCTATGATTAAGATACAGATACCGTTCCACCATA 1854
Qy 1845 CATATATTTCACTTCCAGATCCATTTGTTAACTACAGGCGCTACAAACTTTTGAACATGCC 1904
D 1855 TATTTATTTCACTTCCCAACTCCATAGCTAGACTGCTGCTGAGACATTTGGGACTTTGGG 1914
Qy 1905 GAGCACATACATTTGACGACTACCAAGTGAGATCAGTAAACTCCAAATGCTCTGCACTACTCT 1964
D 1915 TCACAGCTACATTTCAACACTGCCAACTCAGATTTACT-AACTTCGGAGTCTCCGTAGCGCT 1973
Qy 1965 TCGTTGTATAGGACAGTTTCAATTATGACAACTTTTAGTCTAAACCCCAATGAAGTGCAT 2024
D 1974 TCGATGCATGAAGAATATTTTCTCTCTCTTT-----AACAAACATATTT 2018
Qy 2025 AACTAAACATATATGCTGCTTAAAGTATTCACACCTTTTAGTGTGCGGATGATCTGTCG 2084
D 2019 AACTAAACATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2078
Qy 2085 AAAACAAATTCCTGAATTTGACATGGCCACCAAAAGTTGCTGCTGCTGCTGCTGCTGCTGCT 2144
D 2079 TGAACAAATTTCTAAATTTGCACTGGCCACCAAAAGGCTTCCGTTTCAAAATCAAAATGGTGT 2138
Qy 2145 GAAGGTATCCCAAGGAATAGT-----AAGTTTGGAGACTTTCAGGTTTCTAGAGTATGTAG 2200
D 2139 CAAGGTACCAAAAGGAATATGTAATAAAATAAAGCTGACTTAAATAATTTGAGGTAGTGG 2198
Qy 2201 ATATCAGCGGACACAGTATGATGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTGAGGA 2260
D 2199 ATATTAGAAGCTAGCAGTATGAGCAATCAAGAGTTTGGGGCAGTTAAGCAAGCTGAGGA 2258
Qy 2261 AATTAGGTGTACAAACAAAGGTCGACAAAGGAAATATGAAGTATCTTTATTCAGCCA 2320
D 2259 AATTATGTGTGTAACAAAGGGATCCCAAAAGGAAATATGAGATATCTCTATACAGCTA 2318
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Qy 2321 TTGGAAGCTCTCTTCCCTCCAAATCTCTCCATGTGGATGCTGCAAGGAATCTCAGATGGTG 2380
D 2319 TCCAGAAGCTCTGTGTTCTCAATCTCTCAATGTGAATGCTGTGGGATTTTTCAGGTATTG 2378
Qy 2381 GAACACTTTAGTGTCTAGATTTCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2440
D 2379 GAACACTTTAGTGTATAGATTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438
Qy 2441 TGGATGGAATTTCTTGAGGAGATGCTTAACCTGGATTTGAGCAGCTCACTCACCTGAAGAAGA 2500
D 2439 TGAATGGAAGTCTTTGAGGAGATGCTTAACCTGGAATTTGAGCAGCTCAACCTGATGAAGT 2498
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D 2499 TCACTTTATGAGGAGCAAACTAAAGGAAGTAAACCACTGCTATCTTGGTGTCTTCCGCGTTGC 2558
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D 2559 CCAACCTCATGCTCTTCTCATCTTTTATCGGAATGCTTACCTTTGGGAGAGCTAGTATTTC 2618
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Qy 2921 AAGGATCTTCTATAGAAGTGCACACACAGATCCCTGT 2957
D 2915 AAGGATCCCTGTTTGAAGTGAAGCAACAGATCCCTGT 2951
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RESULT 13

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US-10-352-179-84
; Sequence 84, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 2272/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; PRIORITY FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2940)
; OTHER INFORMATION:
US-10-352-179-84
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Query Match      50.4%; Score 1562.2; DB 17; Length 2940;
Best Local Similarity 71.7%; Pred. No. 0;
Matches 2092; Conservative 0; Mismatches 818; Indels 9; Gaps 3;
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Db 1 ATGCGGAGACGGTGTGAGCATGCGAGGTCGCTGGTGGCAGCGCCATCAGCAAGGCC 60
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Db 121 ATCAAGGACGAGCTCAAACTATTTCAGGCATTCCTTAAGAGCTGCTGAAATCAAGAAAG 180
Qy 181 AAAGATGAATCTTAAAGTTTGGGCAAGCAAAATACGTGACCTGTATATGACATTTGAA 240
Db 181 AAAGATGAATCTTAAAGTTTGGGCAAGCAAAATACGTGACCTGTATATGACATTTGAA 240
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Qy 1378 GTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGAGAAAGTTTACTTTAATGACCTA 1437
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Qy 1858 CCCAGATTCATTTGGTAAACTACAGGCGCTCAAACTTTTGAACATGCGCGAGCACATACATT 1917
Db 1858 CCAAGGTCATAGGAAATTTGCAAGTGTGCAAAATTTTGAACATGAGGAGGCAAAATATC 1917
Qy 1918 GCAGCACTACCAAGTGAATCAGTAAACTCCAATGTCGTGATCTCTTGGTTGTATAGGA 1977
Db 1918 TCAGCACTAACTGAGGTGACTAAACTCCGAATCTCCGATAGCCTCCGATGAGCAGG 1977
Qy 1978 CAGTTTCATTTATGACAACTTTAGTCTAA---ACCACCGCAATGGAAGTCATAACTAAACACA 2034
Db 1978 AGTTCAGTCTCTGGTTACTTTAGCATATATAGATATCCCAAGGATGCTTGTATGATCACT 2037
Qy 2035 ATATGCTGCTAAGATTTACACCTTTTGTAGTTCGCGATGATTCGTGCAAAAACAAATT 2094
Db 2038 ATGTGCTTACCGATGGTTTCTCAACTTCAATAAAATTTCACTGACCGGTGTGAAATTAAT 2097
Qy 2095 GCTGAATTTGACATGGGCCACCAAAAGTTGCTGCTGCAATCAATCGGTGTGAAAGTACCC 2154
Db 2098 CTTGAGATATGCAATGCTCATGTTCTACCGTTGGTCTGATACAAAGGGGTGTGAGGGTCCA 2157
Qy 2155 AAAGGAATAGGTAAGTTGGCAGAGACTTGCAGGTTCTTAGATATGTAGATATCAGGCGGACC 2214


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Db 2158 AGAGGAATTGACAACTAAAGAGTTACAGATTCTAGAAAGTGTGGACATCAACAGAACT 2217
Qy 2215 AGTAGTAGAGCAATCAAGAGCTGGGCGAGTTAAAGCAAGCTGAGGAAATTAGGTGTGACA 2274
Db 2218 AGTAGGAAGCGATTGAGAGCTGGGAGGCTAAATTCAGTTAAGAAATTAAGCGTGACA 2277
Qy 2275 ACAACGGGTGCAAAAGAAATGTAAAGATCTTTATGACAGCCATTGAGAAAGCTCTCT 2334
Db 2278 ACAAAAGGCGCACAAATAAAGATATCAGATATTTGTGCAGCGATTGAGAAGCTCTCT 2337
Qy 2335 TCCCTCCAACTCTCCATGTGATGCTGCAGAAATCTCAGATGTTGGAGCACTTGAAGTGC 2394
Db 2338 TCTCTGCAATCTCTCCGTGTGATGCTGAGGAATCTCAGATACCTGGAACACTTGAAGTG 2397
Qy 2395 CTGAGATCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2454
Db 2398 CTCATTTGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2457
Qy 2455 GAGGAGATGCTTAATGATGAGCAGCTCACTCACTGAAAGAACTTACTTATTTGAGG 2514
Db 2458 GCAGATACACAAACTGTTGGAACTTAAAGCACTTAAAGCACTTAAAGCACTTAAAGCA 2517
Qy 2515 AGCAAACTAAAGGAGGTAAACCACTGCTGATCTTGGGCACTGCTGCTGCTGCTGCTG 2574
Db 2518 TGTGTGCTACAGATGGTAAACTATGAGATACCTTGGGCACTGCTGCTGCTGCTGCTG 2577
Qy 2575 CTTCATCTTTATCGAACTTACCTTGGGAGAGCTAGTATTCAAACAGGAGCATTC 2634
Db 2578 CTTCGCTTTATCGCAACGATATCTGACGAGAAATGGCACTTCAAGGGGAACTTC 2637
Qy 2635 CCAATCTTAGAACACTTTGGATTTATGAATTTGATCAGCTAAGAGAGATCAGATTTGAG 2694
Db 2638 CCNAATCTCAGGTGCTTGATATTTACTTGTGAGCAACTTAGAGAGATTAAGATTTGAG 2697
Qy 2695 GACGCACTCACTCTGTTGGAAAGATAGAAATAGGCGAGTGAGGTTGGAATCTGGG 2754
Db 2698 GAGGCACTCGCCCAACAATGAAAGATATAGAAATTTATGTTGTTGAGGTTGGAATCAGG 2757
Qy 2755 ATTACTGTATCATTCACCTTCAAGCTCAAGGAGTTCCAAATTTAGATACGGAATAA 2814
Db 2758 ATTATTTGATACAGCACTTCAAGACTTAAAGATTTTGCCTGAAATATGATGATAA 2817
Qy 2815 GTGGCTGGGCTTGTGCTGAGGAGGAGAGTGAACGACACCCAAATCGCCCGCTGCTG 2874
Db 2818 GTCGGAAGCTTGTGCTGCAAGAGGAGTGAATACACACCCCAATCATACTGAACTG 2877
Qy 2875 CTAATGTACAGTACCGAAGGTATCAGCACTTGGGGCT 2913
Db 2878 CAAATGGCAGGATCGAAGTCAATCATGACCTAGGAGGT 2916
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RESULT 14
US-10-437-963-41016
; Sequence 41016, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41016
; LENGTH: 2925
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; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1
US-10-437-963-41016
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Query Match 50.2%; Score 1557; DB 18; Length 2925;
Best Local Similarity 71.6%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 820; Indels 9; Gaps 3;
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Qy 3 GGCGAGACGGTGTGAGCATGGCGAGGTCTGCTGGTGGCGAGCGCCATCAGCAGGCGCG 62
Db 6 GGCGAGACGGTGTGAGCATGGCGATGTCGGTGTGCTGGCGAGCGCGCTCGGAGAGCGCG 65
Qy 63 CTCGCTGCTGCCGACGAGACAGCAGCTCTCTGCTGGCGCTCGAGAAAGACATCTGTGTAT 122
Db 66 CTCGCGCGCGCGAGGCGCACCTCTCTGCTCGGCATCCAGAAGGAGATCTGTGTACAT 125
Qy 123 CAAAGATGAGCTAAAGAGTGAAGCATGCAAGCATTCCTTAGAGCTGCTGAACCTTATGAAAAGAA 182
Db 126 CAAGGACGAGCTGAAACCTATTCAAGGCACTCTTAAGAGCTGCTGAAGTAAACAAGAGAA 185
Qy 183 AGATGAACTATTAAAGTTTGGCGAGAGCAATAGCTGACCTGTCATATGATGATGAAGA 242
Db 186 AGATGACTTGTCTAAAGGTATGGCGAGCAAGTAGAGATCTGTCTATATAACATTTGAAGA 245
Qy 243 TTCCCTTGTATGAATTTAAAGTTCATATTGAAAGCCAAACCCCTATTTCGTCAGTTGGTGA 302
Db 246 TTGCTAGACGAATTCAGGTTTCATGTTGAGAGCCAAAGCTTGGCAAGCACTAATGAA 305
Qy 303 ACTCAGAGAACCGCACCGAATTTGCTATCCGTATCCCAACCTTAAATCAAGAGTTGAAGA 362
Db 306 GTTGGTGAACCGCATCGAATTTGCTACAGATTCGCAACTTAAATCAAGAAATTTGAAGA 365
Qy 363 AGTGAAGTACGAGAACACACGCTACAGTTTGTAGTCAAGCTTATTTCTCTGG---CACAGA 419
Db 366 AGTGAGCAACAGGAATACACGCTACAGCTTAAATCAAGCCCAATTTCTCTATAACACAGA 425
Qy 420 GATTGACATGATTCCCTATGCAAGAGCATTCGTAATCAGTCAGCTCCCAATGTGGATGA 479
Db 426 GGATGAGAGGATTTCTTACCTAGAGATGCTCGCANTCATCAGGTAGCAACACTGACGA 485
Qy 480 GGCTGAGCTTGTGGGTTTTCTGACTCAAGAAAGGCTGCTTGAATATGATGATACCAA 539
Db 486 GTCAGAACTTGTGGCTTTGCAAGACTAAAGATGAGTTGCTTAAACTGATAGATGTCAA 545
Qy 540 TGCTAATGATGCTCGGCGAAGTAACTGTGTTGTTGGGATGGTGGTTAGGCAAGAC 599
Db 546 TACTAATGACGGTCCAGCTAAAGTGATATGTTGTTGGTATGGGTGGATTTAGGCAAGAC 605
Qy 600 AGCTCTTTCCGAGGAAGATCTTTGAAAGCGAAGAGACATTAAGGAAGAACTTCCCTTGCAA 659
Db 606 TACCTTTGCAAGGAAGGCAATATGAACAAGGAACACAT---GAAGAATTTCTCTGTGTG 662
Qy 660 TGCTTGGATTAACAGTGTACAAATCATTTTCAGAGGATTTGAGTACTTAAAGATATGATACG 719
Db 663 TGCTTGGATCACTGTGCTCAGTCATTTGACAGGAAGAAATTTCTGAAACAAATGATCAG 722
Qy 720 CCAACTTTCTGGCCCCAGTTCTCTGATCAACTCTTGCAGAAATTCGAAGGAAGGAGTGGT 779
Db 723 GCAACTTTCTGGGTGCTGATTCATTATAGACAACTCTCTGAAAGAAATTTAGTGAGAAAGTTGCT 782
Qy 780 GGTCAGAGTACATCATCTTTCTGAGTACCTCTGATAGAGAGCTCAAGGAGAGAGGTACTTT 839
Db 783 CGTCAAGTCCAGCATCTCGCTGATCACTTGGTTGAAGGGCTTAAGGAGAAAGAGTACTT 842
Qy 840 TGTGTTCTTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGATAAATGAAATTTGCAT 899
Db 843 TGTGTTCTTAGATGATCTATGGAATTTTACATGATTTGGAATTTGATATGATATTTGCTTT 902
Qy 900 TCCTAAGAACATTAAGAGGCGAGTCCGAATAGTATTAACCACTCGGAATGTTGATCTTGC 959
Db 903 TCCGAAGATTAACAAACAGAGGAGTGTGTCATTAATAAATAAAGCGGAGAGTGTGCTGCTAGC 962
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Qy	960	GGAGAAAGTGTGCCACAGCCTC	ACTGGTGTATCCACCTTGATTTCTTCGAGATGAACGATGC	1019
Db	963	TGGAAAGGTGTACTCTCTGAA	TCACTTATTTACCACCTTGAACCGTTACATATAGATGATGC	1022
Qy	1020	CATAACATTTCTCTACTGAG	AAAAAACAATAAAAAATCATGAAGACATGGATCAATTAATAA	1079
Db	1023	TATACACTTCTCTACTAG	CAAAAGCAAACTAAGACTTTGAAGACATGGAAATGATGAGGA	1082
Qy	1080	TATGCAAAAGCATGGTTGA	AGCAATTTGATAAATAATGTGGTCGTCTACCAATTAGCAATACT	1139
Db	1083	CTTTGGCAGCATAGTTACA	AAAAATTTGGTAAAGGTGTGGTTATTTACCGCTGGCTATACT	1142
Qy	1140	TACAATAGGAGCTGTGCTT	CGAACTAAACAGGTGTTCAGAAATGGAGGAGAAATTCATGAACA	1199
Db	1143	CACAATAGGAGGCATCTCT	GTACTTAAGAAGATAATGCGAGTGGGAAAAATTTTACAGAGA	1202
Qy	1200	CCTTCTTTCAGAACTAGA	ATAAACCAACCGCTTGGAGCTTTTCAGGAGATGCTGACCCT	1259
Db	1203	ACTTCTTTCAGAGCTTGA	AGCAATCCAGCCCTAGAGCCCATGAGGAGGATGCTGACCCT	1262
Qy	1260	AGGTTACAAACCACTTAC	CACTCCCATTTGAAAACCATGCTTTTGTGTATCTTAAGTATCTTTCC	1319
Db	1263	AAGCTACAACTCACTTAC	CACTCATCTCATCTTAAACCATGCTTCTTTTACTTAAGTATTTCCC	1322
Qy	1320	TGAGGATTTTGAANAATCA	AAAAAGGAATTCGTCTAGTAGGTAGATGGAATAGCAGAGGGTTTGT	1379
Db	1323	TGAAGATTTTGAANAATCA	AAAGAGGCGCCCTGGTAGATAGATGGATAGCAGAGGGTTTGT	1382
Qy	1380	TAGACCAAGAGTTGGATG	ACGACTAAGGATGTCGGAGAAAGTTACTTTTAATCAGCTAAT	1439
Db	1383	CAGAGCCACAGATGGGGT	GAAACATGAGGATGTTGGAAATATGTCACCTTTAATGAGCTTAT	1442
Qy	1440	CAACCGAAGTATGATTTCA	ACGATCAAGAGTGGCGATAGCAGAGGAAAAATTAAGACTTTGTCG	1499
Db	1443	CAACAGAAGTCTGATTTCA	GGCTTCAAAAGTTAGTACAGATGGAGTTGTTTAAGAGATGTGC	1502
Qy	1500	AATTCATGATATCATTCGT	GTATATCAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTT	1559
Db	1503	AATCCATGATATCATTCGT	GTATATCATGTTTCAATTTCTTAGAGAGAAAAATTTTGTGCT	1562
Qy	1560	ATTACCAATGGGAGATGG	CTGATTTAGTTTTCAGGAAAAACACTTCGCCACATAGCATTTCCA	1619
Db	1563	GTTGACTAGGAGAAAGTCA	CTGTTGTAGCGGAGAGAGCATCCGCCATCTAGCATTTCA	1622
Qy	1620	TGGGAGTATGCTCTGCA	AAAACTGGATTTGGAATTTGGAGCATTTTCGATTCATTAAGTATTTT	1679
Db	1623	TGGGAGCAATGCTTCAA	AGATATGCTTTGGAGTGGAAACCATCTCGCTCGATTAACCTTTGTT	1682
Qy	1680	TGTTGACAGACCCAGAGT	CTAGCACATGCACTTTGCTTCAGATCAATTTGAGGATGTTACG	1739
Db	1683	TGGCGACAGACCTGTG	GGGCGAACACTGTCACCTTTGTTTCCCAAAATTTTAGSATGCTGAG	1742
Qy	1740	GGTCTTCGATCTTGAAG	ATGTGACATTTCTTAATCACTCAAAAAAGATTTTCAGCCGATTTGC	1799
Db	1743	AGTGTTCGATCTGGAAG	ATGCAAAATTCAAATTCACAAAAATGATATCAGGAATATAGG	1802
Qy	1800	ATTGTTGTGCCACTTGA	AAATCTTTAGTATTTGGATATTTGTCATTCATATTAATCACTTCC	1859
Db	1803	GTTGTTGCGCCACATGA	AAATATTGAAATTTTGAAGAGCTCAACTATTTTATACACTTCC	1862
Qy	1860	CAGATCCATTTGGTAACT	ACAGGCCCTACAAACTTTTGAAACATGCCGAGCACATACATTGC	1919
Db	1863	AAGTCCATAGGAAAAAT	TTCAGTGTCTGCAAAATTTTGAAACATGAGGAGGCAAAATATCTC	1922
Qy	1920	AGCACTACCAAGTGAG	ATCAGTAACTCCAAATGTCTGCATACTCTTCGTTGTATAGGACA	1979
Db	1923	AGCACTAACCACTGAG	GTGACTAACTCCAGAACTCCGATAGCTCCGATGTCAGCAGGAG	1982
Qy	1980	GTTTCAATTATGACAA	CTTTTATAGTCTAA---ACCAACCAATGAAGTGCATAACTTAACAAAT	2036
Db	1983	GTCTGGTTCTGGTTACT	TTTATAGCAATAATAGATATATCCCAAGGAATGCTTTGATGATCAACAT	2042

2037	ATGCCCTGCTAAAGTAATTTCACACCTTTAGTTCGGAGTCAATCGTGCAGAAACAAATTGC	2096
2043	GTGCTTACCGATGGTCTTTCTTAACTTCATAAATTTTCAGTCACCGTGTGAAGTTAAATTCC	2102
2097	TCGAATTGCACATGGGCCACCAAAAGTTGCTGCTCGAATCAATCGTGTGAAGGTACCCAA	2156
2103	TGAGATATGCATGTCTATGTTCTACCCGTTGGTCTGTATACAAAGGGTGTGAGGGTGC	2162
2157	AGGAATAGGTAAAGTTGCGAGACTTTCGAGGTTCTTAGAGTATGTAGATATCAGCGCGGAC	2216
2163	AGGAATTGACAACTTAAAGAGATTACAGATTCTTAGAAGTCGTGGACATCAACAGAACTAG	2222
2217	TAGTAGACCAATCAAAGAGCTGGGSCAGTTAAGCAAGCTGAGGAAATTTAGGTGTGACAAC	2276
2223	TAGGAAGGGGATGAAGAGCTGGGGGAGCTAATTCAGTTTAAGAAATTAACGTGTGACAC	2282
2277	AAACGGGTGCGAATAAGAGGAAAAATGTAAAGTACTTTATGACGCCAATTGAGAAGCTCTCTTC	2336
2283	AAAAGGCGCCAAATAAGAGTATCAGATATTTGTGCAGCGATTGAGAAGCTCTCTTTC	2342
2337	CCTCCAAATCTCTCAATGTGGATGTGCAAGGAATCTCAGATGGTGGAAACACTTTGAGTGCCT	2396
2343	TCGTGCAATCTCTCCGTGTGGATGTGTGAGGGAATCTTCAGATACTGGAAACACTTTGAGTGGCT	2402
2397	AGATTCTAATTTCAATCTCTCTCCCTACTCAGGACACATCCGTGTTGGATGGAAATTCITGA	2456
2403	CAATTCGATTCGATGCTCTCTCTCCATCTTCTGAAGAGACTCAAGTTGAATGATCTCTTGC	2462
2457	GGAGATGCTTAATCTGGATTGAGAGCTCACTCACTGAAGAAGATCTACTTATTTGAGGAG	2516
2463	AGATACACCAACTGGTTTGGGAACCTTTAAGCAGCTGGTGAAGATGTGCTTTATCCAGATG	2522
2517	CAAACTAAAGGAAGGTAAACCATGCTCATACTTTGGGGCACTGCCAACCTCATGTGCTCT	2576
2523	TGGGCTTAAAGATGTGTAAACCTATGGAAGTACTTTGGGGCACTGCCAACCTTATGGTTCT	2582
2577	TCATCTTTATCGGAATGCTTACCTTTGGGGAGAGCTAGTATTTCAAAAACAGAGCAATTC	2636
2583	TCGCTTTTATCGCAACGCATATGCTGCAGAGAAAATGACATTCAGAAGGGGAAACATTC	2642
2637	AAATCTTAGMACACTTTGGATTTTAGAATTCGATCAGCTAAGACAGATCAGATTTGAGGA	2696
2643	AAATCTCAGGTGCTTGATATTTCTTCTGAGGCACTTAGAGAGATAGATTTGAGGA	2702
2697	CGCGAGCTCACCCCTGTTTGGAAAAGATAGAAATAGCGAGGTGCAGGTTGGAAATCTGG	2756
2703	GGGCACCTCGCCAAACGATGGAAAAGTATAGAAATTTATGGTTGCAGGTTGGAATCAGG	2762
2757	TACTGATATCATTTCACTTCCAAAGCTCAAGAGATTTCCAAATTAGATACGGAAGTAAAGT	2816
2763	TATTCGTATCAAGACCTTCCAAGACTTTAAGATTATTTTCGCTTGAATATGATGTTAAGT	2822
2817	GGCTGGGCTTGTGAGCTGGAGGAGAAAGTCAACGCACACCCCAATGCCCCGCTGCTGCT	2876
2823	CGGGAAGCTTGTATGTGCTGCAAGAGAAAGTGNATACACACCCCAATCATACTGAATTGCA	2882
2877	AATGTACAGTGACGAAGGTATACCACTGGGGCT	2913
2883	AATGGCAGAGGATCGAAGTCAATGACCTAGGAGCTAGGAGGT	2919

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RESULT 15
US-10-656-394A-1
; Sequence 1, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; broad-spectrum resistance gene pi2
; FILE REFERENCES: 035718/232062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: PastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2982

; TYPE: DNA

; ORGANISM: Oryza minuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1) ... (2982)

; US-10-656-394A-1

Query Match 50.1%; Score 1553.4; DB 18; Length 2982;
Best Local Similarity 71.5%; Pred. No. 0;
Matches 2085; Conservative 0; Mismatches 821; Indels 9; Gaps 3;

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Qy 3 GGCAGAGCGGTGCTGAGCATGGCGAGTGTGCTGGCGAGCGCCATCAGCAAGGCGC 62
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Qy 6 GGCAGAGCGGTGCTGAGCATGGCGAGTGTGCTGGCGAGCGCGCTGGGAGGCGCG 65
Db |||||
Qy 63 CTCGCTGCTCCGACGAGACAGCGCTCTGCTGGCGCTGAGAGACATCTGGTATAT 122
Db |||||
Qy 66 CTCGCGCCGCCGACGAGGCCACCTCTGCTGGCATCCAGAGGAGATCTGGTACAT 125
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Qy 123 CAAGATGAGCTAAAAAGCATGCAAGCATTCCTTAGAGCTGCTGAACCTTATGAAAAAGAA 182
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Qy 126 CAAGACGAGCTGAAAACTATTTCAGCATTTCTTAGAGCTGCTGAAGTAAACAAGAGAA 185
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Qy 183 AGATGAACATAATTAAGGTTTGGCGAGAGCAAAATAGTGACCTGTGCATATGACATTGAAGA 242
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Qy 186 AGATGACTTGCTAAGGTTATGCGGAGAGCAAGTACGAGATCTGTCATATACATTGAAGA 245
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Qy 243 TTCCCTTGATGAATTAAGGTCATATTTGAAGCCAAACCCCTATTTTCGTAGTTGGTGAA 302
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Qy 246 TTGCTAGACGAATTCAGAGTTTCATGTTGAGAGCCAAAGCTTGGCAAGCAACTAATGAA 305
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Qy 303 ACTCAGAGAAAGCCACCGAAATGCTATCCGATCCACAACTTAAATCAAGAGTTGAAGA 362
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Qy 306 GCTTGGTGAAGCCATCGAATGCTGTACAGATTGCGAACTTAAATCAAGAAATGAAGA 365
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Qy 363 AGTGAGTAGCAGGAACACACGCTACAGTTTGTAGTCAAGCTATTTCTCTGG---CACAGA 419
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Qy 366 AGTGAGCAACAGGAATACACGCTACAGCTTAATCAAGCCCATTTCTCTATAACCAAGA 425
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Qy 420 GATTGACATGATTCCTATGAGAGAGACATTCGTAATCAGTCAGCTCGCAATGTGGATGA 479
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Qy 426 GGATGAGAGGATTCCTACCTAGAGATGCTCGCAATCGATCAGTAGCAACACTGACGA 485
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Qy 480 GSCTGAGCTGTGSGTTTTCTGACTCCAAGABAGGCTGCTGAAATGATCGATACCAA 539
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Qy 486 GTCAGAACTTGTGGCTTTGCCAAGACTAAAGATGAGTTGCTTAACTGATAGATGTCAA 545
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Qy 540 TGCTAATGATGGTCCGGCCAAAGGTAATCTGTGTTTGGGATGGGTGGTTTAGGCAAGAC 599
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Qy 600 AGCTCTTTCGAGGAGATCTTTGAAGCGAAGAGACATTAAGGAGAACTTCCCTTGCAA 659
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Qy 606 TACCCTTCGAAGGAGGATATGAAAAAAGAGGAAACACAT---GAAGAACTTCTCGTGTG 662
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Qy 660 TGCTTGAATACAGTGCACATCATTTCCAGGATTTGAGTACTTAAAGATATGATACG 719
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Qy 663 TGCTTGGATCACTGTGCTCAGTCAATTTGACAGGAAAGAAATTCGAAACAAATGATCAG 722
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Qy 720 CCAACTTCTTGCCGCCAGTTCTCTGGATCAACTCTTGCAAGAAATGCAAGGGAAGGTGGT 779
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Qy 723 GCAACTTCTGGGTGCTGATTCAATAGACAACTCTTGAAGAAATTTAGTGAAGATTGCT 782
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Qy 780 GGTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAAAGAGGTACTT 839
Db |||||
Qy 783 CGTGCAAGTCCAGCATCTCGCTGATCACTTGTGTAAGGGCTTAAAGGAGAAAGGTACTT 842
Db |||||
Qy 840 TGTGTTCTAGATGATCTATGGATTTTACATGATGGAAATGGATTAATGAAATGCAAT 899
Db |||||
Qy 843 TGTGTTCTTGAAGCTTATGGAACATAGATGCAATGGAATGGAAATGGATTCATGATATGCTTT 902
Db |||||
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Qy 1980 GTTTCATTATGACAACTTTAGTCTAA---ACCACCCAAATGAAGTGCATAACTAAACACAAT 2036
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1983 GTCTGGTTCTGGTTACTTTTAGCATAA TAGATAA TCCCAAGGAA TGCTTGTATGATCACCAT 2042
Qy 2037 ATGCTTGCTTAAAGTATTACACACCTTTAGTTAGTGCAGATGATCGTGCAAAACAAATTGC 2096
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2043 GTGCTTACCGATGGTTTTCTTAACTTCAATAAATTTCAAGTACCGTGTTGAAGTTAAATTCC 2102
Qy 2097 TGAATTGACATGGCCACCAAAAGTTGCTGGTCTGGAATCAATCGGTGTGAAGGTACCCAA 2156
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2103 TGAGNATGCAATGTCATGTTCTACCCGTTGGTCTGTATACAAAGGTGTGAGGGTGCCTAAG 2162
Qy 2157 AGGAATAGGTAAAGTTGCGAGACTTTCAGGTTCTAGAGTATGTAGATATCAGGCGGACCAAG 2216
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2163 AGGAATTGACAACCTTAAAGAGTTACAGATTCTAGAACTCGTGGACATCAACAGAACTAG 2222
Qy 2217 TAGTAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTTAGGTGTGACAAAC 2276
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2223 TAGGAAGCGATTTGAAGAGCTGGGGAGCTAAATTCAGTTAAGAAATTTAAGCGTGACAAAC 2282
Qy 2277 AAACGGGTGCAACAAGGAAATGTAAAGTACTTTTATGCAGCCATTTGAGAAGCTCTCTTC 2336
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2283 AAAAGGCCCAACAATAAGAGTATCAGATATTTTGTGCGCGATTTGAGAAGCTCTCTTC 2342
Qy 2337 CCTCCAATCTCTCCAATGTGATGTGCGAGGAATCTCAGATGGTGGAAACACTTGAATGCCT 2396
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2343 TCTGCAATCTCTCCGTGTGGATGCTGAGGGATTTCTCAGATACTTGGAAACACTTGAATGGCT 2402
Qy 2397 AGATTCTATTTCATCTCTCTCCCTACTGAGGACACTCGTGTGGATGGAAATTCATTGA 2456
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2403 CAATTCGATGTGATGCTCTCTCCATTTCTTGAAGAGACTCAAGTTGAATGGATCTCTTGC 2462
Qy 2457 GGAGATGCTTAACGTGATTTGAGCAGCTCACTCACTGAAGAAGATCTACTATTATTGAGGAG 2516
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2463 AGATACACCAACTGGTTGGAACTTTAAGCAGCTGGTGAAGATGTCCTTATCCAGATG 2522
Qy 2517 CAAACTAAAGGAAGTAAACCATGCTGATACTTTGGGGCACTGCCCAACCTCATGGTCTCT 2576
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2523 TGGGCTAAAGATGTTAAACTATGGAGATACTTTGGGGCACTGCCCAACCTTATGGTTCT 2582
Qy 2577 TCATCTTTATCGGAATGCTTACCTTTGGGGGAAGCTAGTATTCAAAAACAGGAGATTCCC 2636
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2583 TCGTCTTTATCGCAACGCATATGCTGACGAGAAAATGACATTCAGAGGGGAACTTTCCC 2642
Qy 2637 AAATCTTAGAACACTTTTGGATTTATGAATTCGATCAGCTAAGAGAGATCAGATTTGAGGA 2696
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2643 AAATCTCAGGTGCTTTGATATTTACTTGTGAAGCACTTAGAGAGATPAAGATTTGAGGA 2702
Qy 2697 CGGCAGCTCACCCCTGTTGGAAAAGATAGAAATAGCGGAGTGCAGGTTTGGAAATCTGGGAT 2756
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2703 GGGCACCTCGCCACGATGGAAAGTATAGAAATTTATGTTGCAGGTTTGGAAATCAGGGAT 2762
Qy 2757 TACTGGTATCAATTCACCTTCCAAAGCTCAAGAGATTCCAATTTAGATACGGAAGTAAAGT 2816
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2763 TATTGGTATCAAGCACCTTCCAAAGCTTTAAGATTATTTTCGCTTGAATATGATGGTAAAGT 2822
Qy 2817 GGCTGGGCTTGGTCAAGCTGGAGGAGAGTGAACGCACACCCCAATCGCCCGTGTGCT 2876
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2823 CGCGAAGCTTGTATGTGTGCAAGAGAGAGTGAATAACACCCCAATCATCTGAATTGCA 2882
Qy 2877 AATGTACAGTGACCAAGGTATCACGACCTGGGG 2911
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2883 AATGGCAGAGATCGAAGTCATCATGACCTAGGAG 2917
```

Search completed: February 13, 2005, 20:04:19
Job time : 1102.99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 08:34:07 ; Search time 109.873 Seconds
(without alignments)
3632.700 Million cell updates/sec

Title: US-10-656-394A-8
Perfect score: 5268
Sequence: 1 MAETVLSMARSLVGSALSKA.....SQVITLTNDSEIGTAQAG 1032

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5268	100.0	1032	8 ADM72245	Adm72245 O. minuta
2	4942.5	93.8	1091	8 ADI57176	Adi57176 Oryza min
3	4925	93.5	1031	8 ADI57172	Adi57172 Oryza min
4	4906	93.1	1032	8 ADM72241	Adm72241 O. minuta
5	4237	80.4	998	8 ADM72249	Adm72249 O. minuta
6	3072	58.3	993	8 ADM72239	Adm72239 O. minuta
7	3063.5	58.2	979	8 ADI57168	Adi57168 Oryza min
8	2575	48.9	993	8 ADI57170	Adi57170 Oryza min
9	2367	44.9	1054	8 ADI57174	Adi57174 Oryza min
10	2118.5	40.2	660	8 ADM72243	Adm72243 O. minuta
11	1384	26.3	451	8 ADI57178	Adi57178 Oryza min
12	1204	22.9	1251	3 AAY93135	Aay93135 Rice blas
13	1111	21.1	1205	3 AAY49434	Aay49434 Blast dis
14	1111	21.1	1205	8 ADM72280	Adm72280 O. minuta
15	1062.5	20.2	953	3 AAY58854	Aay58854 Sorghum r
16	906.5	17.2	901	2 AAW80251	Aaw80251 An antidi
17	906.5	17.2	901	2 AAY01965	Aay01965 A protein
18	906.5	17.2	901	3 AAY81925	Aay81925 Rice prob
19	906	17.2	949	4 ABB06876	Abb06876 Mla1h pro
20	905.5	17.2	901	2 AAY01966	Aay01966 A protein
21	905.5	17.2	901	3 AAY81926	Aay81926 Rice prob
22	900.5	17.1	958	4 ABB06875	Abb06875 Mla1 prot
23	889	16.9	961	4 ABB06869	Abb06869 Barley M1
24	888	16.9	961	4 ABB06871	Abb06871 Barley M1
25	883	16.8	961	4 ABB06870	Abb06870 Barley M1

26	876.5	16.6	943	4 ABB06877	Abb06877 Rghlbed p
27	873	16.6	967	4 ABB06878	Abb06878 Rghia pro
28	862.5	16.4	956	4 ABB06874	Abb06874 Mla6 prot
29	842.5	16.0	939	4 ABB06879	Abb06879 Rghie/f p
30	823.5	15.6	945	4 ABB06873	Abb06873 Barley M1
31	818	15.5	922	4 ABB06872	Abb06872 Barley M1
32	815.5	15.5	2827	7 ADC08012	Adc08012 Rice prot
33	734	13.9	937	4 AAU02144	Aau02144 Rx 28, mo
34	731	13.9	937	4 AAU02149	Aau02149 Rx 32, mo
35	729	13.8	937	2 AAY52152	Aay52152 Potato re
36	727	13.8	937	4 AAU02145	Aau02145 Rx 72, mo
37	727	13.8	937	4 AAU02143	Aau02143 Rx 25, mo
38	722	13.7	937	4 AAU02146	Aau02146 Rx 39, mo
39	722	13.7	937	4 AAU02148	Aau02148 Rx 7, mod
40	717.5	13.6	1471	8 ADI45353	Adi45353 Rice f8op
41	713	13.5	937	4 AAU02147	Aau02147 Rx 193, m
42	703	13.3	938	3 AAY45004	Aay45004 Protein e
43	701.5	13.3	912	3 AAY44818	Aay44818 Potato Gp
44	692.5	13.1	945	8 ADH51546	Adh51546 Plant inf
45	688	13.1	970	7 ADF17765	Adf17765 Solanum b

ALIGNMENTS

RESULT 1

ADM72245
ID ADM72245 standard; protein; 1032 AA.

XX AC ADM72245;

XX DT 03-JUN-2004 (first entry)

XX DB O. minuta NBS4 polypeptide.

XX KW P12; NBS4; plant protectant; gene therapy; rice; disease resistance.

XX OS Oryza minuta.

XX PN WO2004022715-A2.

XX PD 18-MAR-2004.

XX PF 08-SEP-2003; 2003WO-US027913.

XX PR 09-SEP-2002; 2002US-0409216P.

XX PR 18-MAR-2003; 2003US-0455713P.

XX PR 05-SEP-2003; 2003US-00656394.

XX PA (OHIS) UNIV OHIO STATE.

XX PI Wang G;

XX DR WPI; 2004-257576/24.

XX DR N-PSDB; ADM72244.

XX PT New rice P12-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.

XX PS Claim 1; SEQ ID NO 8; 120pp; English.

XX CC The invention relates to novel broad-spectrum resistance gene P12 and the NBS(1-6) genes present in the P12 gene cluster region. The rice P12-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS4 polypeptide.

XX SQ Sequence 1032 AA;

Query Match 100.0%; Score 5268; DB 8; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MAETVLSMARSLVGSASIKAAASAADETSLLGVEKDIWYIKDELKTWQAFRAAELMKK 60
Db 1 MAETVLSMARSLVGSASIKAAASAADETSLLGVEKDIWYIKDELKTWQAFRAAELMKK 60
Qy 61 KDELKWWAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRQLVKLRERHRIAIRIHNLSRVE 120
Db 61 KDELKWWAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRQLVKLRERHRIAIRIHNLSRVE 120
Qy 121 EVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDTN 180
Db 121 EVSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDTN 180
Qy 181 ANDGPAKVICVVGGMGLGKTALSRIKIFESIEDIRKNFPCNAWITVVSQSFHRIELKDMIR 240
Db 181 ANDGPAKVICVVGGMGLGKTALSRIKIFESIEDIRKNFPCNAWITVVSQSFHRIELKDMIR 240
Qy 241 QLLGPFSSLDQLLQELQGVVVQVHLSLEYLLEELKEKRYFVVLDDLWILHDWNNWINEIAP 300
Db 241 QLLGPFSSLDQLLQELQGVVVQVHLSLEYLLEELKEKRYFVVLDDLWILHDWNNWINEIAP 300
Qy 301 PKNKKGSRIVITTRNVDLAEKATASLVVHLDLFQWMDAITLLLRKTNKHEDMESNKN 360
Db 301 PKNKKGSRIVITTRNVDLAEKATASLVVHLDLFQWMDAITLLLRKTNKHEDMESNKN 360
Qy 361 MQKWERIVNKGRLPLAILTIGAVLATKQVSEWEKFEYHLPSELEINPSLEALRRMVTL 420
Db 361 MQKWERIVNKGRLPLAILTIGAVLATKQVSEWEKFEYHLPSELEINPSLEALRRMVTL 420
Qy 421 GYNHLPShLPCFLYLSIFPEDDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480
Db 421 GYNHLPShLPCFLYLSIFPEDDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480
Qy 481 NRSMIQSRVGIAGKIKTCRTHDIIRIDITVISRQENFVLLPMGDSGLVQENTRHIAFH 540
Db 481 NRSMIQSRVGIAGKIKTCRTHDIIRIDITVISRQENFVLLPMGDSGLVQENTRHIAFH 540
Qy 541 GMSCKTGLDWSIIRLSIAIFGDRPKSLAHAVCPDQLRMLRVLDEVTFLITQKDFRIA 600
Db 541 GMSCKTGLDWSIIRLSIAIFGDRPKSLAHAVCPDQLRMLRVLDEVTFLITQKDFRIA 600
Qy 601 LLCHLKYSIGYSSSIYSLPRSIGKLGQLOTLNMPSTYIAALPSEISKQLCHLRLCIGQ 660
Db 601 LLCHLKYSIGYSSSIYSLPRSIGKLGQLOTLNMPSTYIAALPSEISKQLCHLRLCIGQ 660
Qy 661 PHYDNFSLNHPMKCITWTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSESIGVKVPKG 720
Db 661 PHYDNFSLNHPMKCITWTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSESIGVKVPKG 720
Qy 721 IGLKRLDQVLEYVDIRRTSSRAIKELGOLSKRLGVTGTNGSTKECKILYAALEKLSL 780
Db 721 IGLKRLDQVLEYVDIRRTSSRAIKELGOLSKRLGVTGTNGSTKECKILYAALEKLSL 780
Qy 781 QSLHVDAAAGISDGTLECLDSISSPPPLRLTLVLGDGILEEMPNIWIEQLTKKILYLLRSK 840
Db 781 QSLHVDAAAGISDGTLECLDSISSPPPLRLTLVLGDGILEEMPNIWIEQLTKKILYLLRSK 840
Qy 841 LKEGKTMILGALPNLWHLRYNAYLGEKLVFTGAPPNLRTWIYELDQLREIRPEDG 900
Db 841 LKEGKTMILGALPNLWHLRYNAYLGEKLVFTGAPPNLRTWIYELDQLREIRPEDG 900
Qy 901 SSPLEKTEIGECLRESGITGIHLPKLKEIPIRYGSKVAGLGOLEGEVNAHPNRPVLLM 960
Db 901 SSPLEKTEIGECLRESGITGIHLPKLKEIPIRYGSKVAGLGOLEGEVNAHPNRPVLLM 960
Qy 961 YSDRRYHDLGAEAGSSIEVQTADVPVDAEGSVTVAVEATDPLPEQBGESSQSQVITLTT 1020
Db 961 YSDRRYHDLGAEAGSSIEVQTADVPVDAEGSVTVAVEATDPLPEQBGESSQSQVITLTT 1020
Qy 1021 NDSEIEGTAAQAG 1032
Db 1021 NDSEIEGTAAQAG 1032
```

```
RESULT 2
ADI57176
ID ADI57176 standard; protein; 1091 AA.
XX
AC ADI57176;
XX
DT 22-APR-2004 (first entry)
XX
DE Oryza minuta P19 locus nucleotide binding site (NBS) protein #5.
XX
KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JAN-2003; 2003US-00352179.
XX
PR 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX
(WANG/) WANG G.
PA (LIUG/) LIU G.
XX
PI Wang G, Liu G;
DR WPI; 2004-121064/12.
DR N-PSDB; ADI57175.
XX
Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
Claim 1; SEQ ID NO 93; 136pp; English.
PS
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present amino acid sequence represents an NBS
CC protein encoded by a gene from the Oryza minuta P19 locus.
XX
SQ Sequence 1091 AA;
Query Match 93.8%; Score 4942.5; DB 8; Length 1091;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 987; Conservative 14; Mismatches 31; Indels 59; Gaps 1;
Qy 1 MAETVLSMARSLVGSASIKAAASAADETSLLGVEKDIWYIKDELKTWQAFRAAELMKK 61
Db 1 MAETVLSMARSLVGSASIKAAASAADETSLLGVEKDIWYIKDELKTWQAFRAAELMKK 60
Qy 40 -----YIKDELKTWQAFRAAELMKK 61
Db 61 KDELKWWAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRQLVKLRERHRIAIRIHNLSRVEE 120
Qy 62 DELLKWWAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRQLVKLRERHRIAIRIHNLSRVEE 121
Db 121 DELLKWWAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRQLVKLRERHRIAIRIHNLSRVEE 180
Qy 122 VSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDITNA 181
Db 181 VSSRNTRYSLVKPISSGTEIDMDSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDITNA 240
Qy 182 NDGPAKVICVVGGMGLGKTALSRIKIFESIEDIRKNFPCNAWITVVSQSFHRIELKDMIRQ 241
Db 241 NDGPAKVICVVGGMGLGKTALSRIKIFESIEDIRKNFPCNAWITVVSQSFHRIELKDMIRQ 300
Qy 242 LLGPFSSLDQLLQELQGVVVQVHLSLEYLLEELKEKRYFVVLDDLWILHDWNNWINEIAP 301
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PF 08-SEP-2003; 2003WO-US027913.
XX
PR 09-SEP-2002; 2002US-0409216P.
PR 18-MAR-2003; 2003US-0455713P.
PR 05-SEP-2003; 2003US-00656394.
XX
PA (OHIS) UNIV OHIO STATE.
XX
XX Wang G;
XX
DR WPI; 2004-257576/24.
DR N-PSDB; ADM72238.
XX
PT New rice Pi2-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX
XX Disclosure; SEQ ID NO 2; 120pp; English.
XX
XX The invention relates to novel broad-spectrum resistance gene pi2 and the
CC NBS(1-6) genes present in the pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a rice NBS1
CC polypeptide.
XX
XX Sequence 993 AA;
SQ

Query Match 58.3%; Score 3072; DB 8; Length 993;
Best Local Similarity 62.0%; Pred. No. 2.8e-257;
Matches 614; Conservative 144; Mismatches 223; Indels 10; Gaps 4;
2 AETVLSWARSIVGSAISKASAAADETSLIGVSKDIWIYKDELKTWOAFRAAELMKK 61
3 AETVSWMSVIGSAGVAKASAAADEATLLIGIQEIWIYKDELKTQAFRAAEVTKK 62
62 DELLKVAEQIRDLSDIEDSLDEFKVIHESQTLFROLVKLRERHRIAIRHNLSKRV 121
63 DDLKVAEQVRDLSYNIEDCLDEFKVIHESQSLAKQLMKLGERHRIAVOIRNLSRI 122
122 VSSNTRYSLVKPISS-GTEIDMSYAEEDINQSAARNVDEALVGFSDSKRLEMDTN 180
123 VSNENTRYSLIKPISSTTTEDERSYLEDARNRSNTDSESLVGFATKDELKLDVN 182
181 ANDGPAKVICVWGGGLGKTALSRIKPISESEDIRKNPCNAWITVSQSFRIELLDK 240
183 TNDGPAKVICVWGGGLGKTTLAKAYENKHM-KNFSCCAWIIVSQSPRKEILKQ 241
241 QLLGPFSSLDQLLOELQGVVQVHHLSEYLFEEELKEKRYFVVLDDLLWLDHWN 300
242 QLLGADSLDKLLKEFSEKLLVQVQHLADHLVEGLKEKRYFVVLDDLLWLDH 301
301 POKNKGSRVITTRNVDLAEKATASLVYHLDPLQNDAITLLLRKTNKHEDMESKN 360
302 PKINNRGSRITITRDAGLAGRCTSESILVHLEPHIDDAIHLHLAKTNIRLED 361
361 MQKVERIVNKCGRPLPAITLTIGAVLATQVSEKEVEHLPSELEINPSLEALRM 420
362 LGSIVTKLVKRCGYPLPAITLTIGILATKIMWKGKFRLELPSELEINPSLEAL 421
421 GYNHLPKPCFLYLSIFPEDDFEIKRNLVGRVIAEGFVRPKVGMTTKDVGESYFN 480
422 SYNHLPKPCFLYLSIFPEDDFEIQGRVLDVIAEGFVRATDGVNIEDVGNHFN 481
481 NRSIMQSRVGIAGKIYTCRIHDIIRITVISIQENFVLLPMGGSDGLVQENTRH 540
482 NRSIQPSKVSTDGWVKRCRIHDIIRDIIVISIRENFVLLTREKITVVAEESR 541
541 GSMCKTGLDWSITRSIAIFGDRPKSLAHAVCPQLRMLRVLDIEDVTELITOK 600
542 GSKCKSKCLEWNHURSVTLFGDRVPGVTPALCSQFRLRVLDIEDAKFKPTQ 601
601 LLCHLKYSIGYSSSIYSLPRSIGKLOGLQTLNMPSTVIAALPSEISKLOCLH 660
RCIGQ 660

Db 602 LLRHMKYLNPARASTIYTLPRSIGKLCQLQLLNNREANISALTTEVTYKLNLSRCSR 661
Qy 661 FHYDNFS-LNHPMKCIINTICLPKVFPLVSRDDRAKQIAELHMAKSCWSESIGVKVPK 719
Db 662 SSGYSFIIDNPKECLMITHCLPWFLTSINFSRDKLIFEICMSCSTRSDTKGVVR 721
Qy 720 GIGKJRLDQVLEYVDIRRTSSRAIKELQSLKRLKLGVTGTTNGSTKCKILYAAIEKLSS 779
Db 722 GIDNLKELQILEVVDINRTSRKAIEELGELIQLKLSVTTKGATNKYQIFCAAEIKLSS 781
Qy 780 LQSLHVDAAIGSDGTLLECDSISSPPPLRLTLVLDGILEEMPNWIEQLTKKIYLLRS 839
Db 782 LQSLRVDAEFSDTGTLEWLNISACPPFPFLKRLKLSLADTPNWFNGLKQLVKMCUSRC 841
Qy 840 KLEGGKTMILGALPNLMVLHLYRNAYLGEKLVFKTGAPFNRLTLWIYELDQLREIRPED 899
Db 842 GLKDGKTMELGALPNLMVLRLYRNAYADERMFRRTGTFNRLCLDIYLLKQLREIRFEE 901
Qy 900 GSSPLLEKIEIGECRLSEGITGIHLPKLEIPIRYGSKVAGLQGLEGEVNAHNPRLV 959
Db 902 GTSPTMESIIEYGRLESGIIGIKHLPRLKIIISLEYDGKVKALDVLQEEVNTHPNHT 961
Qy 960 MYSDRRYHLDGAEA-----EGSSIEVQTA 983
Db 962 MAEDRSHHDLGGLASDGDGDDAHDNPALRYQTS 992

RESULT 7
ADI57168
ID ADI57168 standard; protein; 979 AA.
XX
AC ADI57168;
XX
DT 22-APR-2004 (first entry)
XX
DE Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #1.
XX
KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JAN-2003; 2003US-00352179.
XX
PR 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX
PA (WANG/) WANG G.
PA (LIUG/) LIU G.
XX
PI Wang G, Liu G;
XX
DR WPI; 2004-121064/12.
DR N-PSDB; ADI57167.
XX
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
PS Claim 1; SEQ ID NO 85; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present amino acid sequence represents an NBS
CC protein encoded by a gene from the Oryza minuta Pi9 locus.
XX
SQ Sequence 979 AA;

Query Match 58.2%; Score 3063.5; DB 8; Length 979;
 Best Local Similarity 62.9%; Pred. No. 1.5e-256;
 Matches 611; Conservative 141; Mismatches 217; Indels 3; Gaps 3;

QY 1 MAETVLSMARSLVGSATSKAASAADETSLLGVKEDIWIKDELTKMQAFRAELMKK 60
 DB 1 MAETVSMAMSLVGSATSKAASAADETSLLGVKEDIWIKDELTKMQAFRAEYVK 60

QY 61 KDELKVAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRLQVLRHRHRIAIRHNLKSRVE 120
 DB 61 KDELKVAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRLQVLRHRHRIAIRHNLKSRVE 120

QY 121 EVSSRNTRYSLVKPISS-GTEIDMSYAEDIRNQSARNVDAELVGFSDSKRLLEMDT 179
 DB 121 EVSSRNTRYSLVKPISS-GTEIDMSYAEDIRNQSARNVDAELVGFSDSKRLLEMDT 179

QY 180 NANGDPKAVICVGMGGGLKGTALSRKIPESBEDIRKPPCNWITVSQSFHRIELDKMI 239
 DB 180 NANGDPKAVICVGMGGGLKGTALSRKIPESBEDIRKPPCNWITVSQSFHRIELDKMI 239

QY 240 RQLGPSLQDLQLOGLQKVVVQVHHLSLEYLIEELKEKRYFVVLDDLMILHDMNWIIEIA 299
 DB 240 RQLGPSLQDLQLOGLQKVVVQVHHLSLEYLIEELKEKRYFVVLDDLMILHDMNWIIEIA 299

QY 300 PPKNKGSRIVITRNVDLAEKCATASLVVHLDFLQNDAITLLLRKTNKNHDMESNK 359
 DB 300 PPKNKGSRIVITRNVDLAEKCATASLVVHLDFLQNDAITLLLRKTNKNHDMESNK 359

QY 360 NMQKVERIVNKGRLPLAIIITIGAVLATKQVSEKRYEHLPSLEINPSLEALRMVT 419
 DB 360 NMQKVERIVNKGRLPLAIIITIGAVLATKQVSEKRYEHLPSLEINPSLEALRMVT 419

QY 420 LGYNHLSHLKPCFLYLSIPPEDFEIKRNLVGRWIAEGFVRPKVGMTTKOVGSYFVEL 479
 DB 420 LGYNHLSHLKPCFLYLSIPPEDFEIKRNLVGRWIAEGFVRPKVGMTTKOVGSYFVEL 479

QY 480 INRSMIQRVRGIAGKIKTCRIHDIIRDITVISRQENFVLLPMDGSDLVQENTRIHAF 539
 DB 480 INRSMIQRVRGIAGKIKTCRIHDIIRDITVISRQENFVLLPMDGSDLVQENTRIHAF 539

QY 540 HGSMSCTGLDWSIIRSLATFGDRPKSLAHAVCPDQLRMLRVLDEDTPLITQKDFRI 599
 DB 540 HGSMSCTGLDWSIIRSLATFGDRPKSLAHAVCPDQLRMLRVLDEDTPLITQKDFRI 599

QY 600 ALLCHLYLSIGVSSSYSPRSIGKLGQTLNMPSTYIAALPSEISKLOCLHLTRCIG 659
 DB 600 ALLCHLYLSIGVSSSYSPRSIGKLGQTLNMPSTYIAALPSEISKLOCLHLTRCIG 659

QY 660 QHYDNFS-LNHPMKCTINTICLPKFTPLVSRDDRRAQIAELHMAKSCWSEIGYKVP 718
 DB 660 QHYDNFS-LNHPMKCTINTICLPKFTPLVSRDDRRAQIAELHMAKSCWSEIGYKVP 718

QY 719 KGICKLRLQVLEVDYDTRSSRAIKELQGLSKRLKGVNTNGSKCKILYAAIEKLS 778
 DB 719 KGICKLRLQVLEVDYDTRSSRAIKELQGLSKRLKGVNTNGSKCKILYAAIEKLS 778

QY 779 SLQSLHVDAGISDGGTLECLDSTSSPPPLRLTLVLGILEEMPNWIEQLTHLKIYLLR 838
 DB 779 SLQSLHVDAGISDGGTLECLDSTSSPPPLRLTLVLGILEEMPNWIEQLTHLKIYLLR 838

QY 839 SKLKEGTMILGALPNLVLHLYRNAYLGEKLVFKTGAFPNLRLTLIYELDQLREIRFE 898
 DB 839 SKLKEGTMILGALPNLVLHLYRNAYLGEKLVFKTGAFPNLRLTLIYELDQLREIRFE 898

QY 899 DGSFPLEKIEIGCRLESIGTIGIHLPLKIEIPIRGSKVAGLQGLGEVNAHPNPVL 958
 DB 899 DGSFPLEKIEIGCRLESIGTIGIHLPLKIEIPIRGSKVAGLQGLGEVNAHPNPVL 958

QY 959 LMYSDRYHDLG 970
 DB 959 LMYSDRYHDLG 970

QY 960 QMAEDRSHHDLG 971
 DB 960 QMAEDRSHHDLG 971

RESULT 8
 ADI57170
 ID ADI57170 standard; protein; 993 AA.
 XX AC ADI57170;
 XX DT 22-APR-2004 (first entry)
 XX DE Oryza minuta P19 locus nucleotide binding site (NBS) protein #2.
 XX KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
 XX KW plant breeding; transgenic plant; plant.
 XX OS Oryza minuta.
 XX PN US2004006788-A1.
 XX PD 08-JAN-2004.
 XX PF 27-JAN-2003; 2003US-00352179.
 XX PR 25-JAN-2002; 2002US-0352106P.
 XX PR 01-FEB-2002; 2002US-0353304P.
 XX PA (WANG/) WANG G.
 XX PA (LIU/) LIU G.
 XX PI Wang G, Liu G;
 XX WPI; 2004-121064/12.
 XX DR N-PSDB; ADI57169.
 XX PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2 and NBS3, useful for producing plants resistant to Magnaporthe grisea infection.
 XX PS Claim 1; SEQ ID NO 87; 136pp; English.
 XX CC The invention comprises the amino acid and coding sequences of nucleotide binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial blight and rice blast resistance genes). The DNA sequences may be used as markers for resistance to infection with Magnaporthe grisea in plant breeding programs. The present amino acid sequence represents an NBS protein encoded by a gene from the Oryza minuta P19 locus.
 XX SQ Sequence 993 AA;

Query Match 48.9%; Score 2575; DB 8; Length 993;
 Best Local Similarity 54.9%; Pred. No. 4.9e-214;
 Matches 535; Conservative 166; Mismatches 244; Indels 30; Gaps 12;

QY 1 MAETVLSMARSLVGSATSKAASAADETSLLGVKEDIWIKDELTKMQAFRAELMKK 60
 DB 1 MTETVSMAMSLVGSATSKAASAADETSLLGVKEDIWIKDELTKMQAFRAEYVK 60

QY 61 KDELKVAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRLQVLRHRHRIAIRHNLKSRVE 120
 DB 61 KDELKVAEQIRDLSDYDIEDSLDEFKVIHIESQTLFRLQVLRHRHRIAIRHNLKSRVE 120

QY 121 EVSSRNTRYSLVKPISSGTEIDMSYAEDIRNQSARNVDAELVGFSDSKRLLEMDT 180
 DB 121 EVSSRNTRYSLVKPISSGTEIDMSYAEDIRNQSARNVDAELVGFSDSKRLLEMDT 180

QY 181 NANGDPKAVICVGMGGGLKGTALSRKIPESBEDIRKPPCNWITVSQSFHRIELDKMI 240
 DB 181 NANGDPKAVICVGMGGGLKGTALSRKIPESBEDIRKPPCNWITVSQSFHRIELDKMI 240

QY 241 QLLGPSLQDLQLOGLQKVVVQVHHLSLEYLIEELKEKRYFVVLDDLMILHDMNWIIEIA 300
 DB 241 QLLGPSLQDLQLOGLQKVVVQVHHLSLEYLIEELKEKRYFVVLDDLMILHDMNWIIEIA 300

QY 239 QLLGPSLQDLQLOGLQKVVVQVHHLSLEYLIEELKEKRYFVVLDDLMILHDMNWIIEIA 297
 DB 239 QLLGPSLQDLQLOGLQKVVVQVHHLSLEYLIEELKEKRYFVVLDDLMILHDMNWIIEIA 297

QY 301 PPKNKGSRIVITRNVDLAEKCATASLVVHLDFLQNDAITLLLRKTNKNHDMESNK 360
 DB 301 PPKNKGSRIVITRNVDLAEKCATASLVVHLDFLQNDAITLLLRKTNKNHDMESNK 360

Db 298 -GNNMEGSRVVVTRNNKLAGSST-SPVYCLTKLEKEDATKLLRKTGRSLHDIKQD- 354
Qy 361 MQKQVVERIVNKGRLPLAILTIGAVLATKQVSEWEKFEYHLPSELEINPSLEALRRMVTL 420
Db 355 MKEIFEIKLKCGGLPLAITITIGAVLEGKOIKWEIILYAQLPSSLESNPIAEPKKVYTL 414
Qy 421 GYNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480
Db 415 SYNLPKPCFLYLSICIFEDFDIQKRLVHRWIAEGFVRARGGVIVDVAQYFDELI 474
Qy 481 NRSIMQSRVGIAGKIKTCRIHDIRDITVTSIROENFVLLPMGDSLVQENTRHIAFH 540
Db 475 NRSIMQASRVDIENKISCRVHDIRDVMWISISREENFVLLMGDDGTSVVEENIRHLVH 534
Qy 541 GMSCKT-GLDWSIIRSLATFG-DRPKSLAHAVCPDQLRMLRVLDLDDVFTLTKQDFDR 598
Db 535 DTSKCSNIGMDWSHVSRLTLFGNERPKGLSPFCFQPKMLRVLDLQDVKFGMTQDQIG 594
Qy 599 IALLCHLKYLISGYSSISYLSIPRIGLQGLQTLNMPSTYIAALPSEISKLOLTLRCL 658
Db 595 IGLRHUKYVNIHGSHSIYALPRCIGKLDKDLCTUDITDSYITELPTBISKLSQILRCR 654
Qy 659 GQHYDNFSLNHPMKCITNTICLPKFTPLVSRDRRAKQIAELHMAATKSCWSE---SIGV 715
Db 655 GRPNSGDFNLNDPKDCLIAFSCPLLMATDS-DERNKIIAELHVGCSQWSPNGGTGV 713
Qy 716 KVPKIGIKRLDQVLEVDYDRTSSRAIKELGQSLKRLKGLVTTNGSTKECKKILYAAIE 775
Db 714 RVPRGINKLRLQVLEVDYDRTSSRAIKELGQSLKRLKGLVTTNGSTKECKKILCTAIG 773
Qy 776 KLSLSQSLHVDAAIGSDGGTLECLDSSPPPLARTLVLDGILEMPNWIOLTHLKKIY 835
Db 774 KLSLKLTLNARGLDTGTLEWLHSHSLPS-LRIIRLIGYKEMPNWFRELQVLKIH 832
Qy 836 LLRSKLEGTMLTILGALPNLMVLHLYRNAYLGEKLVFKTGAFPNLRLTLMIYELDLREI 895
Db 833 LQNSQLEEDKTEILGELPNLMVLFLSWRA-----VLIIIRNQKQKEV 875
Qy 896 RFEDGSPPLBKIBIGECRLBSGTIGIHLPKLKEIPRYGSKVAGLGQLEGEVNAHPNR 955
Db 876 RFEEGTSPMERIDIRECRLTSGIAGIKHLPRLKEISLEYSAKVVRVLQGLEVENGTHPNR 935
Qy 956 PVLAMYSRRVHDIG 970
Db 936 PMLRFGERSRHDIG 950

RESULT 9

ADIS1714

ID ADIS1714 standard; protein; 1054 AA.

XX AC

XX AC

XX AC

DT 22-APR-2004 (first entry)

XX DE

DE Oryza minuta p19 locus nucleotide binding site (NBS) protein #4.

XX nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;

XX plant breeding; transgenic plant; plant.

XX OS

XX Oryza minuta.

XX PN

XX US2004006788-A1.

XX XX

XX PD

XX 08-JAN-2004.

XX XX

XX 27-JAN-2003; 2003US-00352179.

XX XX

XX 25-JAN-2002; 2002US-0352106P.

XX PR

XX 01-FEB-2002; 2002US-0353304P.

XX XX

XX (WANG/) WANG G.

PA (LIUG/) LIU G.

PI Wang G, Liu G;

XX WPI; 2004-121064/12.

DR N-PSDB; ADI57173.

XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2

PT and NBS3, useful for producing plants resistant to Magnaporthe grisea

PT infection.

XX Claim 1; SEQ ID NO 91; 136pp; English.

PS The invention comprises the amino acid and coding sequences of nucleotide

XX binding site (NBS) proteins from the Oryza minuta p19 locus (bacterial

CC blight and rice blast resistance genes). The DNA sequences may be used as

CC markers for resistance to infection with Magnaporthe grisea in plant

CC breeding programs. The present amino acid sequence represents an NBS

CC protein encoded by a gene from the Oryza minuta p19 locus.

XX Sequence 1054 AA;

SQ Query Match

Best Local Similarity 50.3%; Pred. No. 6.7e-196;

Matches 516; Conservative 149; Mismatches 266; Indels 94; Gaps 22;

Qy 1 MAETVLSMARSLVGSATSKAASAADETSLLLGVEKDIWYIKDELTKMQAFLRAELMKK 60

Db 1 MADTVLSIAKSLVGSASVSVASVAADQIMLLGVQKQEIWIKDELQTIQAFIAAE-ASK 59

Qy 61 KDELKLVWAEQIRDLSDIEDSLDEDFKVIHIESQTLFRQLVKLRERHRIAIRHNLSRVE 120

Db 60 KSILLKVVWQVRDLSYDIEDCLDEFVHVGSQLSRQLMKLKDHRHIAIQIRNLRIE 119

Qy 121 EVSNRTRYSLVK-PISSGTEIDMSYAEIDRQSNARNDVAELVGSQKRLLEMDT 179

Db 120 EVSTNRIRYLIENDLTCTTTDERNLFEMDIRNQ-ANNIEADIVGSGPKRELLDIDV 178

Qy 180 NANGGPAKVICVGMGGLGTALSRKIFESEEDIRKNFPNCNMTVTSQSFHRIELKDMI 239

Db 179 HANDGPKVVCVGMGGLGKTTIARKIYESKEDIAKPFSCCAWITVSQFVRVELLDLM 238

Qy 240 RQLGPSLQLLQELQGVVQVHLSYELIEBELKEKRYFVVLDDLWLHDMWNINEIA 299

Db 239 VKLFGEEVLKRLRELEGK-VPQVDDLASLYRLTELNERRYFVLDNVWSTDQKWINIA 297

Qy 300 FP-KNNKGSRIVITTRNDVLAEKATASLYVHLDLFLQMDAITLLRKTWNHEDMESN 358

Db 298 FPRNNKGSRIVITTRDVLGTKECTSELLIYQLKPLEINYAKELLARKANKAIGDMESD 357

Qy 359 KMQQKQVVERIVNKGRLPLAILTIGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMV 418

Db 358 K-MSDIITIKIKKGYLPLAILTIGVLSLTKREWEFTFYQIPESELESNLSAMRRIV 416

Qy 419 TLGYNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNE 478

Db 417 TLSYNLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNE 476

Qy 479 LINRSMIQSRVGIAGKIKTCRIHDIRDITVTSIROENFVLLPMGDSLVQENTRHIA 538

Db 477 LINRSMIQSRVGIAGKIKTCRIHDIRDITVTSIROENFVLLPMGDSLVQENTRHIE 536

Qy 539 FHGSMSC-KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDDVFTLTKQD 597

Db 537 FHGSKYCSSETSLDWSIIRSLTMFGERSVLEHSCSSQLRMLRVLDLDDVFTLTKQD 596

Qy 598 RIALLCHLKYLISG-----YSSSIYSLPRS-----IGKQLQGLQTLNMPSTYIAALPS 644

Db 597 NIVLCHLKYLICKIPIPTIYLTSTIHTANSADIGLSDGVHFTAN--SDY----- 648

Qy 645 EISKLOCLHTLRCIGQHYDNFNSLHMPKCIITNTICLPKFTPLVSRDRRAKQIAELHMA 704

Db 649 ----LRSLRSLRCMKKEYFSSSLT-----LTNTLCLPMTIPTFPVSTSDRSETIAKLHMA 699


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XX Wang G, Liu G;
PI WPI; 2004-121064/12.
DR N-PSDB; ADI57177.
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
XX Claim 1; SEQ ID NO 95; 136pp; English.
PS
XX The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present amino acid sequence represents an NBS
CC protein encoded by a gene from the Oryza minuta P19 locus.
XX
XX Sequence 451 AA;
SQ
Query Match 26.3%; Score 1384; DB 8; Length 451;
Best Local Similarity 51.6%; Pred. No. 5.7e-111;
Matches 281; Conservative 73; Mismatches 93; Indels 98; Gaps 3;
Qy 1 MAETVLSMARSLVGSALSKAASAAADETSLLLGVKEDIWIKDELKTWQAFRAAELMKK 60
Db 1 MADTVLSIALKSLVGSANVSKVASVAADKWILLGVQKEIWFIKDELQTIQAFMAAE-ASK 59
Qy 61 KDELKVAEQRDLSYDIEDSLDFKVIHESOTLFRQLVKLRERHRIAIRIHNLSKRV 120
Db 60 KSILLKVVQVQVRLSDIEDCLDEFTVHVGSQTLRQLMKLKDRIAVQIRNLRTIE 119
Qy 121 EVSSRNTRYSLVPISSGTEIDMDSYAEIDINQSARNVDEALVGFSDSKKLEMDTN 180
Db 120 EVSSRNTRYNLINDLTSTTGERNFIMEDIENESANNIEAEALVGFSGPKRELLDLVDH 179
Qy 181 ANDGPAPKVICVVGMLGKLTALSKRPIFESEDIRKNPCNAWITVSQSFHRIELDKMIR 240
Db 180 AKDQPTKVCVVGMLGKLTIAKIYESKEDIAKNFSCCAWITVSQSFVLELLKDLV 239
Qy 241 QLLGSSLDQLLQELQGVVQVHLLSEYLFELKEKRYFVLDLWILHDWNWNIAP 300
Db 240 KLFGEVLKRLRELEGK-VPQVDDLASYLRTLNERRRYFVLDVWVSTDSWKWINSIAF 298
Qy 301 PKNKKGSRVITITNVDLAKCATASLVYHLDFLQWDAITLLRKTNNKHEDMESKN 360
Db 299 PRNNKGSRVITVTRDVLAKECTSELIYRLKPLEITYAKELLRLKANKKIEDKSDKK 358
Qy 361 MOKWVERIVNKCGRPLAIIITIGAVLATKQVSEWEKFEYHLPSPLEINPSLEALRRVTL 420
Db 359 MSDIITKLVKCGVPLAIIITIGVLA TK----- 387
Qy 421 GYNHLSHLKPCFLYLSIFPEDFBIKRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480
Db 388 ----- 387
Qy 481 NRSMIQSRVGIAGIKTCRIHDIIRDITVISIQENFVLLPMGDGSDLVQENTRHIAFH 540
Db 388 -----DPSRAGVRGEFKSCRIHDMRDIAISISEENFILLPEGTDYDVVHGNTRHIAFH 442
Qy 541 GMSGC 545
Db 443 GSKYC 447
RESULT 12
AAAY93135
ID AAAY93135 standard; protein; 1251 AA.
XX
AC AAAY93135;
XX
DT 08-NOV-2000 (first entry)
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```
XX Rice blast fungus-resistance protein Pi-b from rice.
DE
XX Rice blast fungus; Pyricularia grisea; Magnaporthe grisea;
KW resistance gene.
XX
OS Oryza sativa.
XX JP2000125885-A.
XX
XX 09-MAY-2000.
PD
XX 29-MAR-1999; 99JP-00087305.
XX
XX 21-AUG-1998; 98JP-00235884.
PR
XX (KAGA-) KAGAKU GIJUTSU SHINKO JICYODAN.
PA (NORQ) NORINSUISANSO NOGYO SEIBUTSU SHIGEN.
XX
XX WPI; 2000-379868/33.
DR N-PSDB; AAA11349, AAA11350.
XX
XX A blast-resistant gene and related genes, useful for creating a rice
PT grade of high blast resistance.
XX
XX Claim 26; Page 20-23; 36pp; Japanese.
PS
XX The invention relates to the isolation of novel rice blast fungus
CC (Pyricularia grisea; also known as Magnaporthe grisea) resistance genes
CC from rice strain BI-1. The genes are designated Pi-b (AAA11349) and Pi-b'
CC (AAA11351). The genes can be used for creating rice which has high blast
CC fungus resistance. This sequence represents the protein encoded by the Pi
CC -b gene
XX
XX Sequence 1251 AA;
SQ
Query Match 22.9%; Score 1204; DB 3; Length 1251;
Best Local Similarity 27.4%; Pred. No. 1.4e-94;
Matches 353; Conservative 200; Mismatches 367; Indels 368; Gaps 36;
Qy 1 MAETVLSMARSLVGSALSKAASAAADETSLLLGVKEDIWIKDELKTWQAFRAAELMKK 60
Db 1 MEATALSVGKSLVNGALGYAKSAFAEEVALQGLGKQDHTFVADLEMMRSMFMEAEHQD 60
Qy 61 KDELKVAEQRDLSYDIEDSLDFKVIHESOTLFRQLVKLRERHRIAIRIHNLSKRV 120
Db 61 NSKVKTWVQVQVRLSDIEDCLDEFTVHVGSQTLRQLMKLKDRIAVQIRNLRTIE 120
Qy 121 EVSSRNTRYSLVPISSGTEIDMDSYAEIDINQSARNVDEALVGFSDSKK 172
Db 121 DVSGRNRYHLIKGSAKAT-----INSTEQSSVIATATFGIDARRAAKQDNQRV 170
Qy 173 -LLEMIDTNDANDGPAPKVICVVGMLGKLTALSKRPIFESEDIRKNPCNAWITVSQSFH 230
Db 171 DLVQLI--NSEDQDLKVIWVGTSQTLRQLMKLKDRIAVQIRNLRTIE 227
Qy 231 RIELKDMIRQLLGPSSLDQL----- 252
Db 228 PROFVQSLVNLQHLATQGVAEALLEKEKTEQDLAKFKNGCVNDRKCLIVLNDLSTIEWDQI 287
Qy 253 -----QELQG----- 257
Db 288 KKCFQKCRKGSRIIVSSTQVEVASLCAQGESQASELQLSADQTLAYFDKGSQIIBDSV 347
Qy 258 ----- 257
Db 348 KPVSIQSDVAITSTNNHTVAHGEIIDDQMDADEKKVARKSLTRIRTSVGAEEESQLIGRE 407
Qy 258 KVVVQVHHL----- 266
Db 408 KEISEITHLILNDSQQQVVISVWGMGLGKTTLLVGVSQVPSRLSDPKDKVFTIWRPF 467
Qy 267 -----SEYLTIE-----LKEKRYFVVLD 284
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Db 468 ILVLLSLRLAQHLKSGSKSELEENRVSSKSLASMEDTELTGQLKRLLEKSKCLVLVD 527
Qy 285 DLWLHLDNWNWINEIAPFNKKNKGSRIIVITTRNVDAEKCATAS-LVYHLDPLQNDATIL 343
Db 528 DFDSTSEWDQIKPTLPL-LKTSRIIVITTRKENIANHCSGKGNVHNLKVLKENDALCL 586
Qy 344 LLRT--NKNHEDMESKNQKQKVERIVNKCGRPLAILITGAVLAT--KQVSEWEKPYE 399
Db 587 LSEKVFEEATYLDQNNPELVKEAKQIKKCDGLPLAIVVIGFGLANRPKTPPEWRKLINE 646
Qy 400 HLPSELEINPLEALRMVTLGYNHLPLKPCFLYLSIPPEDFEIKRNLVGRWIAEGF 459
Db 647 NINAELENPELMIRVLEKSYDGLPHLKSCTFLYSIPPEDQIISSRRLLVHWAAGY 706
Qy 460 VRPKVGMTTQDVGESYFNEINRSMI---QSRVGIAGK-IKTCRIHDIIRDIVTSISRQ 515
Db 707 STAAHGKSAIBANGYFMELKNRSMILPFOQS--GSSRKSIDCKVHDLMEDIAISKSTE 764
Qy 516 ENFVLLPMGDSLVQENTRHIA----FHGMSCKTGL-DWSIIRSLAIFGDRPKSLAHA 570
Db 765 ENLFRVVEEGSAYIHGAIRHLAISNNWKGDKSEFEGIVDLRSIRLSLFGDMKPPFFVYG 824
Qy 571 VCPQLMRVLVDLEDTFLITQKDFRIALLCHLVLSIGYSSSIYSLPRSICKLQGLQ 630
Db 825 ---KMFIRVLDPEG-TRGLEVHLDQIWKLNHLKFLSLRGCTYRIDLLPLDGLNLRQLQ 879
Qy 631 TLNMPSTYIAALPS---EISKLQCLHLRCITGQPHYDNFSLNHPMK---CITNTICLPKV 684
Db 880 MLDIRGYVVKALPTIINKLQKQVIHAGRKTDYVWEKHSIMQCRKVGCICATCCLPLL 939
Qy 685 FTPLVSRDRRAQIAELH--MATKCSWS-----BSIGVKVPKGIKLRDL 727
Db 940 -----CEMYGPLHKLARLDAMTFACCVKFPSTMTGVHEEGAMVPSGIRKLKDL 989
Qy 728 QVLEYVDIRTSRAIKELGOLSKLKLGYTTNGSTKECKILYAAIEKLSLOSILHDA 787
Db 990 HTLRNINVR--GNAILRDIGMLTGLHLGLVA--GINKNGRAFLAIISNLNKLESLSVSS 1046
Qy 788 AGISDGTGLECLDISPPPLRLTLVDGILEEMPNIIEQLTHLKKIYLLRSKLKE-GKT 846
Db 1047 AGMP--GLCGCLDDISSPENLQSLKLYGSLKTLPEWIKELQHLVKLKLVSTRLLEHVA 1104
Qy 847 MLILGALPNMLVHLRYNAVYGEKLVFK---TG-AFPNRLTLWLYELDQREIRFEGSS 902
Db 1105 MEFLGELPKVEILVI--SPFKSEIHFEPQGTGAFVSLRVLKLGLWGIKSVKFEFGTM 1162
Qy 903 PLEKIEI-GECLRESGITGIIHLPKLEIPRY-----GSKVAGL----- 942
Db 1163 PKLERLQVQRIENIEIGFSGLEPLQINIEVQLSVWFPTDHDRIARAARAAGADYETAWE 1222
Qy 943 -----GOLEGBVN---AHPNRPVL 958
Db 1223 VQEARRGKGLKRIQRLARNFNQPII 1250

RESULT 13
AAY49434
ID AAY49434 standard; protein; 1205 AA.
AC AAY49434;
XX
XX
DT 17-MAR-2000 (first entry)
DE Blast disease-resistance (Pi-b) protein.
XX Blast disease; rice; pi-b gene; blast disease-resistance gene.
XX
XX Oryza sativa.
XX
XX EP969092-A1.
XX
XX 05-JAN-2000.
```

```
XX 11-JUN-1999; 99EP-00111443.
XX
XX 12-JUN-1998; 98JP-00181455.
XX
XX (NORQ) NAT INST AGROBIOLOGICAL RESOURCES.
XX
XX Yano M, Iwamoto M, Katayose Y, Sasaki T, Wang Z, Yamanouchi U,
XX Iehimaru L;
XX
XX WPI: 2000-064864/06.
XX
XX N-PSDB: AAZ46679, AAZ46680.
XX
XX Novel polypeptide and DNA encoding it used to produce plants resistant to
XX fungal blast disease.
XX
XX Claim 1; Page 8-14; 46pp; English.
XX
XX The invention provides a protein which confers resistance to blast
XX disease onto plants. The blast disease-resistance (Pi-b) protein can be
XX expressed by standard recombinant methodology. The novel Pi-b gene is
XX used to produce transgenic plants resistant to the rice blast disease,
XX which will control the disease and increase crop yields. The present
XX sequence represents the rice Pi-b protein. The resistance gene Pi-b is
XX located at the end of the long arm of rice chromosome 2 and displays
XX resistance to blast fungi
XX
XX SQ Sequence 1205 AA;
XX
XX Query Match 21.1%; Score 1111; DB 3; Length 1205;
XX Best Local Similarity 26.9%; Pred. No. 1.6e-86;
XX Matches 334; Conservative 188; Mismatches 351; Indels 368; Gaps 36;
XX
XX Qy 48 MQAFRAELMKKKDELKVAEQIRDLSDYIEDSLDFEKVHIESQTLFQVLKLRHR 107
XX Db 2 MRSFMEAHQEONSKVKVTWQVQRTAYDVEDSLQDFVHLKRPSPWRPRTLLERHR 61
XX
XX Qy 108 IAIRIHLKSRVEVSRNTRYSLVKPFISSGTEIDMSYAEIDINQSNARNYDEALVGFS 167
XX Db 62 VAKQMKELRNKVEDVSQRNVRYHLKGSAT-----INSTGSSVIATAFGID 111
XX
XX Qy 168 DSKR-----LLEMIDTNDANDGPAKVICVVGWG-LGKTALSRLKPISESEDIRKPF 217
XX Db 112 DARRAAQDNQORVDLVQL--NSEDQLKVIATVWGTSMDGMGQTTIIRMAVEN-PDVQIRF 168
XX
XX Qy 218 PCNAWITVSQSFHRIELKDMIRQLLGPSSLDOLL----- 252
XX Db 169 PCRAWVVMHPPFPRDFVQSLVNLQHLATQGVALLKEKTEQDLAKKFGNCVDRKCLIV 228
XX
XX Qy 253 -----QELQG----- 257
XX Db 229 LNDLSTIEWDQIKKCFQCKRKSRIIVSSTQVEVASLCAGQESQASELKLSADQTLYA 288
XX
XX Qy 258 ----- 257
XX Db 289 FYDKGSIIBDSVKPVSISDVAITSTNNHTVAHGEIIDDQSDMADEKKVARKSLTRITS 348
XX
XX Qy 258 -----KVVQVHHL----- 266
XX Db 349 VGASESOLIGREKEISEITHLILNDSQQVQVIVSWGMLGKLTTLVGVQSPRLSDK 408
XX
XX Qy 267 -----SEYLLIE----- 273
XX Db 409 FDYVFTVIMRPFILVELLSLAELQHLKSGSKSELEENRVSSKSLASMEDTELTGOLK 468
XX
XX Qy 274 --LKEKKYFVVLDDWLILHDNWNWINEIAPFNKKNKGSRIIVITTRNVDAEKCATAS-LVY 330
XX Db 469 RLLEKSKCLVLDDDFDSTSEWDQIKPTLPL-LKTSRIIVITTRKENIANHCSGKGNVH 527
XX
XX Qy 331 HLDPLQNDATILLLRKT--NKNHEDMESKNQKQKVERIVNKCGRPLAILITGAVLAT 388
XX Db 528 NLKVLKNDALCLLSEKVFEEATYLDQNNPELVKEAKQIKKCDGLPLAIVVIGFGLAN 587
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Qy 389 --KQVSEKFEYHLPSELEINPSLEALRRMVTGLYGNHLPKPCFLYLSIFPEDFEIK 446
Dy 588 RPKTPEWRKLNENINAELEWNPGLMTRTVLEKSYDGLPHLAKSCFLYLSIFPEDQIIS 647
Qy 447 RNLVGRWIAEGFVRPKVGMVTKOVGSYFNELNRSMI---QSRVGIAGK-IKTCRIH 502
Dy 648 RRLVHRWAAEGYSTAAHGKSAIBIANGYFMELKNRSMILPFOQS--GSSRKSDSCKVH 705
Qy 503 DIIRDITVISROFNVLPMGDSGLVQENTHIA---PHGSMCKTGL-DWSIIRSL 557
Dy 706 DLMRDIAISKSTEENLFRVEEGCSAYIHGAIRHLAISNNWKGDKSEFEGIVDUSRIRSL 765
Qy 558 AIFGDRPKSLAHAVCPDQLRMLRVLDDVDTFLITQKDFDRIALLCFLKYLISGYSSSIY 617
Dy 766 SLFGDWKPFYVG---KMRIRVLDPEG-TRGLEHYHLDQIKWLNHLKFLSLAGCYRID 820
Qy 618 SLPRSIGKLOGLQTNMPSTVIAALPS---BISKLOCLHTURCTIGQHYDNFSLNHPMK- 673
Dy 821 LLPDLGNLRLOQLMDIRGTYYKALPKTIKLOKQVTHAGRKTDYVWEKSHSLMQRCK 880
Qy 674 --CITNTICLPKVTPLVSRDDRKAQIAELH--NATKSCWS-----BSIG 714
Dy 881 VGCICATCCCLP-----CEMYGPLHKLARRDAWTFACCVPPSMTGVHBEEG 930
Qy 715 VKVPKGIGKLDLOVLEYVDIRRTSSRAIKELGQSLKRLKLGVTGTNGSTKECKKILYAAI 774
Dy 931 AMVPSGIRKLDLHTLRNINVR-GNALRDIGMLTGLHLGVA--GINKKNGAFRLAI 987
Qy 775 EKLSSLOSLHVDAGISDGGTLECLDISPPPLRLTLVLDGILEEPMNTEQTLHKKI 834
Dy 988 SNLAKLESLSVSSAGMP--GLCGCLDDISSPPENLQSLKLYGSLKTLPEWIKELQHLVKL 1045
Qy 835 YLLRSKLKE-CKTMLIILGALPNLAVLHLYRNAYLGEKLVPK--TG-AFPNLRTLWIYEL 889
Dy 1046 KLVSTRLEHDVAMEFLGELPKVETVI--SPFKSEEHFKPPOTGTAFVSLRVKLKAGL 1103
Qy 890 DQLEIRPEDGSSPLLEKIEI-GECLRESGITGIIHLPKLEIPIRY-----GSK 938
Dy 1104 WGIKSVFEEGTMPKLERLQVQGRINEIGFSGLEFLQINELVSVWFFPDHDIRAAR 1163
Qy 939 VAGL-----GOLEGEVN-----AHPNRPVL 958
Dy 1164 AAGADYETAEWEQVARRKGGLKRLKIREQLARNPNQPII 1204

RESULT 14
ADM72280
ID ADM72280 standard; protein; 1205 AA.
AC ADM72280;
AC
DT 03-JUN-2004 (first entry)
XX
DE O. minuta Pi2 gene predicted amino acid sequence.
XX
KW Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance.
XX
OS Oryza minuta.
XX
FN WO2004022715-A2.
XX
PD 18-MAR-2004.
XX
XX 08-SEP-2003; 2003WO-US027913.
PF
XX 09-SEP-2002; 2002US-0409216P.
PR
XX 18-MAR-2003; 2003US-0455713P.
PR
XX 05-SEP-2003; 2003US-00656394.
XX
XX (OHIS ) UNIV OHIO STATE.
PA
XX Wang G;
XX
```

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DR . WPI; 2004-257576/24.
XX
PT New rice Pi2-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.
XX
PS Disclosure; Fig 5; 120pp; English.
XX
CC The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents an O.
CC minuta Pi2 gene predicted amino acid sequence
XX
SQ Sequence 1205 AA;

Query Match 21.1%; Score 1111; DB 8; Length 1205;
Best Local Similarity 26.9%; Pred. No. 1.6e-86;
Matches 334; Conservative 188; Mismatches 351; Indels 368; Gaps 36;

Qy 48 MQAFLRAAELMKKDELLKVMAEQIRDLSDIEDSLDEFKVHIESOTLFRQLVKLRHRH 107
Dy 2 MRSFMENAEHEEQNSKVVTWVKQVRTAIDVEDSLQDFAVHLKRPKSWRPPRLLERHR 61
Qy 108 IAIRIHNKLKSRVEEVSERNTRYSLVKPISSTGTEIDMDSYAEIRNQSNARNVDEALVCF 167
Dy 62 VAKMKELRNKVEDVSQRNVRYHLIKGSAKAT-----INSTQSSVIATAIFGID 111
Qy 168 DSKKR-----LLEMIDTNANDGPAKVICVGMCG-LQKTALSRKIPESEEDIRKNF 217
Dy 112 DARRAAQDNQRVDLVQLI--NSEDDQLKVIAMVGTSGDMGQTTIIRMAYEN-PDVQIRF 168
Qy 218 PCNAWITVSOSFRIELDKMIRQLGLPSSLDQL-----QELQG----- 252
Dy 169 PCRAWVRMHPFPRDFVQSLVNLQHLHATQGVAEALLEKTEQDLAKKFNCGVDRKCLIV 228
Qy 253 -----QELQG----- 257
Dy 229 LNDLSTIEWDQIKKCFQKCRKGSRIISVSTQVEVASLCAGQESQASSELKLSADQTLA 288
Qy 258 -----KVVVVVHHL----- 257
Dy 289 FDKGSGIIEDSVKPVSIISDAITSTNNHTVAHGEIIDDQSDMADEKKVARKSLTRTS 348
Qy 258 -----KVVVVVHHL----- 266
Dy 349 VGASESOLIGREKEITSEITHLIINDSQQVQVIVSMGGLGKTTLVSGVYQSPRLSDK 408
Qy 267 -----SEYLIEE----- 273
Dy 409 FDKYVFTVIMRPFILVELLSLABQLHKSGKKEELLENRVSSKKSLASMEDTETLQGLK 468
Qy 274 --LKEKRYFVVLDDLWILHDNWNINEIAPKNNKSGSRIVITTRNVDLAEKCATAS-LVY 330
Dy 469 RLLEKKSCLIVLDDFSDTSEWDQIKPTLPPL-LEKTSRIIVTTRKENIANHCSGKGNVH 527
Qy 331 HLDPLQWMDAITLLRKT--NKHEDMESNKQWKQVERIVNKGRLPLAITLTIGAVLAT 388
Dy 528 NLKVLKNDALCLLSEKVFEEATYDDQNPPELVEAKQILKCDGLPLAIVLGGFLAN 587
Qy 389 --KQVSEKFEYHLPSELEINPSLEALRRMVTGLYGNHLPKPCFLYLSIFPEDFEIK 446
Dy 588 RPKTPEWRKLNENINAELEWNPGLMTRTVLEKSYDGLPHLAKSCFLYLSIFPEDQIIS 647
Qy 447 RNLVGRWIAEGFVRPKVGMVTKOVGSYFNELNRSMI---QSRVGIAGK-IKTCRIH 502
Dy 648 RRLVHRWAAEGYSTAAHGKSAIBIANGYFMELKNRSMILPFOQS--GSSRKSDSCKVH 705
Qy 503 DIIRDITVISROFNVLPMGDSGLVQENTHIA---PHGSMCKTGL-DWSIIRSL 557
Dy 706 DLMRDIAISKSTEENLFRVEEGCSAYIHGAIRHLAISNNWKGDKSEFEGIVDUSRIRSL 765
Qy 558 AIFGDRPKSLAHAVCPDQLRMLRVLDDVDTFLITQKDFDRIALLCFLKYLISGYSSSIY 617
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Db 336 LKEDEAWLFSNKAPPASLEQCRONTLEPTIARKLVERCOGLPLAIAISIGSMSTTKFESE 395
 Qy 394 WEKEVEYHLPSELETPNSLEALRRMWTGYNHLPKPCFLYLSIFPEDPEIKENRLVGR 453
 Db 396 WKYVSTLNWELNNHLEKUVRSIMFSDPLPKRCFLYCSLFPVYVNMKRRKLIRM 455
 Qy 454 WIAEGFVRPKVGMTKDVGESYFNELNRSMIORSRVGIAGIKTKICRHIIDITVTSIS 513
 Db 456 WMAQRFVEPIRGVKAEEVADSYNELVYRNMLVILWNPFRPKAFKMHVDVWEIALSVS 515
 Qy 514 ROENF--VLLPMGSGSLVQ--EN--TRHIAFGHSMCKTGLDMSIIRSLAIFGDRPKSL 567
 Db 516 KLERFCVDYNDSDGDAETMENYGRSLCIQKEMT--PDSIRATNLHSLIIVCSSAKHKM 574
 Qy 568 AHAVCPQLMRVLIDEDVTFLITQDFDRIALLCHLKYLISIGSYSIYSLPSIGKIQ 627
 Db 575 --ELLP--SLNLRALDLEDSI--SKLPDCLVTFMFLKYLNLGS--KTQVKELPKNFHKL 627
 Qy 628 GLQTLNMPSTVIAALPS---BISKQLCHLTCIGQHYDNFSLNHPMKCITNTICLPKV 684
 Db 628 NLETLNTYKSKIELPLGMWKLKRLVITFR--RNEGHDSN----- 667
 Qy 685 FTPLVSRDRAKOIAELHMAKTSQWSESIGVKVPKGIKRLDQVLEVDIRRTSSRAIK 744
 Db 668 -----WNYVLGTRVVPKIQWQLDQW---DCFNAEDELIK 700
 Qy 745 ELGQSLKRLKLGVTNGSTKECKILYAAIEKLSLQSLHVDAGISDGGTLECLDIS 804
 Db 701 NLGCMQTQTRISLVN--VRREHGRDCLSLNKKIRIFLSL--TSIDEEBLEIDDLIAT 756
 Qy 805 PPLRLTLVDIGILEEMPNTIEQTHLKKIYLLRSKLKEGKTMILGALPNMLVHLN 864
 Db 757 AS--IEKFLAGLKVPSWNTLQNTLYGLRSGSQE--NAULSIQTLPLWLVSFY-N 812
 Qy 865 AYLGKLVFTKGFAPNRLTLWIYELDQRLREIRFDGSGPPLLEKIEIGECR----LESGIT 920
 Db 813 AYMGPRLRFAQG--FONLKILBIVQMKHLETVVIEDGAMFELQKLYVRACRGLEYVPRGIE 871
 Qy 921 GIHLPKLKEIPI--RYGSKVAGIQLQE 946
 Db 872 NLINQLQELHLHVSQNLVERIRGSGVD 899

RESULT 2
 G96621
 Probable disease resistance protein F23H11.10 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: G96621
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: G96621
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-906 <STO>
 A;Cross-references: UNIPROT:Q9XIF0; GB:AE005173; NID:G5080812; PIDN:AAD39321.1; GSPDB:GN
 C;Genetics:
 A;Gene: F23H11.10
 A;Map position: 1

Query Match 15.7%; Score 826; DB 2; Length 906;

Best Local Similarity 27.9%; Pred. No. 8.3e-40;

Matches 270; Conservative 182; Mismatches 373; Indels 144; Gaps 34;

RESULT 3

T12377

hypothetical protein T6H20.240 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)


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Qy 459 FVRPKVGMTTKDVGESYFNEILNRSMIQSRVGIAGIKTKICRIHDIIRDTIVSISROENF 518
Db 453 IYD---GSTIEDSEYILEELVRNLVIADNYSQSKYCOMEDMREVCLSKAEENF 509
Qy 519 ---VLLPMGSGSLVQENR-----HIAFGSMCKTGLOWSIIRSLAI----- 559
Db 510 LQIIIDTCTSTINAQSPSRRLSIHSGRAFHILGHKN---KTK-----VRSLIVPRFE 561
Qy 560 --FGRPKSLAHAVCPDQLRMRLVLDLEDVTFITLTKDQDRIALLCHLYLSIGYSSIIY 617
Db 562 EGYWIRASVPH-----NLTLRLVLDLSWVKFEGGKLPCS-IGGLIHLRYLSL-YEAKVS 614
Qy 618 SLPRSIGKLOGLQTLNMPSTVIAALPSEISKLOQLH---TLRCICQGFHYDNFSLNHPMKC 674
Db 615 HLPSTMRNLKLLYLNL-----RVDEEPIHVPNLVKEMQLRY-----LSLPLK- 659
Qy 675 ITNTICLPKVFTPLVSRDDRAKQIAELHMAKSCWSSEISGVKVPKGIGKLRDLQVLEYVD 734
Db 660 -----MDDKTKL-----ELGDLVNLEYLY 678
Qy 735 IRRPSSRAIKELGOLSKLRKLGVTNGSTKEKC--KILYAAIEKLSLSLOSLH----- 784
Db 679 GFSTQHSVTDLLRKLRYLAV-----SLSERCNFETLSSSLRELRLNLETINFLFSLEY 734
Qy 785 -VDAAGISDGTLECLDSISSPPPLRLTLVDGLILEEMPNIWIEQLTHLKIIYLRSKLKE 843
Db 735 MVDYNGEF-----VLDRFH-----LQQLGLAVRMSKIPDQHQFPHLVHLFLYCGMEE 784
Qy 844 GKTWLIILGALPNLMVLHLRYNAYLGEKLVFKTAGPPNLRTLMIYELDQLREIRPEDGSSP 903
Db 785 -DPMPILEKLLHLKSVRLARKAFLGSRMVCCKGFPOLCVIEISKESELEWIVEEGSMP 843
Qy 904 LLEKIEGECHLESIGITGIHLPLKLEIP--IRGSKVAGLQLEG 947
Db 844 CLRTITIDDCR-----KLKELPDGLKYITSLKEL-KIEG 876

RESULT 5
P96573
protein F12M16.25 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: P96573
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: P96573
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-1584 <STO>
A;Cross-references: UNIPROT:Q9WAG6; GB:AE005173; NID:g7769860; PIDN:AAF69538.1; GSPDB:GN
C;Genetics:
A;Gene: F12M16.25
A;Map position: 1
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Query Match 15.2%; Score 803; DB 2; Length 1584;
Best Local Similarity 27.0%; Pred. No. 4e-38;
Matches 263; Conservative 191; Mismatches 365; Indels 156; Gaps 35;

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Qy 10 RSLVGSIAKSAASAADETSLLGVKXDIWIYKDELTKMQAFRAAEALMKKKDELLKQWA 69
Db 316 KAVVSFGVEKLWELLSRESARELNGIDEQVGLKQGLQSLKLDADAKNTERVRNFL 375
Qy 70 EQIRDLSDYIDSLDEF-----KVHIESQTLFRQLVRLKRHRHIAIRHLKS 117
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Db 376 EDVKDIVDADDIESFLNLNELRGKEGIKKQVRTLACF-----LVDRRRFPASDIEGITK 430
Qy 118 RVEEV---SSRTRYSLVKPISSGTEIDMSVAEDIRNOSARNVDAEALVGFSDSKRL 173
Db 431 RISEVIVGMSLGIQHI---ADGGRSLSQERQREIRQTFSRN-SESDLVLGDQSVF-- 484
Qy 174 LEMIDTNANDGPARKVICVGMGGGLGTALSKRKIFESEEDIRKNPKNAMITVSQSFRHIE 233
Db 485 -ELVDHLVENDSVQVVSVMGGMGIGTKTTLARQVPH-HDIVRRHFDGFSWVCVSQOFTF-- 540
Qy 234 LLKDMIRQLLPGSSLDLQQL-----OGKVVVQVHHLSYELIEBELKEKRFVVLDDWL 289
Db 541 --KDV-----WQRILODLRPYDEGIIQMDIEYTLQGELFELLESRGVLLVDDVWKE 589
Qy 290 HDNNWINEIAPKNNKKGSRIVITRNVDLAEKATASLVVHLDLQMDNDAITLLLRKTN 349
Db 590 EDMIRIKAV-FP--HKGWKKLLTSRNEGGLHJADPTCFAPRPRILTPGOSWKLPERIVS 646
Qy 350 KNHEDMESNKNMOKWVERIVNKCQRLPLAILITIGAVLATKQ-VSEWEKFFEHLFSELEIN 408
Db 647 SRDKTEF-KVDEAMGKEMTYTCGGLPLAVKVLGGLAKKHTVLEWKRVHSNIVTHIVGK 705
Qy 409 PSL-----EALRMVTGYNHLSHLKPCFLYLSIFPEDFEIKNRLVGRWIARGFVRP- 462
Db 706 SGLSDDDNSNVYRVLSSLYEDLPWQLKHCFYLAAHFPEDYKIDVKILFNWVAEGIIITPF 765
Qy 463 KVGWTTKDVGESYFNEILNRSMIQSRVGIAGIKTKICRIHDIIRDTIVSISROENF--V 519
Db 766 HDGSTIOTGESYLEELVRRNMVVMVVEESYLTSRLEYCOMHDMREVCLSKAEENFIRVV 825
Qy 520 LLPMGDGSDLVQEN---TRHIAFH--GSMCKTGLOWSIIRSLAIFGD-----RPKSLAH 569
Db 826 KVPTTTTINAQSPCSRRLVHLSGNALHMLHGNKAKRSVLIFGVEEKFWKPRGFQ- 884
Qy 570 AVCPDQLRMRLVLDLEDVTFITLTKDQDRIALLCHLYLSIGYSSSIYSLPRSIGKLOGL 629
Db 885 --C---LPLRLRLDLSYVQF-EGGKLPSSIGDLIHLRFLSL-YEAGVSHLPSLSLGNLKL 937
Qy 630 QTLNM--PSYIAALPSEISKLOCLHTLRCIGQPHYDNFSLNHPMKCITNTICLPKVFTP 687
Db 938 LCLNLGVADRLVHVPNLVKEMOELRYLR-----DLVNLSLNTFSTKHGSVTDLL 1002
Qy 688 LVSRDDRAKQIAELHMAKSCWSSEISGVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELG 747
Db 970 -----SMPAKTKLEIG---DLVNLSLNTFSTKHGSVTDLL 1002
Qy 748 QLSKLRKLGVTNGSTKEKC--KILYAAIEKLSLSLOSL-----HYDAAIGSDGGLTECL 799
Db 1003 RMTKLSVLNVIFSG---ECTFETLLSLRELRLNLETLSLFDHDFOKVSVV--NHGELLVL 1056
Qy 800 DSISPPPLRLTLVDGLILEEMPNIWIEQLTHLKIIYLRSKLKEGKTMILLGALPNLMVL 859
Db 1057 DFTH-----LKDITLSMHLPRFPDQYRPPPHLAHILWIGCRMEB-DPMPILEKLLHLKSV 1110
Qy 860 HLYRNAYLGEKLVKPGAFPNLRTLMIYELDQLREIRFEDGSSPLLEKIEIGEC-RLESG 918
Db 1111 YLSGAFGLGRMVCCKGFPQLLAKMSYKELVEMVEEGSMELRTITIDNCKKQL 1170
Qy 919 ITGIIHLPLKLEIPI 933
Db 1171 PDGLKYVTCLELKI 1185
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RESULT 6
T48898

disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C;Accession: T48898
R;McDowell, J.M.; Dhandaaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl
Plant Cell 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolution
A;Reference number: Z24999; MUID:99030193; PMID:9811794

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A/Accession: T48898
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-906 <MCD>
A/Cross-references: EMBL:AF089710; NID:G3928861; PIDN:AAC83165.1; PID:G3928862
A/Experimental source: Landeberg erecta
C/Genetics:
A/Gene: RPP8
A/Introns: 293/1; 342/1
C/Function:
A/Description: promotes resistance to Peronospora parasitica

Query Match      14.9%; Score 786; DB 2; Length 906;
Best Local Similarity 25.9%; Pred. No. 1.7e-37;
Matches 257; Conservative 203; Mismatches 347; Indels 184; Gaps 333

Qy      8 MARSLVGSIAKSAASAADETSLLGLVSKDIWIYKDELTKMQAFRAAELMKKKDQLLVK 67
Db      1 MAEAFVFGLEKLDLLSRESERLQGVDEQDGLKRQRLSLOSLKLDADAKKHGSDRVN 60
Qy      68 WAEQIRLDYSIDPSLDEF-----KVHIESQTLFRLVK-LRERHRIAIRHN 114
Db      61 PLEDVKDLVFAEDIEDIESVYLNKLKGEKGKGV-----RRLARFLTDHKKVASDIEG 114
Qy      115 LKSVEEVSSRNTRYSLVKPISSTGTEIMDS---YAEDIRNQSARNVDEAEVLGFSDSKK 171
Db      115 ITRKISDVGEMQSGFIOQIIDGVRSLSLQERQVRQREIR-QTPYDSSSESLVGVEQSVK 173
Qy      172 RLL-EMDITNANDGPAKVICVVGGMGLKGTALSRIKFISEEDIRKNFPCNAMIIVSQSPH 230
Db      174 ELVGHVLVENDVH---QVVSITAGMGIGIKTTLARQVFH-HDLVRHFGFQFVWCVSQPT 228
Qy      231 RIELLKDMIRQLLQPGSSLDQLLELQ---GKVV-VQVHHLSYLLIEELKEKRYFVVLDDL 286
Db      229 QKHVWQ-----RIILQELPHDGDILQWDEVALQKLFQLEAGKYLVLDDV 275
Qy      287 WILHDWNWINEIAFPNNKNGSRIVITTRNVDLAEKCATASIVYHLDPLQMDAITLLR 346
Db      276 WKEDMDVIKAV-FPR--KRGWKMLLTSRNEGVIHADPTCLTFRASILNPESWKLCEB 332
Qy      347 KT--NKHHEMESKNQMKQVERIVNKGCRPLAIIITIGAVLATKQ-VSEWEKFFEHLPS 403
Db      333 IVFPRRDETEVRLDEEMAEAMGEMVTHCGGGLPAAVKVLGGLLANKHTYPEWKRVSNDTGS 392
Qy      404 E-----LEINPSLEALRWMTLYGNHLPShLKPCLYLSIPPEDEFKRNRLVGRWAE 457
Db      393 QIVCGSCLDN-SLNSVYRIISLSVEDDPLTKHRLFLAHPPEYSKISAYDLFNWAVE 451
Qy      458 GFVRPKVGMTTKDVGESYFNELINRSMIQRSRVGIAGIKTCRIHDIIRDITVSIROBN 517
Db      452 GIYD---GSTIQDSGEYLEELVRRNLVIADNRYLSSHSKNCQMDDMMREVCLSKAKEN 508
Qy      518 FVLPLMGDGLVQENTHRIAFHSGMSCKTGLDWSI-----IRSLAI-----FGDRPK 565
Db      509 FLQI-IKDPTSTINAQSPSRRLSTHSGKAFHLLGHQNTKVRSLIVWDEDFGIRSA 567
Qy      566 SLAHAVCPDQLRLRLVLDLEDVTLITQKDFRIALLCHLKYLISGYSSSIYSLSPRSITG 625
Db      568 SVFH-----NUTLARVLVDLYVWKP-----EGKLFSSITGG 597
Qy      626 LQGLQTLNMPSTYIAALPSBISKLQCLHLTRLCIGQHYDNFSLN-----HPMKCITNTIC 680
Db      598 LIHLRYLSLFLAGVSHLPS-----TWNRKLKLLYLNLSVNNKEPIHVPNVLKEMIQ 648
Qy      681 LPKVFTPLVSRDDRAKQIAELHMAKTCWSBSSIGVKVPKGIGKLDQLQVLEVDVIRPTSS 740
Db      649 LRYLSLPL-KKDDTKL-----ELGDLVNLFLFPGFSTQH 682
Qy      741 RAIKELGQLSKRLKLVTTNGTSTKEKC--KILYAAIEKLSSIQSLHVDAAAGISDGGTLEC 798
Db      683 SSVTDLLHMTKRLAYLAV---SLSRCNFETLSSSLRNLNLETIYV----- 725
Qy      799 LDISSSPPPL-----LRTLVLVDGILEEMPNIWTEQUTHLKKIYLLRSKLE 843

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Db 63 IKDIYDIEDIEFILKEKEMKIMKIRKIPASTIMDRRELASDGGISKISKVIQ 122
Qy 125 RNTSYLVKPISSGTEID--MDSYAEDIRNQSARNVDEAEVLGFSDSKRLLEMDITNAN 182
Db 123 DMQSGVGOIITDGRSSHPLOQRQRMHTFSRD--SENDPVGMEANVKLVGLV---VE 178
Qy 183 DGPVKVGVGGLGKTALSRKIPESBEDIRKPPCNANITVSQSFHRIELLMKMIQ 242
Db 179 KDDVQIVSLTGMLGGLKTTARQVP--NHDVVKDRPDGFAMVSVSQEFTRISSVMQITQNL 237
Qy 243 LGPSSLDQLLELQGVVQVHLSLEYLIEBLKEKRYFVVLDDLWILHDMNINEIAPPK 302
Db 238 TSKERD----EIQNKKEADLH---DDLFRLESKTLIVLDDIWEKEDMDLIIKPI--PPP 289
Qy 303 NNKKGSRIVITRNVDLAECATASLVYHLDLQWDAITLL--LRKTNKHEDMESNKN 360
Db 290 --KKGWVLLTSRTESIAMRGDITVISPKKCLSI PDSWTLFQSIAMPRKDTSEFKVDEE 347
Qy 361 MOKVVERIVNKGRLPLAIIITIGAVLATK--QVSEWEKFEYHLPSEL--EINPSLEALRM 417
Db 348 MENNGKMKIKCGGLSLAVKVLGLLAAKYTHDMKRLSENIGSHIVERTSGNNSDIHV 407
Qy 418 VTLGVNHLPSHLKPCFLYLSIPDPFEIKRNLVGRWIAEGFV--RPKVGWTTKDVGESY 475
Db 408 LSVSFEELPNLKHCFLYLAHFPDSEIDVSKLHYWAAEGISERRRYDGETIRDTGDSY 467
Qy 476 FNELINRSMIOQRVGIAGKIKTIRIHDITIVSISROENFVLL-----PMG 524
Db 468 IEELVRNMVISEDVMTSRETCLHDMMEICLPKAKENFLQIVSNHSPTSNPQTIG 527
Qy 525 DGSOLVQEN--TRHIAFHGSMCKTGLDWSIIRSLAI-----FGDRPKSLAHAVCPDQLRM 578
Db 528 ASRRFVLHNPPTLHVERYKNN-----PKLRSILAVVYDDIGNRWNLSGSIF--TRVKL 578
Qy 579 LRVLDDLEVDVTLITQKOPDRALLCHLKLYLSIGYSSSIYSLPSRIGKLGLOTLNMPSTY 638
Db 579 LRVLDDLVOAKP-----KGGKLPDSIDGKLIHLRLSLKDAK 613
Qy 639 IAALPSEISKLOCLHLRCIGQHYDNFSLNHPMKITNTICLPKVTPLVSRDDRAKQI 698
Db 614 VSHLPSSLRLNVLIIYLDIRDF-----TDIFVNVPMGM--RELRYLEL 656
Qy 699 AB-LHMAATKSCWSSSIGVVKPGIGKRLDQVLEVDIRTSRAIKELGQSLKRLKGV 757
Db 657 PRFMHEKTKL-----ELSNLEKLEALENFSTKSSSLEDLRGMVRLRLVI 701
Qy 758 TTNGSTKEKKILYAAIEKLSSLOSLAV--DAAGISDGGTLECLDSISPPPLRLTLVDG 816
Db 702 ILSEGT--SLQTLASVCGRLHLENPKIMENAGVNRNGEERMVLDFT-----YLKGLTSLI 755
Qy 817 ILBEMPNNWIEQLTHLKKIYLLRSKLGKTKMLILGALPNMLVHLRYNAVILGEKLVFKTG 876
Db 756 EMPPLPKIQLHPSHLTVLIDLSYCCLEB--DMPLEKLELLEKDLSDLYLSFGSKNVCAG 814
Qy 877 APPNRLTWIYELDQLEIRFEDGSSPLLEKIEICEGRLESIGITGIIHLPKLKEI 931
Db 815 GFPOLRLALDEQEEWIEVEGSMGRSLTSLISWSSTLKLPLDGLRPYISLKNL 869

RESULT 13
T12979
hypothetical protein T6H20.260 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12979
R;Choisné, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, July 1999
A;Reference number: 217586
A;Accession: T12979
A;Molecule type: DNA
A;Residues: 1-847 <CHO>
A;Cross-references: UNIPROT:Q9STE5; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.260

A;Experimental source: cultivar Columbia; BAC clone T6H20
C;Genetics:
A;Gene: ATSP:T6H20.260
A;Map position: 3
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat
Query Match 13.7%; Score 723.5; DB 2; Length 847;
Best Local Similarity 27.0%; Pred. No. 6.3e-34;
Matches 249; Conservative 178; Mismatches 382; Indels 113; Gaps 31;
Qy 8 MARSLGSAISKAASAAADSETLLGVKEDIWYIKDELTKMQAFRAELAKKKDELKLV 67
Db 1 MVDAITFVVGKIDNYLIEAPMLIGVDDLEUKTELTCLQVYLKUNVECDKDEVSKE 60
Qy 68 WAEQIRLSYDIEDSLDEFKVIHESQTLFRLVKL-----REHRIAIRIHNKLKSRVE 120
Db 61 WTKLVLDIAYDVEDVLTDFYFLKELRLHRLGLMELTWIISDKDAYNILLDDIKTLKRTL 120
Qy 121 EYSSRNTRYSLVRPISSGTEIDMDSYAEDIRNQSARNVDEAE--LVGFSDSKRLLEMDIT 179
Db 121 DVTRKLEMYG--IGNFNEHRRVASTSRVREVR--ARSDDOEERVVGLTDDAKVLLTKLLD 177
Qy 180 NANDGPAKVICVCMGGLGKTALSRKIPESBEDIRKPPCNANITVSQSFHRIELLMKMI 239
Db 178 DGDGNKLYMISIFGMEGLGKTSLARKLFNS--SDVKSFEYRVWTVNVSCECNTRDILMRII 236
Qy 240 RQLLGPSLDQLLELQGVVQVHLSLEYLIEBLKEKRYFVVLDDLWILHDMNINEIA 299
Db 237 -----SSLSETSEGELEKAAQ--ELEVLHDLIOEKRYLVVDDIWESEALSLSKR-A 287
Qy 300 FPKNKGSRIVITRNVDLAECATASLVYHLDLQWDAITLLLRKTNKHEDMESNK 359
Db 288 LP-CSYQGSRIITTSIRVVAEGDRKRVYTHNIRFLTFKESWNLFEXKAFR--YILKVDQ 344
Qy 360 NMOKVVERIVNKGRLPLAIIITIGAVLATKOVSEWEKFEYHLPSELINPSLEALRMV 419
Db 345 ELQIKGEMVQKCGGLPRTTIVLAGLMSRKKPNENVDW-----SSLVKODNIHVSLFD 400
Qy 420 LGYNHLPSHLKPFLYLSIPDPFEIKRNLVGRWIAEGFVRPKVGMTTKDVGSYFNE 479
Db 401 LSPKMGHELKLCFLYLSVFPEDYEVNDVEKLIQLLVAGFIQEDDEMTMEDVARYIIDL 460
Qy 480 INRSMIQ---RSRVGIAGKIKTIRIHDITIVSISROENFVLLPMDGSDLVQENRTH 536
Db 461 VYISLVEVVRKK---GKLSFRIHDLVREFTIKKSKELNFV--NVYDEQHSSTTSRRE 514
Qy 537 IAFH---GSMCKTGLDWSIIRSLATGDRPKSLAHA--VCPDQLRMLRVLDLEDVTLIT 592
Db 515 VVHLLMDDNYLCDRRVN--TQMRSPFLFPGKRNDITYVETITLKLKLRVLNGLGLHF--- 570
Qy 593 QKDFDRIALIHLKLYLSIGYSSSIYSLPSRIGKLGLOTLNMPSTYIAALPSEISKLOCL 652
Db 571 -----ICQ-----GYSP--WSLPDVIGGLVHLRYGIADTVVNNLPDFISNRLFL 613
Qy 653 HTLRCIGQHYDNFSLNHPMKITNTICLPKVTPLVSRDDRAKQIAELHMAATKSCWSES 712
Db 614 QTLDAAG---NSFERMTDLNLSLRLHTRGRTGELLIGD--AVNLQTLASISSYSMSK- 667
Qy 713 IGKVPKGIKRLDQVLEVDVIRTSRAIKELGQSLKRLKGV-----TTNGSTKEKCK 768
Db 668 --LKHELLI--NLRDLRIEYEF--HYLNDQIKVPLDVLVSLSKLNLRLVKIEVVSFLPSEET 723
Qy 769 ILVAAATEKLSLOSQVADAGISDGGTLECLDSISPPPLRLTLVLDLILEMPNWIQL 828
Db 724 VRELLVKL---TLHCDVRLP-----RMDLIIF---PSLESITLVNLOQEDP----- 765
Qy 829 THLKTYLLRSKLKKEGKTMILGALPNMLVHLRYNAVILGEKLVFKTGAPNRLTWIYE 888
Db 766 -----MPTLQKLRLENILVYSCVYPCAKMFINAQGFRLRLKLV- 806
Qy 889 LDQLRIREFDGGSPPLEKIEI 910
Db 807 IKRLDELEIEEAMPCLMKLNL 828

Qy	246	SSLDOLLOELQKVVVVQHHLSEYLIBE-----LAEKRYFVVVLDLWILHDWNWINEIAP	300
Db	218	QNGD-----ISHMDEHTLQKFLKLETTGRYLVLVLDVWKEEDWDRIKAV-F	263
Qy	301	PKNKKGSRVITTTENVDLAEKATASLVYHLDFLOMNDATITLLRKTNKHONHEDMESKN	360
Db	264	PR--KRGWMLLTSRNEGVGIHADPKSGFKTRILTPBESWKLCSKIVPHRDETGTGLSD	321
Qy	361	MQRWVERIVNKCGRLLPAILAITGAVLATKQ-VSEMEKFEV-----HLPSELEINPSEALR	415
Db	322	MEAMGKENVTCGGPLPLAVKVLGGLATKHTVPWKRVYDNIGPHLAGRESSLDDNLSIY	381
Qy	416	RMVTLGVYNHLSHLKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPK-VGMTTKDVGES	474
Db	382	RVLSSYENLPMCLKHCFYLAHPPEYIEIHKVLFNVLAAEGIITSSDDGTTIQDKGED	441
Qy	475	YFNELINRSMTORSEVGTAGIKTCRIIHDITRTVTSRQENFV-LIPMGDGSOLVQ--	531
Db	442	YLEBLARNMTITDKYVNFRLKCHCOMHDMREVCLSKAKENFLEIFKVSATSGAINAR	501
Qy	532	--ENTRHTIAFGMSCKTGLDWSI---IRSLAIFGDRPKSL---AHAVCPDOLRMLRVLD	583
Db	502	SLSKSRRLSVHGG-NALPSLGQTNKVRSLLYFAFEDEFCEILESTTTCFSLPLRLRVLD	560
Qy	584	LEDVTFATITQKDFORIALLCHLYLSIGVSSSIYSLPRSIGKLOGLQTLNMPSTVIAALP	643
Db	561	LSRVKPF-----EGGKLPSIGDLIHLRPLSLHRAWISHLP	595
Qy	644	SEISKLOCLHTLRCIGQPHYDNFSLNHPMKCITNTICLPKVFPTPLVSRDDRAKOI-ABHL	702
Db	596	SSLRNLKLL-----LYNLNGFN-----GMVHVPNVLKEM--QELRYLQLPMSWH	637
Qy	703	MATKSCWSESIGVVKPKIGIKRLDLOVLEYVDIRTTSSRAIKELGOLSKRLKLV-TTNG	761
Db	638	DKTKL-----BLSDLVNLSESLMNFSTKYASVMDLHLHSLTKLELSLFTIDG	682
Qy	762	STREKCKILYAAIEKLSLQSLHV-----DAAGISDGG--TLECLDSISSPPPLRLTLVLD	815
Db	683	SS-----DTLSSSLGQLRSLEVLVHLVDRQEPVAYHGGIIVLNCIH-----LKELEU-	729
Qy	816	GILEMPNWI BQL---THLKKIYLLRSKLKEGKTMLLIGALPNLMLVHLRYNAYLGEKLV	872
Db	730	--AIHMPRPDQYLPHPLSHLYLWCCSWEB-DPIPIELRULLHLKASVILTCGAFVGRMV	786
Qy	873	FKTGAPNVLRTIWIYELDQLREIRFEDG	900
Db	787	CSKGGFPOLCFPLKLEELSEBIEWIIEEG	814

Search completed: February 9, 2005, 08:54:44
Job time : 34.6479 secs

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Qy 241 QLLGSSLDQLLOELQGGVVVQVHLSYLIIEELKEKRYFVVLDDLWLHDMWNINIAF 300
Db 241 QLLGTELLRQCLKELEK-AVHVEDLASYLEKLEDMRYFVLDLWTDIDAWMIKSIAP 299
Qy 301 PNNKKSRIIVITRNVDLASKCATASUVYHDLFQWMDAITLLLRKTNKHEDMESKN 360
Db 300 PIRNKDSRIIITRDVGLAAKCTSDSLIYHLKLIQIEDATNLLLRKSRKTWEDKNDKK 359
Qy 361 MQKQVETVVKGRPLPLAILITGAVLATKQVSEWEKPYEHLPSLEINPSLEALRRMVTL 420
Db 360 MNAVVKMKVCKGGLPLAVLTIGGMANKVKTEWESIYKQIPSELESNPSLEARRVITL 419
Qy 421 GYNHLSHLKPCFLYLSIFPEDFEIKRNLVGRMIAEGFVRPKVGMTTKOYGESYFNELI 480
Db 420 SYNHLPSHLKSCFLYLSIFPEDFEIKRRLVDRIAEGFVARSGVNIEDVGISYFTLTI 479
Qy 481 NRSIMQSRVGIAGIKTKCRTHDIIRDTVTSIRQENFVLLPMGDSGLVOE-NTRIAP 539
Db 480 NRSIMQSKVIEGHVKSRCVHDMRDVWVMSISREENFVYL-AGDNSTRVAEGNFRHVA 538
Qy 540 HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLEDVTFELITOKDPRI 599
Db 539 HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLEDVTFELITOKDPRI 598
Qy 600 ALLCHLKYLSI---GYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSEISKLOCLHLR 656
Db 599 GSLRHLKYLTLPRLPLNMHKLPAISIGKLOGLSLDGLGYSCITITLPTAISKLSGLRTL 658
Qy 657 CIGGFHYDNFSLNHPMKCITNTICLPKVFTPLVGRDRRAKQIAELHM--ATKCSWSESIG 714
Db 659 CRNORYSNYPNEDSCERWFIWCVPLVAS--BPDQRASFABELPMWCMSTGFGPKSYG 716
Qy 715 VKVPKGIKLDQLVLEVDIIRRTSSRAIKELGOLSKRLKLGVTNGSTKECKILYAAI 774
Db 717 VKLPKGINLKEQLILEYVDIKRTSSRAIQELGETQLKURVTIKGATEKKCSLFWEAI 776
Qy 775 EKLSSLOSLHYDAAGISDGTLECLDISSSPPPLRTLVLDGILEEPMNTEQIHLKKI 834
Db 777 QKLSILYSLYV-----DGENLEWLSVSVFAPPLMRSIKWNGSLLEIPNWIGSLMHLVKL 830
Qy 835 YLLRSKLKEG-KTMLIIGALPNLMVLHLYRNAYLGEKLVFTKGAPPNLTUWIELDQLR 893
Db 831 MLYCDGLKEGSRSEMLGALPNLMVLLRGLFSDTIGEKLVFVAETFPNLRNLGVTVMHGLR 890
Qy 894 EIREDESSPLEKIEIGECLESIGTGIHLPKLKEPIRYGSKVAGIGOLEGVNAHP 953
Db 891 EVRFEEGALPQIAIRISQGLSVGITGIKHPLMKLEISLVGQGGVAGHLGVQGEVNSHP 950
Qy 954 NRPVLLMYSDRRYHDLGAEBGSSITEVQTADVPDAEGSVTVVAEATDPLPEQEGESS 1011
Db 951 NHPVLRSLNKLTPQQLG-----DVV--VQGSNAIQVE-----EAMGESS 987

RESULT 2
Q9LWW7 PRELIMINARY; PRT; 1007 AA.
AC Q9LWW7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to gene for Pib.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP001168; BAA90798.1; -.
DR Gramene; Q9LWW7; -.
DR GO; GO:0005524; P:ATP binding; IEA.
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DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR00767; Disease_resist.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERISIT.
SQ SEQUENCE 1007 AA; 114793 MW; F96F2CE09AE808E3 CRC64;

Query Match 48.2%; Score 2539; DB 2; Length 1007;
Best Local Similarity 53.6%; Pred. No. 3.5e-127; Indels 32; Gaps 14;
Matches 546; Conservative 152; Mismatches 231;

Qy 1 MAETVLSMARSLVGSIAISKAASAADETSLLGVEKDIWYIKDELKTQAPLRAAELMKK 60
Db 1 MAETVLSMARSLVGSIAISKAASAADETSLLGVEKDIWYIKDELKTQAPLRAAELMKK 60
Qy 61 KDELKVAQIRDLSDYIDEDSLDEFKVIHIESQTLFQVLKLRERHRIATRIHNLKSRVE 120
Db 61 KDLKLVAAEQVRSLSYDIEDCLBEFVHVGNQSLQQLTNLKDHRHIAVKIRNLKSRLE 120
Qy 121 EVSSRNTRYSLAVKPISSGTEIDMDSYAEDIRNQSARNVDAELVGFSDSKRLLEMDTN 180
Db 121 EVSSRNTRYSLAVKPISSGTEIDMDSYAEDIRNQSARNVDAELVGFSDSKRLLEMDTN 180
Qy 121 EVSSRNTRYSLAVKPISSGTEIDMDSYAEDIRNQSARNVDAELVGFSDSKRLLEMDTN 179
Db 121 EVSSRNTRYSLAVKPISSGTEIDMDSYAEDIRNQSARNVDAELVGFSDSKRLLEMDTN 179
Qy 181 ANDGP-AKVICVGMGGIGKTALSRIKIFESSEDIRKNPNCNAWITVSQSFRHIELKDMI 239
Db 180 ANDDDHCRVLCVGMGGIGKTALSRIKIFESSEDIRKNPNCNAWITVSQSFRHIELKDMI 239
Qy 240 RQLLGPSSLDQLLOELQGGVVVQVHLSYLIIEELKEKRYFVVLDDLWLHDMWNINIA 299
Db 240 SOLLGHS-----LKRFEK-PIRAHDLGTHLRDGLKELRYFVVPDDLWTDHWEIRFA 294
Qy 300 PPKNKKSGSRIVITRNVDLAEKATASLVVHLDLQWMDAITLLLRKTNKHEDMESKN 359
Db 295 LPSKNNKRSRVITRDLGVANACTTPTFVRLKLLTECAIDLLLRKESKEDMKNDN 354
Qy 360 NMQKQVRIYVVKGRPLPLAILITGAVLATKQVSEWEKPYEHLPSLEINPS--LEALRM 417
Db 355 NLKSIYVQLVKKCGCLPLAIVTIGAMFANKPSSKWEEMCRQLPSELENNPSGVEAIRV 414
Qy 418 VTLGYNHLSHLKPCFLYLSIFPEDFEIKRNLVGRMIAEGFVRPKVGMTTKOYGESYFN 477
Db 415 VTLGYNHLSHLKPCFLYLSIFPEDFEIKRNLVGRMIAEGFVRPKVGMTTKOYGESYFN 474
Qy 478 ELNRSIMQSRVGIAGIKTKCRTHDIIRDTVTSIRQENFVLLPMGDSGLDQVNTRH 537
Db 475 ELNRSIMQSRVGIAGIKTKCRTHDIIRDTVTSIRQENFVLLPMGDSGLDQVNTRH 534
Qy 538 AFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLEDVTFELITQK 594
Db 535 SCHGNYPIVGMDFSRVSLTVFGEFQDRPMLVGSSICSAQFTMLRVLDLENVAFSVTQK 594
Qy 595 DFPRIALLCHLKYLS---IGYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSEISKLOCL 652
Db 595 DINKIGLLRHLRYLNTHTRRSTIYALPSSIGKLOQLVLDIRESEISTLPTDISKLML 654
Qy 653 HTLRCL--GQPHYDNFSLNHPMKCITNTICLPKVFTPLVSRDRAKQIAELHMAKSCWS 710
Db 655 RIURCSGPMWTFYFPDDEPKICLKHLRMLPLMTPLVGSAAKNYITAEUHRAYSSHWS 714
Qy 711 ESIGVKVPKGIKLDQLVLEVDIIRRTSSRAIKELGOLSKRLKLGVTNGSTKECKKIL 770
Db 715 ETPGVRVPTGISKLEQLVLEVDLKLTKSAIEELGELRWLQKLRVSTKGAQDKKRTL 774
Qy 771 YAAIEKUSLQSLHVDAAIGSDGTLKCLDIS--SPPLRLTLVLDGILEEMPNWIEQLT 829
Db 775 CEATIEKLSLQSLCVYEGYFITGTLWELGFCNFPPLLRKLHGRIRVMPDPSFRNLK 834
Qy 830 HLKVIYLRSLKLEKGMKMLIIGALPNLMVLHLYRNAYLGEKLVFTKGAPPNLTUWIEL 889
Db 835 QLRKIFLRLSEL-DGRAIEITGLTLPNLMVLLRGLFSDTIGEKLVFVAETFPNLRNLGV 893
Qy 890 DQLREIRFEDGSSPLLEKIEIGECLESIGTGIHLPLKLEIPIRYGSKVAGLQGEV 949
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Db      894  ||| ||| : : : ||| : ||| ||| ||| ||| : : ||| ||| ||| 951
Qy      950  NAHNPRLMYSDRRYHDLGAEAGSIEVQTADPVPDAEGSVTVAAEATDPLPEQEGE 1009
Db      952  KAHKPTPALRLQDRSKDIDGLPV-----VLTKD-----EGS-NVEEAKESVHDDAGE 999
Qy      1010  SSQ 1012
Db      1000  SSQ 1002

RESULT 3
ID Q651S9 PRELIMINARY; PRT; 953 AA.
AC Q651S9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to NBS-LRR type resistance gene.
GN Name=P0702F05.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0702F05.1";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005828; BAD46438.1; -.
SQ SEQUENCE 953 AA; 108557 MW; DAFD5081E707261C CRC64;

Query Match 24.6%; Score 1294.5; DB 2; Length 953;
Best Local Similarity 33.3%; Pred. No. 1.1e-60;
Matches 336; Conservative 207; Mismatches 342; Indels 125; Gaps 34;

Qy 1 MAETVLSMARSLVGSATSKAASAAADETSLLLGYEKDIWIKDELTKTQWAFRAELMKK 60
Db 1 MEGAIPVAECTVRSLLSKLSQSWSFVRGVGHGDIQYIKDELSENNAFLRYLVLED 60

Qy 61 KDELKVAEQIRLSYDIEDSLDEFKVIHESQT----LFRQ----LVKLRERHRIARIH 113
Db 61 HDTQVRIWMKQVREIAYDAEDCIBQFTHLGESSGIGFLYRLIYLGLKCCRRIAMQLQ 120

Qy 114 NLKSRVEVSRRNTRYSLVKPISSGTEIDMDSYAEIDRNQSRNVD-----EAEV 164
Db 121 ELKARAQDVSRSSRYEYMLP-----KTLQAGAPRLTRHASRLDPQLHALPTEEAQLV 175

Qy 165 GFSDSKRLLEIMIDTNDANDGPAKVICVGMGLGKTALSRKIPSEEDIRKNPFCNAWIT 224
Db 176 GLDPRDKLVWV--MEADPCRRVLAIVGFGLGKTLARWCVENPMVKGADFHCCPLFI 233

Qy 225 VSQSFHRIELKDMIRQLL-GPS-----SLDQLLQELQ-GKVVQVQVHLSYL 270
Db 234 VSQTFNIRTLFQYIMIRELIQRPNKAWAVAGGKHGHTDGNMGMEVEAVLAEKVRQYL 293

Qy 271 IEELKEKRYFVLDLILHNDWNINEIAPFNKNGKSRIVITTRNVDLAKCATA--SL 328
Db 294 LD-----KYIVIFDDIWTISAWESI-RCALP-DNKGSGRVITTRNEDVANTCGSPQDQ 346

Qy 329 VYHLDPLQMDAITL-LLRKTNKHEDMESKNQKQKVERIVNKGCGRLPLAILTIGAVLA 387
Db 347 VYKMQ--RLSDAASRELFFKFIQFSGADISSNEDEVSNSILKKCGGLPLAIVSIGSLVA 404

Qy 388 TK---QVSEWEKPYEHLPSLEINPSLEALRMVTLGYNHLPKPCFLYLSIFPDPE 444
Db 405 SKTNRTKEEWKICDNLGSELETNPTLEVAQVLTLSYNDLPYHLKACFLYLSIFPENYV 464

Qy 445 IKRNLVGRWTAEGFVRPKVGMTKTKVGSSEYFNELINRSMIQSRVGIAGKIKTRHDI 504
Db 445 IKRNLVGRWTAEGFVRPKVGMTKTKVGSSEYFNELINRSMIQSRVGIAGKIKTRHDI 504

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Db      465  IRRGPLVRRWIAEGFVNQRHGLSMEEVAESYDFEVSARSIVQPKIDWSGKVRTCRVHDM 524
Qy      505  IRDTVTSISQENFVLLPMGDSGLV--QENRTHIAFGHSMSC--KTGLDWSIIRSLAIFG 561
Db      525  MLEVIISKSLEENFASPLCDNGHPLVCHDKIRRLSIHNSHNSVQTRVSVSHVRSFTM-- 582
Qy      562  DRPKSLAHAVCP---DQRLMLRVLDLSDVTFITQKDFDRIALLCILKYLKYLKYLKYLK 618
Db      583  ----SASVEEVPMPFPQMRLLRVLDLQSSCL--NNSTLNYICKPYQLKYLTL--RTNIGK 636
Qy      619  LPRSIGKLGLOTLNMPSTVIAALPSBISKLOCL--HTLRCIGQPHYDNFSLNHPMKCITN 677
Db      637  LPRILGNLKYLETLDIRATRIKRLPASASNLSCUKHL-----VGHKVQ-LTR 683
Qy      678  TICLPKVFTPLVSRDDRAKQIAELHMYATKSCWSSSIGVKPKGIGK-LRDIQVLEYVDIR 736
Db      684  T-----TSVKCFRPSDGLMTEAGVVKNMNAQLSLAHIVVK 718
Qy      737  RTSRAIKELGOLSKRLKLGVTNGSTKECKIILYAAIEKLSSLOSQSLHVDAAIGSD-CGT 795
Db      719  ERPA-VLSEIGLOKLOKLVNLFGRVEENWNAFLQSLVKLTGSLRSLSIHILDEKHSSS 777
Qy      796  LECDSISSPPPL--LRTLVLGDGILEMPNMTIEQLTHLKIYLLRSKLEKGTMLILGALP 854
Db      778  LEYLALIAESPPPLFIRNFSKGLQRPWPPIPSLRNVSRI--TFRDTGLHAEIAGVLGOLP 836
Qy      855  NLMVLYRNAYLGEKLVFKTGAPNRLTIWYELDQIREIRFEDSGSPLEKEIGISCR 914
Db      837  NLLCLKLYQRSYADDDHFFAHGNPLKRLMLVIDNMENIRNVHFEKGSVPNLEWLTIAFLQ 896
Qy      915  -LSGGITGIHLPKLKEIPRIYRG-----SKVAGLQLEGEVNAHNRP 956
Db      897  EPKDGITGLENLKLEIEF-FGDIIILSMVTKVASC-----MKAHPNRP 939

RESULT 4
ID Q651T2 PRELIMINARY; PRT; 954 AA.
AC Q651T2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to NBS-LRR type resistance gene.
GN Name=P0702F05.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0702F05.1";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005828; BAD46435.1; -.
SQ SEQUENCE 954 AA; 108010 MW; 0F8BEBB635D2750 CRC64;

Query Match 23.4%; Score 1233; DB 2; Length 954;
Best Local Similarity 32.5%; Pred. No. 2.1e-57;
Matches 331; Conservative 189; Mismatches 356; Indels 144; Gaps 32;

Qy 1 MAETVLSMARSLVGSATSKAASAAADETSLLLGYEKDIWIKDELTKTQWAFRAELMKK 60
Db 1 MEGAIPVSLTGAATVRSLLCKLGLLTEDTLVQGVHGEIQYIKDELSENNAFLNLTTSQI 60

Qy 61 KDELKVAEQIRLSYDIEDSLDEFKVIHESQT-----LFRQLVKKLRERHRIARI 112
Db 61 HDQVRIWMKQVREIAYDSEDICDEP-IHNLGESSEMGFFGLISMLRKLACRHRIALQL 119

Qy 113 HNLKSRVEVSRRNTRYSLVKPISSGTEIDMDSYAE---DIRNQSARNVD-----E 160
Db 120 QELKARAQDVGRSSRY-----GVELAKATHEEAHPRLTRHASLHIDPQLHALFAEE 171

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Qy 161 AELVGFSDSKRLLEMDITNANDGPAKVICVVGMLGKLTALSRKIPSEEDIRKNFPCN 220
Db 172 AOLVGIDPRNELVSWL--MEEDLRRLVAIVGFGELGKTTILARWCGSPVVKADQCC 229
Qy 221 AMITVSQFRIELKDMIRQLLQSSJDLQLE-----LQKVVV 261
Db 230 PLFIISQTFNIRALFQHMVR-----ELIQEPHKAWAIGAGCKHGLITDYLEGMRW 280
Qy 262 QVHLSYELBELKEKRYFVVDLWILHDWNWINEIAFPKNNKGSRIVITTRNDLAE 321
Db 281 EVAALTKNLRYPQDKRYIVILDDITWVSAMEST--RCALP--DNLKGSRIIVTTRNADV 338
Qy 322 KCAT--ASLVHLDPLQWMDAITLLRKTNNKHEDMESKMKQKVERIVNKCGRPLAI 379
Db 339 TCCSRPQRIYINQLSTTSRELFKKIFGADDKSPTDFEFVSNVSKCCGGLPLAI 398
Qy 380 LTIGAVLATK---QVSEWEKFEYHLPSELEINPSLEALRRMVTLYGNHLPGLKPCFLYL 436
Db 399 VNIGSLASKNTRTKEEQKQCNNGLSELENNPTLEGVKQVLTILSYNDLPVHLKACFLYL 458
Qy 437 SIFPDEFIKNRLNGRIAGFVPKVGMTTKDVGESYFNELINRSMIQRSRVIAGKI 496
Db 459 SIFPENYVIKRGPLVRRWIAEGFVSQRHGQSMQLAESYDFEFVARSTVQPVRTDWTGKV 518
Qy 497 KTCRIHDIIRDTVYSIQENFVLLPMGDGSDLV--QENTRIAHFGS--MSCKTGLDWSI 553
Db 519 RSCRVDHMLMDVTVSRSTEEENFASPLCDNGSTLASHDKIRRLSHSYNSQKTSANVSH 578
Qy 554 IRSIAIFGDRPKSLAHAVCP---DQRLMLRVLDDVTLTKQDFDRIALLC---HLKY 607
Db 579 ARSFTM-----SASVEVPFFPQLRLRLVLDLQGCCLSN---ETHCWRFFQLKY 628
Qy 608 LSGVSSYISLPSRIGKLOGLTNMPSYIAALPSEISKLOCLHTURCIGQHYDNFS 667
Db 629 LSL--RNTNVSKLPHLLGNLKHLETDIRATLIKLPASAGNLSCLKHL-----F 676
Qy 668 LNHMKCITNTICLPKVTFLVSRDRRAKQIAELHMATKSCWSESIGVKVPKGIGK--LRD 726
Db 677 AGHKVQ--UTRT-----ASVKFLRQSGLEAVATGVKMWVA 710
Qy 727 LQVLEYVDIRTSRAIKELGQSKRLKGLVTTNGSTKECKKILYAAIEKL--SSLQSLHV 785
Db 711 LQSLVHI--VVKDKSPVLAIEIGLQNLTKLNVLLRG--VEENNNAFLESLSKLPGLRSLSI 768
Qy 786 DAAGISDGG--TLECLDSTSSPPPLRLTVLDGILEMENWIEQLTHLKKIYLLRSKXEG 844
Db 769 HTLDEKHSLSLDNLAFVESPPLFTKFSLAGELERLPWPISLRNVSRFALRTEL--HA 827
Qy 845 KTMLTILGALPNMLVHLVRYNAYLGEKLVKTAGPAPNLATLTIYELDQLRREIRFEDGSSPL 904
Db 828 DAIGVLGDPNLLCLKUKYHKSADNCIVFCHGKFVKLKLIIIDNLERIKQFDMGSVTN 887
Qy 905 LEKIEIGECR--LESGITGIHLPLKLEIPRIYRG-----SKVAGLGOLEGEVNAHPNR 956
Db 888 LERLTSLRBPKYGISGLENLPLKLEIEF--FGDIILSVVTKVASC-----VKAHNP 940
```

RESULT 5

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Q8H5A7
ID Q8H5A7 PRELIMINARY; PRT; 1494 AA.
AC Q8H5A7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative disease resistance protein RPH8A.
GN Name=QJ1634 B10.108;
OS Oryza sativa (japonica cultivar-group);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
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RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OJ1634 B10.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003840; BAC15497.1; -.
DR Gramene; Q8H5A7; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; P:defense response to pathogen; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR008940; Prenyl_trans.
DR Pfam; PF00560; LRR_1; 3.
DR Pfam; PF00931; NB-ARC; 1.
DR Pfam; PF01535; PPR; 4.
DR PRINTS; PR00364; DISEASERSIST.
DR TIGRFAMs; TIGR00756; PPR; 4.
SQ SEQUENCE 1494 AA; 168313 MW; 15BB15F247C3446B CRC64;

Query Match 23.3%; Score 1225.5; DB 2; Length 1494;
Best Local Similarity 32.4%; Pred. No. 9.8e-57;
Matches 332; Conservative 188; Mismatches 361; Indels 145; Gaps 31;

Qy 1 MAETVLSMARSLVCSAISKAASAADETSLLLGVEKDIWIYKDELKTMQAFRAAELMKK 60
Db 514 MEHAVSAAGAIHTLGLKGTIVLQEAQLGGIRGELQHLKDELSMTAFQLDLSGRDE 573
Qy 61 KDELLKYWAEQIRLSYDIEDSLDEFKVIHESQT-----LFRQ----LVKLRRHR 107
Db 574 CGKQVKIWKHVREIAYDIEDCIDFKHQLDSSAGSGSPVVFRRKATHILQTRVRHQ 633
Qy 108 IAIRHNLKRVSRVSRNTRYSLVKPISSTETDMSYABDIRNQARNVD----- 159
Db 634 IAKQIBELKRTNMISARNRYSANHLISGTAGNSMAAYDS---QANLLNVDTTALFP 690
Qy 160 -EAEVLGFSDKLELMDITNANDGPAKVICVVGMLGKLTALSRKIFSEEDIRKNFP 218
Db 691 ERRLQVGLRFPQGNLHWL--LEAHVQQLRVSVIFGFGGLGKTTIAMTYQLSLSRNGP 749
Qy 219 CNAMITVSQSFHRIELKDMIRQL-----LGPSSLDQLLQELQGVVVQVHH 265
Db 750 CQAFVTVSQSPDKVLMARDILLQITQPVNQPSSPTGAGKGPMEGLLKGMENAVVQ--- 806
Qy 266 LSEYLIBELKEKRYFVVDLWILHDWNWINEIAFPKNNKGSRIVITTRNDVLAECAT 325
Db 807 LASILRQOLENKRYLIVLDDIWSMTAWEGI--RFSLPDSN--NGSRIVVTTRIRAVHTCC- 863
Qy 326 ASLVYHLDPLQWMDAITLLRKTNNKHEDMESN-----KNMKQKVERIVNK 371
Db 864 -----FHYDRAYEI-----KPLTDCESRDLPFRIPGSSICEHLEDISAKILGK 909
Qy 372 CGRLPLAILITGAVLATKQVSE---WEKFVEHLPSELEINPSLEALRRMVTLYGNHLP 428
Db 910 CGGTPLSIVSIFAGLASKPVHISKLEIYSSLSGSEIETNFSLDRLKILSELYNDLPYH 969
Qy 429 LKPCFLYLSIPPEDFEIKNRLNGRIAGFVPKVGMTTKDVGESYFNELINRSMIQRS 488
Db 970 LKTCFLYLSIYPEDHNIRRTKILRRWIAERFVTGKGLSVFEVAESYDFEFINRSIIQPV 1029
Qy 489 RVGTAGIKTKCRIHDIIRDTVYSIQENFVLLPMGDGSDLV--QENTRIAHF--GSNSC 545
Db 1030 TTSPTGKVKTRVHDVHMLIEIVSKSIDENFTTL--VGEQNTLPQEKIRLRTVTHSRGVKY 1088
Qy 546 KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQRLMLRVLDDVTLTKQDFDRIALLCHL 605
Db 1089 ATRILCHVRSLSIFAD-----GETLQFGWKKMLRLLDLEGYEF--RNRDLKDLCLRLQL 1142
Qy 606 KYLSIGYSSSIYSLPSRIGKLOGLTNMPSYIAALPSEISKLOCLHTLRCIGQHYDN 665
Db 1143 EYLN--RRTHITELPAQIGNLKKLETLDIRDTAKHLPPGTTNLP--HLANLLG---GR 1195
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Qy 944 -----OLEGEVNAHNPVRVL 958
Db 1199 YDQTYTFEKEQLQKQLDNKNKPNL 1223

RESULT 7
ID Q9MBF2 PRELIMINARY; PRT; 1226 AA.
AC Q9MBF2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE pibH8 protein.
GN Name=pibH8;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Tohoku IL-9; TISSUE=Green leaf;
RX MEDLINE=99348180; PubMed=10417726;
RA Wang Z., Yano M., Yamanouchi U., Iwanoto M., Monna L., Hayasaka H.,
RA Katayose Y., Sasaki T.;
RT "The pib gene for rice blast resistance belongs to the nucleotide
RT binding and leucine-rich repeat class of plant disease resistance
RT genes."
RL Plant J. 19:55-64 (1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Tohoku IL-9; TISSUE=Green leaf;
RX MEDLINE=21582385; PubMed=11725950; DOI=10.1023/A:1012457113700;
RA Wang Z.X., Yamanouchi U., Katayose Y., Sasaki T., Yano M.;
RT "Expression of the pib rice-blast-resistance gene family is up-
RT regulated by environmental conditions favouring infection and by
RT chemical signals that trigger secondary plant defences."
RL Plant Mol. Biol. 47:653-661 (2001).
DR EMBL; AB013451; BAA93618.1; -.
DR Gramene; Q9MBF2; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; P:defense response to pathogen; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 3.
DR PRINTS; PR00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERSIST.
SQ SEQUENCE 1226 AA; 138086 MW; F45F3EBCF9F0251A CRC64;

Query Match 23.0%; Score 1209.5; DB 2; Length 1226;
Best Local Similarity 27.4%; Pred. NO. 5.3e-56;
Matches 352; Conservative 197; Mismatches 347; Indels 389; Gaps 30;

Qy 1 MAETVLSNARSIVGSAISKAASAADETSLLGVKEKDIWYIKDELKTWQAFRAELMKK 60
Db 1 MEATAVSVGKSVLGGALSYAQTAIEAGALKLGVRQDSFIRDELEMMQSFLLAAD--KE 58

61 KD-----ELKKVAEQIRLDSDIEDSLDEFKVHIESQTLFRQLVKL-RERHRIAIRIHNL 115
Db 59 HDGHHHEVIRTWKQVRDAVDVEDCLQDYAARLKKPPWWSLPTVHRRERRIGNEMKEL 118

116 KSRVEVSSRNTRY-----SLVKP 134
Db 119 RAKVEDVSQRMRYHGVSAAPQSSVTAELLQSTAAIDIDEARRAAKQKQKVDLVKL 178

135 IS-----SGT-----ETDMSYADI 150
Db 179 ITNQGQGLRVIAVLETRSGPAGTVVVRVAAVQKLKGFECHAWVRLMHMSFDANQIFGSL 238

151 RNQARNVDEA-----ELVGFSDSKRLL----- 174

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RESULT 8

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Db 239 VRQKANSREGTGKTPQGTSPGVSVLNEMEAQDYNLLHDFTGYVTNKYLVLNGLSTIE 298
Qy 175 -----EM 176
Db 299 EMDWIKTYLPNNHNGSRVLVCTQQAEEVASCCTCTDDKVKVSEIQHEGFSFKPLVVFKEV 358
Qy 177 IDTNAN-----DGP----- 185
Db 359 VSQPVNSDSTKMKSETSSMEGASTTSDSKTVPDSGVIQEDGPKDLPESLPPHLNRDSN 418
Qy 186 -----AKVICVVMGGLGKTKALSRIKIFESER 211
Db 419 TVSVKELSRSTTQIGRGKEKDDVIKLLSDCNPIRQIVISVMGMGGIKTTLVKSIIYQSS 478
Qy 212 DIRKNFPCNAWITVSQSFHRIELDKMIRQLQLGSSLDQLLOELQGVVQVHHL----- 266
Db 479 LEKLGERRAAWTVLRPFQUTELLRSUQ-----RLVKSPGKKVSIPOGLARSGL 529
Qy 267 ----SEYLIBELKE----KRYFVVLDDLWILHDMWINEIAFPKNNKKGSRIVITTRNVD 318
Db 530 STWGSEELDKLQDLTGKKYLIVLDDLSTTTEWDSIIR-NLPINN-NGSRIILTRFKL 587
Qy 319 LAEKCATAFL-VYHLDPLQNDALITLLRTKNKNHDMESKNMKNQKVRIVNKGRLPL 377
Db 588 VAQCHSKKEMNMHNIIEGLTDGDALEFLTKVRMDGDESELKPDILKEBAKIIKKCGRLPL 647
Qy 378 AILTIGAVLAT--KQVSEWEKFEYHLPSELEINPSEALARMVTLGYNHLPSHLKPCFLY 435
Db 648 AVATVGGLSARPNIIIEWREFSDRISEEDFNPNSEMIKKILASSVEGLTYHLKSCFLY 707
Qy 436 LSIPPEDFEIKRNLVGRWIAEGFVRPKVGWTTTKDVGESYFNELINRSMTQRSGVAGK 495
Db 708 MSIPEDSDIRYRELLRRWTAEGYSRATRSNEKVAEQFTALLNKSQKSTIASGK 767
Qy 496 IKTCRIHDIIRDITVSIROENFVLLPMGDSGLVQENTRHIAFHGSMCKTG-----LD 550
Db 768 TGFQCVYNLMHEIISKESEENLVLDLDDHITSRSKDKVRHLVVSXSKSRKNDQMIVD 827
Qy 551 WSIIRSLAIFGDRPKSLAHAVCPQLARMLVLDLDEVTFLITQKDFRIALLCHLKVLSI 610
Db 828 VSHIRSLTVFGEW-KSF---FLSKMKNLRLVLDLEDAEGL-QDPDLVPIGKLHLKLYLSL 882
Qy 611 GYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSEISKLQ----- 650
Db 883 RGSFGVENLPNSFGNLLNLETLDIRGTWTKLPATIGRLQNLKYVHAGSLDDEDDQPIIK 942
Qy 651 CLHTLRICIGFHYDNPISLHNPCKITNTI CLPKVFTPLVSRDDRRAKQIAELHMAKSCWS 710
Db 943 LLHQFRSIREEMGTFRFAVSIMLFI-----AWL 971
Qy 711 ESI---GVKYPKGIGKLDLQVLEYVDIRTSRAIKELGOLSKRLKLGVTNGSTKEKC 767
Db 972 RNLDCVGKVPGRGIRLRSIHTLSIVNIAR-GKALLKNLKKLTOLCKLGV--GINKNKC 1028
Qy 768 KILYAAELKSSLSQSLHVDAAAGSDGCTLECLDSISSPPPLLRTLVLVDIGILEENPMIEQ 827
Db 1029 KELCSALADHCRQLSLLLRAG--NAGLEGCLDNWSOPKDKSLQLYGNLVTLPENIKD 1086
Qy 828 LTHLKKTYLRSKLEKGTWMLILGALPNMLVHLRYNAYLGEKLVFTKGAPFNRLTIWY 887
Db 1087 LKILQKLSLRLNTLKAADTMEVLGNLPMALAILQDNACBEEELCFGPERFTGLTLELL 1146
Qy 888 ELDOLRIREDGSSPLEKIEICEGR--ESGITGIHLHPKKEIPIRYGSKVAGLG-- 943
Db 1147 NWESLKSVKFERGATPKLKVLLHHCWOIHNGSGSGETLSTLKEVSI-----LGYN 1198
Qy 944 -----OLEGEVNAHNPVRVL 958
Db 1199 YDQTYTFEKEQLQKQLDNKNKPNL 1223

```

Q69MT5 PRELIMINARY; PRT; 963 AA.

AC Q69MT5; 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Putative resistance protein.

GN Name=OSJNB0034812.23;

OS Oryza sativa (Japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

EN [1]

RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Katayose Y.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC clone:OSJNB0034812.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP005735; BA033830.1; -

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0042829; P:defense response to pathogen; IEA.

DR InterPro; IPR00767; Disease_resist.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR002182; NB-ARC.

DR Pfam; PF00560; LRR_1; 3.

DR Pfam; PF00931; NB-ARC; 1.

DR PRINTS; PR00364; DISEASERISIT.

SQ SEQUENCE 963 AA; 109012 MW; 5E808C349CBFA3C6 CRC64;

Query Match 22.9%; Score 1209; DB 2; Length 963;
 Best Local Similarity 33.0%; Pred. No. 4.1e-56;
 Matches 335; Conservative 209; Mismatches 348; Indels 124; Gaps 37;

Qy 1 MAETVLSMARSLVGSATSKAASAADETSLLGVEKDIWIYKDELKTWQAFRAELMKK 60
 Db 1 MEATVLSMARSLVGSATSKAASAADETSLLGVEKDIWIYKDELKTWQAFRAELMKK 60

Qy 61 KDELKLVWAEQIRLSYDIEDSLDEPKVHIE-----SQTFLRQLVKLRERHRAIRHNL 115
 Db 61 ADDTVRTVWQVRLADYVDESLDFALFDATLSSSSSSSWLFWRAEHRVVAARREL 120

Qy 116 KSRVEVSSNRNYSLV--KPISS---GTEIDMDS-----YAEDIRNQSRNVDEAE 162
 Db 121 KASVEELNQFLRYRIVVEHPRASRGCGASDQQLDHDGQYYSAEIAFO-----ESD 174

Qy 163 LVGFSDSKKLLEMDITNDNGPA-----KVICVGMGGLKTKALSRKIFESSEDIRKN 216
 Db 175 IIGRAEKAETVALVLSGCGGDDVGGGALGVSWGMGGMGKSSLVRMVY-NDPELLDA 233

Qy 217 PFCNAWITVSQSPHRIELKMDIRQLLQPSLDDQLLOELQGVV-----QVHLSLEYLIE 272
 Db 234 PDCDAWTVP---HPLD-----SADEFVRLRHLAAGKQDVH-----A 270

Qy 273 ELKEKRYFVVDLWLMDWNIWINEIAPPKNKKGSRIVITTRNVDLAERKATA-----S 327
 Db 271 YLREKRYVIVDDLSRESEHIIWPV-LHVDGGKGRVVTTRREDVARHCAGLVREGHG 329

Qy 328 LVYHLDPLQNDAILTLRKNKHEMESKNQKQWIRVKNCGRLPLAILTIGAVLA 387
 Db 330 HVYELRLPGREESKDLFCQKYKSTEYI-LEKEMEDLAGPLIKRCRGLPLAISTIGLLA 388

Qy 388 TKQVS--EWEKFFVHLPSELEINPSLEALRWMTLGVNHLPSHLKPCFLYLISIPPEDEI 445
 Db 389 NRPTGLEWIKLDEHGALE-SSDLRNTKIVSSYDGLPYDLYLISIPPEHNEI 447

Qy 446 KRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELINRSMIQ--RSRVGIAGKIKTCRIHD 503
 Db 448 RCTELLRWAAEGFIAKNRDMPVEEVQGRFYNELINRSMIQPSKRISPSVSDRCVHS 507

Qy 504 IIRDTIVSIRQENFVLLPMGDGSDLVQENTRHIA----FHGSMCKTKGLDWSIIRSLAIF 560
 Db 504 IIRDTIVSIRQENFVLLPMGDGSDLVQENTRHIA----FHGSMCKTKGLDWSIIRSLAIF 560

Db 508 MVLIQIILSKSIEBNQLFIKKHCNEVPQSKIRHLVSRWKRDRERLENINFSYRSLTVF 567

Qy 561 GDRPKSLAHAVCPDQLRMLRVLDLVDVTLITOKDFDRIALLCHLKLKYLSSYSSISLSP 620
 Db 568 GDCPASL---ISP-KMELLAVLDLED-SLNLKNEDLRHVGELHHLRVLCL-RGTEISKLP 621

Qy 621 RSTGKLGLOTLAMPSTYIAALPSEISKLQCLHTLCIGQPHYDNFSLNHPMKCITWTIC 680
 Db 622 -SFQNLRYLETLDIQTKVQTPDGIAKLEKRYL-----LAGVNFSE-----L 665

Qy 681 LPKVFTPLVSRDDR-AKOIAELHMAWKSCWS-----ESIGVKVPKGIKLRDLQVL 730
 Db 666 LHKVEQP--ETDRKANQLGNM-LSCLYCNSSDYCGISSLDVRVSVRAPEGVEKURDLHML 722

Qy 731 EYVDIRTSRAIKELGQSLKRLKLVTTNGSTKKECKILYAAIEKLSLQSLHVDAGI 790
 Db 723 GVINVGH-GNGVGVKIKKLTNLRILGV--SGVLKEEGQDLCKSEKLSRLQRLERS--- 776

Qy 791 SDGTTLECL-DSISSPPPLRLTLVLDGILEMPNWIQLTHLKKIYLLRSKLKGGKTMLI 849
 Db 777 ---DSLKFLAESFPAAPKHLLSRLYGNLVRLPKWIGSLNDLAKLKLGTQLKQGRIN-H 832

Qy 850 LGALPNLWLVHLYRNAVILGEKLVFKTCGAFPNLRLTLWIYELDQREIRFEDGSSPLLEKIE 909
 Db 833 LGLRNLAFLGLWDNSYVGYSLHFGPTFPKLPFLDIDGLKNITETVAIENGAMPESQLW 892

Qy 910 IGECR--LES--GITGIHLPLKKEIPI-RYGSKVAGLQGLEGVNAHPNRPVLLM 960
 Db 893 VNDCKGLDSKDGSLGVPVHLTNLNLVAVKCKEKENMEILOTVQVSEHSKEPKPLI 948

RESULT 9

Q6WSR3 ID Q6WSR3 PRELIMINARY; PRT; 1169 AA.

AC Q6WSR3; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Resistance protein Tl0rga2-1A.

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Triticeae.

OX NCBI_TaxID=4565;

EN [1]

RP SEQUENCE FROM N.A.

EX PubMed=14645721; DOI=10.1073/pnas.2435133100;

RA Feuillet C., Travella S., Stein N., Albar L., Nublat A., Keller B.;

RT "Map-based isolation of the leaf rust disease resistance gene Lr10 from the hexaploid wheat (Triticum aestivum L.) genome.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:15253-15258 (2003).

DR EMBL; AY270159; AAQ01786.1; -

DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0042829; P:defense response to pathogen; IEA.

DR InterPro; IPR00767; Disease_resist.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR002182; NB-ARC.

DR Pfam; PF00560; LRR_1; 2.

DR Pfam; PF00931; NB-ARC; 2.

DR PRINTS; PR00364; DISEASERISIT.

SQ SEQUENCE 1169 AA; 131589 MW; A64E186A3664C6CA CRC64;

Query Match 22.9%; Score 1204; DB 2; Length 1169;
 Best Local Similarity 28.5%; Pred. No. 9.8e-36;
 Matches 351; Conservative 201; Mismatches 345; Indels 334; Gaps 37;

Qy 1 MAETVLSMARSLVGSATSKAASAADETSLLGVEKDIWIYKDELKTWQAFRAELMKK 60
 Db 1 MEETVLSVGKSLVNGAVRYAQSAIEVALQGVRRDOVFITNELEMMQAFLAANDEGD 60

Qy 61 KD-ELKLVWABQIRDSYDIEDSLDEPKVHIESQTLFRLQVLRERHRAIRHNLKSRV 119
 Db 61 KD-ELKLVWABQIRDSYDIEDSLDEPKVHIESQTLFRLQVLRERHRAIRHNLKSRV 119


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Db 228 PRDFVSLVNLQAHATQGVVEALLEKEKTEQDLAKFNGCNDKRCIKLVLDLSTIEWDQI 287
Qy 253 -----QELQG----- 257
Db 288 KCKFQCKRGRSIIIVSSTOVEVASLCAQESQASLQKLSADQTLVAFYDKGSIIEDSV 347
Qy 258 ----- 257
Db 348 KPVSIISDAITSTNNHTVAHGEIIDDQSDADEKKVARKSLTRITSVGASEESQLIGRE 407
Qy 258 KVVQVQVHL----- 266
Db 408 KEISEITHLIILNDSQQVQVIVSVGMGLGKTLVSGVYQSPRLSDFKDKTVFTIWRPP 467
Qy 267 -----SEYLIE-----LKEKRYFVYLD 284
Db 468 ILVELLSLABQLHKSGSKEELLENRVS SKKSLASMBEDTELQGLKRLLEKSKCLIVLD 527
Qy 285 DLWILHDWVINEIAPKPKNGKGRIVITTRNVDLAEKCATAS-LVYHLDPLQNDAILT 343
Db 528 DFDSTEDQIKPTLFLP-LKTSRIIVTTKRIANHCSCGNGVNHNLKVLKNDALCL 586
Qy 344 LLRKT--NKNHEDMESKNQMKVRIIVNKGRLPLAILTIGAVLAT--KQVSEWEKPYE 399
Db 587 LSEKVFPEATYDDQNNPELVKQILKCDGLPLAIVIGGFLANRKPTEPWRKLINE 646
Qy 400 HLPSELEINPLEALRRMTVLYGNHPSLHPCFLYLSIFPEDPEIKRNLVGRWIAEGF 459
Db 647 NINAELENNPELMIRTVLEKSYDGLPYHLASCFLYLSIFPEDQIISRRLLVHRWAEGY 706
Qy 460 VRPKVMTTKDVGSYFNELINRSMI---QSRVGIAGK-IKTCRIHDIIRDTIVTSISRQ 515
Db 707 STAAHGKSAIBIANGYFNMELNRSMILPFOQS--GSSRKSIDSCVHDLMDRIAISKTE 764
Qy 516 ENFVLLPWGDSGLVQENTHIA---PHGSMCKTGL-DWSIIRSLAIGDRPKSLAHA 570
Db 765 ENLVRVEEGCSAVIHGAIRHLAISNNWKGDKSBEFGLVDLSRISLSLFGDWKPFVYG 824
Qy 571 VCPQLRMLRVLDDVDTFLITQDFORIALLCHKLYLSIGYSSISYSLPSRISGLQGLQ 630
Db 825 ----KMFIRVLDFEG-TRGLEVHLDQIWKHLKFLSLRGCVRIDLLPLGLNLRLQ 879
Qy 631 TLNMPSTVIAALPS--EISKQLCHLTRCTGQFHYDNFSLNHPMK---CITNTICLPKV 684
Db 880 MLDIRGTVVKALPTIILKQLQVIHAGRKTDYVWEKHSIMQRCRKVGICATCCCLPLL 939
Qy 685 FTPLVSRDDRKAQIAELH--MATKSCWS-----PSIGVKVPKGIGKRLDL 727
Db 940 -----CEMYGPLHKLARDAWMTFACCVKFPSSIMTGVHBEEGAMVPSGIRKLKDL 989
Qy 728 QVLEYVDIIRTSRAIKELQSLKRLKLVGTNTGSTKECKILYAAIEKLSLSQLSHVDA 787
Db 990 HTLRNINVR--GNAILRDIGMLTGLKLGVA--GINKNGRAFLAISNLNKLSELSVSS 1046
Qy 788 AGISDGGTLECLDISPPPLRLTAVLDGILEEMPNWIEQIHLKYLKSLKLE-GKT 846
Db 1047 AGMP--GLCGCLDISPPENLQSLKLYSLKTLPEWIKELQHLVKLKLVSTRLEHDVA 1104
Qy 847 MLIIGALPNLMVHLRYNAYLGEKLVK---TG-APNLRILTWTIYELDOLREIFEDGSS 902
Db 1105 MEFLGELPKVEILVI--SPFKSEIHFPPQTGFVSLRVLKLAGLWNGKSVKPEEGTM 1162
Qy 903 PLLSKIEI-GSCRLESGITGIHLPKLEIPIRY-----GSKVAGL----- 942
Db 1163 PKLERLQVQRIENIEFGSLFELQINIEVQLSVWFPTDHDRIARAAGADYETAWEEE 1222
Qy 943 -----GOLEGEVN-----AHPNRPVL 958
Db 1223 VQEARNGGELKRIKIRELARNPQPII 1250

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RESULT 11

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Q947C8
ID Q947C8 PRELIMINARY; PRT; 1169 AA.
AC Q947C8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative resistance protein.
GN Name=RGA-2;
OS Triticum monococcum (Einkorn wheat) (Small spelt).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4568;
XP [1]
SEQUENCE FROM N.A.
MEDLINE=2132852; PubMed=11439119;
Wicker T., Stein N., Albar L., Feuillet C., Schlagenhauf E.,
Keller B.;
"Analysis of a contiguous 211 kb sequence in diploid wheat (Triticum
monococcum L.) reveals multiple mechanisms of genome evolution.";
RL Plant J. 26:307-316(2001).
DR EMBL; AF326781; AAK84082.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR_1; 3.
DR Pfam; PF00931; NB-ARC.
DR PRINTS; PRO0364; DISEASERSIST.
SQ SEQUENCE 1169 AA; 131599 MW; 0563D1ABC6D7B891 CRC64;

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Query Match 22.8%; Score 1200; DB 2; Length 1169;
Best Local Similarity 28.5%; Pred. No. 1.6e-55;
Matches 351; Conservative 201; Mismatches 345; Indels 334; Gaps 37;
Qy 1 MAETVLSMARSLVGSATSKAASAADETSLLLGVEKDIWYIKDELKTWQAFRAAELMKK 60
Db 1 METTVLSVGKVLNGAVRYAQAIAEVALQLGVRRDQVFITNELEMMQAFLMAANDEGD 60
Qy 61 KD-ELLKVAEQIRDLSDYIEDSLDEPKVHIESQTLPRQLVKLRERIRIHNLSRV 119
Db 61 GDSKVRVWYKQVRDLAYDVEDSLQDFAVRLEKQPMWR--ILLKDRQVAKQMKGLRANV 118
Qy 120 EYSSRNTRYSLVKPITSSGT*EIDMD-----SYAEDIRNQSR-NVDEAELVGFS 167
Db 119 EDYSQRNWRHLKGSAGSNPASTDQGSATGTAMTWSSTEDARRQREKAKADLVQLIKM 178
Qy 168 DSKRRLLEMDITNANDGPAKVICVVGMGGLGKTALSRIKIPESBEDIRKN--PPCNAMITV 225
Db 179 DRLRLVIAVWGTSST-----VGETSVIKRAF--EDLKKHNRFDCHAWIKV 221
Qy 226 SQSFHRIELKDMIRQ-----LLGPSSLDQLLOELQGVVQVHLSYELIELEKRYFV 281
Db 222 MCPFNSYEFVRSIIRQFIYNLLQDPVENMDAQVLRGMGMKKENDLVDFEKSILNDSYLI 281
Qy 282 VLDDLWILHDWVINEIAPFKNKKGSRIVITTRNVDLA----- 320
Db 282 VIDGMTTEEDQIKP-CFP-NNKGRSRIIVSTKQVEVASLCAQPNVADPHKQLSIDQD 339
Qy 321 ----- 320
Db 340 TLYAFPEKSGDGDSTEVGSSSTNTTTTASHILVNNKILTRMETTLAAFKFQLIGREKE 399
Qy 321 -----BKCATASL----- 328
Db 400 KSEIIQLVTNGDGRQFEVISVCGMGGLGKTTVVRDVYQSQELRGKPEKCACTIMRPFNC 459
Qy 329 ----- 328
Db 460 DELLKNLAGQGYEDVADVMVRHLEGGKCLIVLDLSTSTREWDALIPHFTALETSSRIIVT 519

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Db 888 KKCGRLPLAVAGGFLSTRPNIREWKFSDHISTELDENPSLEMIKKILISSTEGLSY 947
Qy 428 HLKPCFLYLSIPPEDFEIKRNLVGRVIAEGVRPKVGMTTKDVGESYFENELINRSMIQR 487
Db 948 HLKSCFLYLSIPPEDHDRIYGRLLRWIAEGYSRAKRNNNAEKEAEQFTALLNKSMLIQ 1007
Qy 488 SRVGTAGIKTCRIHDITDITVSROENFVLLPMGDSLDVQENTRHIAFHGMS--- 544
Db 1008 SRTVTGTGFCQVHDLREISIAKSEENLVLDHESISSKDKVRHLVISQWSREQ 1067
Qy 545 -----CKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTELITQKDFRI 599
Db 1068 KKNNDQNVIVSHRSLTVGEW-KSF---FLSKOMRLRVLDLED-TDGLHEDHIVPI 1122
Qy 600 ALLCHLYLSIGYSSYIYSLPRISCKLQLOTLNMPSTYIAALPSEISKLOCLHLRCIG 659
Db 1123 GKHLHLKYLRLSGSATILNLPSSFGNLLNLETDIRGTWTKLPATIGRLQNLKYLHA-G 1181
Qy 660 QPHYDNFSLNHPMKCITWICLPKVTPLVSRDRA-----KOIAELHMAWKSCHSESI-- 713
Db 1182 MPDDEDTRSWVP--TPPSAILEAFREYNQEEVGMGKILFVSLMFLISGMLNNDL 1239
Qy 714 -GVKPKGIGKLRDLQVLEVYDIRTSRAIKELGQLSKRLKLGVTWTTNGSTKECKILYA 772
Db 1240 FGKVPKRIKRLRSIHTLSVWISR-GKAMUKNLKLTQLRRKLGVT--GINKNCEBELCS 1296
Qy 773 AIEKLSSLSQSLHVAAGISDGTLE-CUDSISSPPPLRLTLVLCILSEMPNWTLEQLTHL 831
Db 1297 VIVKHGCLQSLLLRAEG-KDG--LEGCLDGLSPPKDLESQLYGNLVKLPENVKLENL 1353
Qy 832 KKIYLLRSLKKEGKTMILGALPNLMLVLRNAYLGEKLVFKTGAPFNLRITLMIYELDQ 891
Db 1354 QKLSRSTNLSEADATMQLGLPLMDIILRLQDKACKENELRFPDCTFNLRALIELISMG 1413
Qy 892 LREIRFEGSSPLEKIEIGICRL--ESGICITHLPKLKEIPR--YGSKVAGLQLE 946
Db 1414 LKSVIFEGATPKLEVLVLDHCCSIDAEGFPGIENLATLKEVSLQGYYYTFFKKKLQOOL 1473
Qy 947 GEVNAHPNRPVL 958
Db 1474 NMIEPRNLRL 1485

AC Q9LJ10 PRELIMINARY; PRT; 1011 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to Oryza sativa gene for Pib.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arihara K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idenuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katsagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa Y.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,

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RA Yano M., Jiang J., Gojobori T.;
RL "The genome sequence and structure of rice chromosome 1.";
RT Nature 420:312-316(2002).
DR EMBL; AP001073; BAA89580.1; -.
DR Gramene; Q9LJ10; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR000630; Ribosomal_S8.
DR Pfam; PF00560; LRR_1; 2.
DR Pfam; PF00931; NB-ARC; 2.
DR PRINTS; PR00364; DISEASERISIT.
DR PROSITE; PS00053; RIBOSOMAL_S8; UNKOWN 1.
SQ SEQUENCE 1011 AA; 114012 MW; 14EDDB8A31A4835C CRC64;

Query Match 21.7%; Score 1144; DB 2; Length 1011;
Best Local Similarity 31.2%; Pred. No. 1.3e-52;
Matches 329; Conservative 193; Mismatches 374; Indels 158; Gaps 37;

Qy 1 MAETVLSMARSLVGSATSKAASAAADSTLLGVKEKDIWIKDELKTMOAFLR--AAELM 58
Db 1 MEAAVSTEGTVRILLAKLGEFLSKYVLSGVYRHEIQELKDDLESNNACLDLAAVGD 60
Qy 59 KKDELKLVAAEQIRLDISYDIEDSLDEPKVHIES-----QTLPRQLVKL 102
Db 61 YHQSQQRTWTKQVREYVAYDAEDCIDSPRYHVGGRNDEGLLVAGWLRRTALRPLTL 120
Qy 103 RERHRIAIRIHNLSRVEEVSRRYSLVKP--ISSGTEIDMSYAEADIRNQSARNVDE 160
Db 121 RAMYKLAVEVQSLKARALKVSRRLRYRLEPFAAASSGSEYAPRCYDDLRRLPALSVDE 180
Qy 161 AELVGFSDSK--RLLEMDITNANDGPA--KVLICVMGGLGKTALSRKIPSEEDIRK 215
Db 181 SRLVGVRSKRAIKLLEHKGDDGDDGLARKKVAVVGFGGLGKTTLAAMYKS--PAVQ 238
Qy 216 NFPCNAVITVSSQPHRIELKDMIRQLLGP--SLDOLLOELQKGVVQ 262
Db 239 GIHHRAPFVTVTRSCNLRAMLESLEQLPAPARDPRCSRKEITAMEKDBILAGIETKPIQ 298
Qy 263 -VHLSBYLIELKEKRYFVVDLILHLDNWNINEIAPKPKKGSRIVITTRNVDLAE 321
Db 299 LLACSTH---LSDKRYFIVVDLWSLEDWASLKP-AFPDNDKH-SRIITITRNROVAE 352
Qy 322 KCAT--ASLVVHLDPLQWDAITLLRKT--NKHEDMESKNQKQKQVIRVKNCGRLPL 377
Db 353 SCCSLPGDRVHFMDVLP-NQOSRELFFKTVFQKHCPS--YRSLEGISGDLITKCGGLPL 410
Qy 378 AILTIGAVLA---TKQVSEWEKFEHLPSLEINPSLEALRMVMTLGYNHLPSHLKPCFL 434
Db 411 AIVSVGGMLAAQENKTPVETKVCGLSGSLSTSAAVRGMRILSLSYHDLPYHLKACFL 470
Qy 435 YLSITPDPDEFKRNRLVGRWIAEGFVRPKVGMWTKDVGESYFENELINRSMIQRVGTAG 494
Db 471 YLSVFREGYEIKRGPLVRRWAAEGFVGGRGSEWTPPEAAGKYIDBFVGRSIVTPTRVATNG 530
Qy 495 KIKTCRIHDIRDITVSIHQENFVLLPMGD-----GSDLVQENTRHIAF 539
Db 531 VVRCCKVHDIMLEVMTAKVEENFISL-LGSVTSYGRHQHTAAATTTGHDKI-----RRLSV 585
Qy 540 HGS-----MSCKTG-----LDWSIRSLAIFGDRPKSL 567
Db 586 HGSHPQSQSGSGGDEIFRFRRRKKGEQDDVLSVSDLSCLARSLLMLRCIEKPL 645
Qy 568 AHAVCPDQLRMLRVLDLEDVTELITQKDFRALLCHLYLSIGYSSYIYSLPRISCKLQ 627
Db 646 P-SISFKRLKLLRVLDLEGCRWL--SSRELDICKLSLLRYLSL-RDTGVQRLPRSVGRLK 702
Qy 628 GLQTLNMPSTYIAALPSEISKLOCLHLRCIGQHYDNFSLNHPMKCITWICLPKVTPL 687
Db 703 QLMTLDVRETDVRELPTITRLGHRHL-LSGRYR--YTRSHRV-----KLPEP 749

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:38:22 ; Search time 27.2998 Seconds
(without alignments)
2821.919 Million cell updates/sec

Title: US-10-656-394a-8
Perfect score: 5268
Sequence: 1 MAETVLSMARSLVGSALSKA.....SOVITLTNDSEIGTRAQAG 1032

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1111	21.1	1205	3 US-09-330-330-1	Sequence 1, Appli
2	955	18.1	920	3 US-08-930-996A-8	Sequence 8, Appli
3	641.5	12.2	928	4 US-09-336-946B-2	Sequence 2, Appli
4	641.5	12.2	928	4 US-09-993-170-58	Sequence 58, Appli
5	636.5	12.1	928	4 US-09-336-946B-4	Sequence 4, Appli
6	621	11.8	1402	3 US-09-004-838-11	Sequence 11, Appli
7	609	11.6	905	3 US-09-360-186-3	Sequence 3, Appli
8	609	11.6	905	4 US-09-864-680A-3	Sequence 3, Appli
9	607.5	11.5	1240	3 US-08-930-996A-4	Sequence 4, Appli
10	577.5	11.0	1220	3 US-08-930-996A-2	Sequence 2, Appli
11	564	10.7	1824	2 US-08-680-327-3	Sequence 3, Appli
12	564	10.7	1824	3 US-09-228-246-2	Sequence 2, Appli
13	561.5	10.7	1247	4 US-09-803-286A-2	Sequence 2, Appli
14	557	10.6	1206	4 US-09-245-928A-19	Sequence 19, Appli
15	557	10.6	1243	4 US-09-245-928A-17	Sequence 17, Appli
16	557	10.6	1257	4 US-09-245-928A-18	Sequence 18, Appli
17	552	10.5	1255	3 US-08-947-823-3	Sequence 3, Appli
18	549	10.4	1257	3 US-08-947-823-5	Sequence 5, Appli
19	539	10.2	784	3 US-09-004-838-12	Sequence 12, Appli
20	469	8.9	553	3 US-09-004-838-16	Sequence 16, Appli
21	405.5	7.7	909	2 US-08-310-912A-142	Sequence 142, App
22	405.5	7.7	909	3 US-09-301-085-142	Sequence 142, App
23	405.5	7.7	909	5 PCT-US95-04589-142	Sequence 142, App
24	403	7.6	885	2 US-08-310-912A-2	Sequence 2, Appli
25	403	7.6	885	3 US-08-841-089-2	Sequence 2, Appli
26	403	7.6	885	3 US-09-301-085-2	Sequence 2, Appli
27	403	7.6	885	5 PCT-US95-04570-2	Sequence 2, Appli

Query Match 21.1%; Score 1111; DB 3; Length 1205;
Best Local Similarity 26.9%; Pred. No. 6.9e-89;

ALIGNMENTS

RESULT 1
US-09-330-330-1
; Sequence 1, Application US/09330330
; Patent No. 6274789
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; APPLICANT: Iwamoto, Masao
; APPLICANT: Katayose, Yuichi
; APPLICANT: Sasaki, Takuji
; APPLICANT: Wang, Zi-Xuan
; APPLICANT: Yamanouchi, Utako
; APPLICANT: Ishimaru, Liesa
; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,330
; FILING DATE: 11-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 10-181455
; FILING DATE: 12-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/032001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1205 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-330-330-1

Sequence 2, Appli
Sequence 7, Appli
Sequence 108, App
Sequence 9, Appli
Sequence 6, Appli
Sequence 111, App
Sequence 88, Appli
Sequence 108, App
Sequence 108, App
Sequence 108, App
Sequence 2, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 125, App

Db 764 -----AANEG-----FGSLKYFMFV-----CTAPCMTFVEGAMPSVQRL----- 797
Qy 891 QLRIRPFDGSSPLEKIEGCRLESIGTIIHLPKLKEIPRYG-----SKVAGLG 943
Db 798 ---NLRFNANEFK-----QYDSKETGLEHLVALAEISARIGGTTDDDESINKTEVES 844
Qy 944 QLEGEVNAHPNRPVLLMYSDRRYHDLGAEAGSSIEVQTA 983
Db 845 ALRTAIRKHPTPTLMV--DIQWVDWIFGAEGRDLEDLA 882

RESULT 4
US-09-993-170-58
; Sequence 58, Application US/09993170
; Patent No. 6743969
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara
; APPLICANT: Bryan, Gregory
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene
; TITLE OF INVENTION: Specificity and Method for Engineering Altered
; TITLE OF INVENTION: Specificity
; FILE REFERENCE: BB1385 US NA
; CURRENT APPLICATION NUMBER: US/09/993,170
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/248,335
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 58
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-993-170-58

Query Match 12.2%; Score 641.5; DB 4; Length 928;
Best Local Similarity 24.2%; Pred. No. 1.9e-47;
Matches 257; Conservative 168; Mismatches 380; Indels 255; Gaps 35;

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Db 1 MAPAVASQGVIMKSLTSKLSLLQPPPPPPQPSLSRKGERRKILLRGLDRHLDD 60
Qy 50 AFLRA---AELMKKKDELLKVAEQIRDSLYDIEDSLDEFKVIH----- 90
Db 61 YLLVLEPSPDAPPDSTAAACWAKEVRELSYVDVDFDELDTQLLHRRGGDGSSTAGAK 120
Qy 91 --ESQTLFRQVLKURRHRRIAIRIHNLSKRVVEVSSRNTRYSLVKPISSTGTEIMDSVAE 148
Db 121 KWISSMIARLGEINRRRIADVTLFRARVKEAIRRHESYHLGRRTSSSRPREDD--D 178
Qy 149 DIRNQSARN-----VDEA-----ELVGFSDSKRLLEMDITNANDGP-AKVICV 192
Db 179 DDREDSAGNERRRFLSLTFGMDDAAVHQLVGRDISMQVRLW---ADGEFKLVKVASIV 235
Qy 193 GMGGLGKTRKIFES-EDIRKNFPCNAVITVSQSFHRIELKDMIRQLLGPSSLDQL 251
Db 236 GSGGVGKTLTATEFYRLHGRDLDPDCEAFVTRPRKPDWTKILTDMLSQL-----RP 288
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Qy 372 CGRLPLAILTIGAVLATQVSEWKFYEHL-----PSELEINPSLEALRNMVTIGYNHLP 426
Db 407 CGGLPLAI-TTARHFKSLLDGGQWQNHIOKSLTTSNLKNPTLQNRQVNLINYNLP 465
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Db 466 HCLKACLLYLSIYEDYIIRKANLVQRWMAAGFINSIENKVMEEVAGNYFDELVGRGLVQ 525

Qy 487 RSRVGIAGKIKTCRIHDIIRDITVSIHQENF-VLLPMGDSGLVQENTRIAHFGHMSC 545
Db 526 PVDVCKNEVLSVCVHVMVLNFIKCKSIEENFSTLQHSQTTVRHADKVRSLSLHFSNAH 585
Qy 546 KT-----GLDWSIRSLAIFGDRPKSLAHAVCPDQ-----RMLRVL-----DLEDVTFLIT 592
Db 586 DTTPLAGLRLSQVRSMAFFG-----QVKMPSIADYRLRLRVLILCFWADQEKTSY--- 635
Qy 593 QKQFDRIALLCHLKYSIGYSSSIYSLPRSIGKLGQTLNMPSTYIAALPSEISKLOCL 652
Db 636 --DLTSIFELLQRLYKLTGNITV-KLPEKIQGLQHLQTLADARATAVL-LDIVHTQCL 691
Qy 653 HTLRICIGQHYDNPSLNHPMKCIINTI--CLPKVFPTPLVSRDDRDAKQIAELHMAKSCWS 710
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Db 712 ----SIPKWTGKLNNRLINI-----AVMQISQ----- 735
Qy 771 YAAIEKLSLSQLSHVDAAGISDGGTLECLDSISSPPPLRLRLTLVLDGILEEMPNIQULTH 830
Db 736 -----DLDLTKGLSLTALSLLVRTAPQRIV----- 763
Qy 831 LKKIYLLRSKLKEGKTMILLGALPNLMLYRNAYLGEKLVFKTGAPPNLRLTLWIYELD 890
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RESULT 5
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; Sequence 4, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E.I. du Pont de Nemours and Company
; TITLE OF INVENTION: A P1-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-336-946B-4

Query Match 12.1%; Score 636.5; DB 4; Length 928;
Best Local Similarity 24.2%; Pred. No. 5.3e-47;
Matches 256; Conservative 166; Mismatches 385; Indels 251; Gaps 35;

Qy 1 MAETVLSMARSLVGSATSKAAS-----AADETSLLLGVEKDIWYIKDELKTM--Q 49
Db 1 MAPAVASQGVIMKSLTSKLSLLQPPPPPPQPSLSRKGERRKILLRGLDRHLDD 60
Qy 50 AFLRA---AELMKKKDELLKVAEQIRDSLYDIEDSLDEFKVIH----- 90
Db 61 YLLVLEPSPDAPPDSTAAACWAKEVRELSYVDVDFDELDTQLLHRRGGDGSSTAGAK 120
Qy 91 --ESQTLFRQVLKURRHRRIAIRIHNLSKRVVEVSSRNTRYSLVKPISSTGTEIMDSVAE 148
Db 121 KWISSMIARLGEINRRRIADVTLFRARVKEAIRRHESYHLGRRTSSSRPREDD--D 178
Qy 149 DIRNQSARN-----VDEA-----ELVGFSDSKRLLEMDITNANDGP-AKVICV 192
Db 179 DDREDSAGNERRRFLSLTFGMDDAAVHQLVGRDISMQVRLW---ADGEFKLVKVASIV 235
Qy 193 GMGGLGKTRKIFES-EDIRKNFPCNAVITVSQSFHRIELKDMIRQLLGPSSLDQL 251
Db 236 GSGGVGKTLTATEFYRLHGRDLDPDCEAFVTRPRKPDWTKILTDMLSQL-----RP 288
Qy 252 LQELQGVVQVHHLSEVLEBELKEKYFVVVLDLWILHDWNWINEIAFPQNKKGSRIV 311
Db 289 QHQRQSSDVWEVDRLLLETIRTHLQDKRYFIIEIDLWASSMMDIVSR-GLPDNN-SCSRIL 346
Qy 312 ITRRNVDLAEKATASLVYHLDLFLQMDAITLLARKTNKGNHEDNESKMKQKQVIRVVK 371
Db 347 ITTIEPVALACCGVNSHHIKIDPLGDVSSQLFFSGVVGQGNFPGHLETVSHDMIKK 406
Qy 372 CGRLPLAILTIGAVLATQVSEWKFYEHL-----PSELEINPSLEALRNMVTIGYNHLP 426
Db 407 CGGLPLAI-TTARHFKSLLDGGQWQNHIOKSLTTSNLKNPTLQNRQVNLINYNLP 465
Qy 427 SHLKPCLYLSIFPEDFEIKNRVLGRVWIAAGFVRPKVMTTKDVGSYSFNNELNRSIMQ 486
Db 466 HCLKACLLYLSIYEDYIIRKANLVQRWMAAGFINSIENKVMEEVAGNYFDELVGRGLVQ 525

Db 2 EIGLAVGAFSSALNVLFDRAPNGDILNFRKDHVK-LLKKLKWTLRGIQIVLSDA 60
Qy 63 ELLKVAEQIRDSYDIEDSDEFKVHIESQTLFRQLVKLRERHRIARHN----- 114
Db 61 ENKQASNPVRDNLNEURDAVDSAEENLIEVNYEALRLKVEGQHFQNFSETSNQOVSBFF 120
Qy 115 -----LKSRYEVSRRNTRYSLVKPISSGTIEDMSYAEIDRNSARNVDEAEVLGFS 168
Db 121 LNIKDKLEDTIETKDLQEQIGLL-----GLKEYFDSTKLETRPSTSLIDEPDIFG-- 172
Qy 169 SKKRLLEMDTNANDGPA-----KVICVGMGGLKGTALSRKIFSEEDIRKNPCNMIT 224
Db 173 RQSEIEDLIDRLSEGASGKLTVPVIGMGLGKTTAKAVY-NDESVKNHFDLKAFC 231
Qy 225 VSQSFRIELKDMIRQLLGPSSDQLLOELQGVVVVQVHLSYVLEELKEKRYFVLVD 284
Db 232 VSEAYNAFRITKGLLEIGSIDLVDDNQLQVQ-----LKERLKEKFLVLVD 280
Qy 285 DLW--ILHDMWINEIAPPKNKKGSRIVITRNVDLAECATASLVVHLDLQWDAIT 342
Db 281 DVNDNTNNEWDELNRVFN--QGDIGSKIIVTRKDSVALMNGEQI--SMGNLSTEASWS 336
Qy 343 LLLRKTNNKHEDMESNKNMQRVERIVNKCGRPLAILTIGAVLATK-QVSEWEKRYEHL 401
Db 337 LFQRHAFENMDPM-GHSELEBVGRLAAKCKGLPLAKTLTAGMLRSKSEVEBEWKCILRSE 395
Qy 402 PSELEINPSLEALRWTLGNHLPKPCFLVLSIPPEDEFEIKRNLVGRWIAEGFVR 461
Db 396 IWEIRDNDILPAL-----MLSYNDLPAHLKRCFCFAIPPKDYPFRKQGVHLWANGLV- 450
Qy 462 PKVGMTTKDVGESYFNELINRSMIORSRVAGIKTC-RIHDIIRDITVSISRQENFVL 520
Db 451 PVEBEIIODLGNQFLELSRSLPERVNPPEGNIKELFLMHDLVNDL-AQLASSKLCIR 509
Qy 521 LPMGDGSLDQENTRHTAFHSGMSCKTGLD-----WSIIRSLA-----IFGRPX 565
Db 510 LEESQGHML-EQCRHLSY--SMGYDGGFEKLTPLYKLEQLRTLPTCSSVNYFYNPLTK 566
Qy 566 SLHAVCPDQRLMLRVLVDLEVTPLITQKDFRALLCHLKYLSIGVSSISYSPRSIGK 625
Db 567 RVLHNLIP-TLRSRLALSLSH--YKMEELPNDLFIKLLRFLDIS-RTNKRPLPDSLCV 622
Qy 626 LQGLQTLNMPGTYYAALPSEISKQCLHLTRCIGQFHDNPSLNHPMKCIITNTICLPKVF 685
Db 623 LYNLETLSSCKLEELPLOWEKL-----INLRHLD-----ISNT----- 657
Qy 686 TPLVSRDDRAKQIAELHAWTKSCWSESGVVPKGIGKRLDQVLEVVDIRRTSSRAIKE 745
Db 658 -----WH-----LQMLHLRLKSLQVLV-----GAKP 680
Qy 746 LQQLSKRLKLVTTNGSTKECKILYAAIE--KLSSL-----QSLHVDAAGIS 791
Db 681 LVGVWRMEDLGEAQN-----LYGSLSVVVKLENVVDRREAVKPKRKNHVEQL--- 728
Qy 792 DGGTLECLDSTSSPPPLARTLVLDGI-----LEEM-----PNWIEQLTHLKKIYL 836
Db 729 ---SLEWSESISANSONQTERDILBELRPHKIQEVKIIGYGTGFPNVAWDPFLKVL 785
Qy 837 LRSLKEGKTMILIGALPNMLVHLRYNAYLGEKLVFKT--GAPPNRLTLWIYELDQURE 894
Db 786 SLRNCKDCYSLPALQQLPCLPFLSV--KGMHGIRVVTEEFYGRLLSSKK-----PFCLEK 838
Qy 895 IRFED-----GSSPLEKIEIGECRLSEGITGIHLPKL-EIPIRGS----- 937
Db 839 LEFEDMTWKQWALGIGEFTLEKLSIINC-----PELSLEIPIQFSSLRKF 886
Qy 938 KVAGL-----GOLEG 947
Db 887 RVFCGPVVFYDAVLRSQLG 907

RESULT 10

US-08-930-996A-2

; Sequence 2, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; TITLE OF INVENTION: 12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-2

Query Match 11.0%; Score 577.5; DB 3; Length 1220;
Best Local Similarity 23.6%; Pred. No. 1.4e-41;
Matches 241; Conservative 191; Mismatches 371; Indels 219; Gaps 45;

Qy 3 ETVLSMARSIVGSAISKAASAAADETSLLGVEK--DIWVIK--DELKTQAFRAAE 56
Db 2 EIGLAIGGAFSSALNVLFDRAPNGDILNFRKDHVK-----LQVLSDAE 61
Qy 57 LMKKDKLLKVAEQIR-----DLSYDIEDSDEFKVHIESQTLFRQLVKLRERHRIAR-- 111
Db 62 NKASQNFVQWLHLKLTAVDAENLIEQVNYEALRLKVFETSNQOVSDL---NLCLSD 117
Qy 112 -IHNLSRVEVSRRNTRYSLVKPISS-GTEIDMDSYAEIDRNSARNVDEAEVLGFS 169
Db 118 FFLNIKKLEDTIKK--LEVLEKQIGRLGKHEHFIKQETRPSTSLVDDSGIFGRKNE 175
Qy 170 KK-----RLLEMDTNANDGPAKVICVGMGGLKGTALSRKIFSEEDIRKNPCNMITV 225
Db 176 IENLVGRLLSM-DTRKRN--LAVVPIVGMGMGKTTAKAVY-NDERVQKHFGTAMPCV 231
Qy 226 SOSPHRTELKDMIRQLLGPSSL--DQLLOELQGVVV--QVHLSYVLEELKEKRYFV 281
Db 232 SEAYDAFRIPKGLLOE-IGSTDLCADDNLQVLKADNINQLVKLEKNGKRLV 290
Qy 282 VLDDLV--ILHDMWINEIAPPKNKKGSRIVITRNVDLAECATASLVVHLDLQWDAIT 339
Db 291 VLDDVMDNYPWDRLNLF--QGDIGSKIIVTRKESVALMMDSGAI--YMGILSSED 346
Qy 340 AITLLLRKTNNKHEDMESNKNMQRVERIVNKCGRPLAILTIGAVLATK-QVSEWEKRY 398
Db 347 S-WALFKRHSLEHKDPKEHPFEFVEGVQIADKGLPLAKTAGMLRSKSEVDEWRNI- 404

Qy 399 EHLPSL-EINPSLEALRRMTLGNHLPKPCFLYLSIFPEDFEIKRNLVGRMAE 457
Db 405 --LRSEIWLPSGNGILPALMSTNDLFAHLKQCLAYCAIYKPYQPRKEQVHLMTAN 462
Qy 458 GFVRPKVGMTTKGVESYFNELINRSMIQSRVGIAGIKTCRIHDIIRDITVSIHQEN 517
Db 463 GLVH-----QFHSGNQYFIELRSLSPEMASEPSESDVEFLMDLVNDL-AQIASNH 515
Qy 518 FVLPMGDSGLVQENTHIAFHGSMCKTGLDWSIIRSLAIFGDR-----563
Db 516 CIRLEDNKGSHML-EQCRH-----MSYSIQDGEFEKLKSLPKSEQLRTLLPIDIOPHY 568
Qy 564 ----PKSLAHAVCDQLRMLRVLEDVTLITQKD-PDRALLCHLKYSIGYSSSIYS 618
Db 569 SKLSKRVLHNLIP-TURLRALSLSHYQIEVLPNDLPIKLT---LRFDLDS-ETSITK 623
Qy 619 LPRSIGKIQIGIQTLMPS-TYIAALPSEISKLOCLTLRCIGQPHYDNFSLNHPMKCTN 677
Db 624 LPDSIFVLYNLETLLSSCEYLEELPQMEKL-----INRHLD-----ISN 665
Qy 678 TICLPKVTPLVSRDRRAKQIAELHMAKSCWSESIGVKVPKIGIKLRDLQVL-----730
Db 666 TRRL-----KIPHLRLSLKSLQVLVGAFLV 691
Qy 731 ----EYVDIRTSRAIKELQGLSKRLKLVTTNGSTGKECKILYAAIEKLSLSQSLHV 785
Db 692 GGMWMEYL-----GEAPNLYGSLISILENVV-----DREAVKARMEKKNHVEQL--737
Qy 786 DAAGISDGTLECLDSTSSPPPLRTLVLDGIL-----EEMPWIEQLTH 830
Db 738 -----SLEWSESISADNSQTERDILDLRPHKIKAVEIYGYGTGTFPNVADPLF 788
Qy 831 LKITYLLRSKLKEGKTMILIGALPNMLVHLRYNAYLGEKLVFKT--GAPFNLTLYE 888
Db 789 VKLVHLRLNCKDCVSLPALQCLFELSI--RGMHGIRVVTSEFYGRLLSKK-----P 841
Qy 889 LQURERTREP-----GSSPLEKIEIGECRLSESGITGIHLPLK-LRIPRY 935
Db 842 FNSLVKLRFEDMPKWKQWHTLIGEFPTLEKLSKNC-----PELSLEIPIQF 889
Qy 936 GS 937
Db 890 SS 891

RESULT 11

US-08-680-327-3

Sequence 3, Application US/08680327

Patent No. 5859321

GENERAL INFORMATION:

APPLICANT: Staekawicz, Brian S., Oldroyd, Giles Edward,
APPLICANT: Salmeron, John M., Rommens, Caius
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT
TITLE OF INVENTION: PATHOGEN RESISTANCE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Kiarquist Sparkman Campbell Leigh &

ADDRESSEE: Whinston

STREET: One World Trade Center

STREET: 121 S.W. Salmon Street

STREET: Suite 1600

CITY: Portland

STATE: Oregon

COUNTRY: United States of America

ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/680,327

FILING DATE: July 11, 1996

Db

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,912

FILING DATE: September 22, 1994

CLASSIFICATION: 800

APPLICATION NUMBER: 08/227,360

FILING DATE: April 13, 1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Alan. E.

REGISTRATION NUMBER: 35,123

REFERENCE/DOCKET NUMBER: 5151-45038

TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391

TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1824 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-680-327-3

Query Match 10.7%; Score 564; DB 2; Length 1824;

Best Local Similarity 23.6%; Pred.No. 4.4e-40;

Matches 248; Conservative 189; Mismatches 373; Indels 240; Gaps 45;

Qy 17 ISKAASAAADETSILLGVERKDIMVYKDELTKMQAFL-RAAELMKKQDELKQVWAEQIRDL 75

Db 959 LGKLELLRLSKLDLIIDLKHQIESVKEGLCLARSFIDHFSYDEHDEACGLIA-RVSV 1017

Qy 76 SYDIEDSLDE-----FKV-----HISQTLFROLV-KLRHRHRIARIHNLKGRVE 120

Db 1018 AYKAEYVIDSLAYSHPLWKYKLVMISEVLENIKLVNKVGTGTCRRNIETVTHEVAKTTT 1077

Qy 121 EVSSRNTRYSLVPISSGTIDEIMDSYAEDIRNQSARNVDEAELVGFSDSKRLLEMDTN 180

Db 1078 YVAPSPSAYT-----ORANE-----EMEGFOOT-----IDELKDKL 1108

Qy 181 ANDGP-AKVICVVMGGLKGTALSRKIFESSEDIRKNPCNAMIIVTSQSFHRIELLKDMI 239

Db 1109 LGSPPELDVLSIVGMPLGKGTLLAKKIY-NDPEVTSRFDVHAQCVVQLYSWRELLTIL 1167

Qy 240 ROLLGSSLDQLLOELQGVVVQVHLSEYLIIBELKEKRYFVVDLWILHDMWINEIA 299

Db 1168 NDVLEPSDRN---EKEDGEIADELRRP-----LTKRFLILLDDVDYKVDNLQWCF 1217

Qy 300 FPKNNKGSRIIVLTRNVDLAEKATASLVYHLDPLQMDAITLLLRKTNKHEDMESNK 359

Db 1218 SDVSNR--SRIILTRNDVAEYVKCESDPHHLRLFRDDESWTLLQKEV---FQGESCPP 1272

Qy 360 NMOKMVERIVNKGRLPLAILITIGAVLATKQ--VSEWEKFEVHLPSLEINPSLEALRRM 417

Db 1273 ELEDVGEISKSCRGPLSVLVAGVLKQKKTLDLSWKVVEQSLSSQ-RIG-SLEESISI 1330

Qy 418 VTIGYNHLPKPCFLYLSIFPEDFEIKRNLVGRVIAESGFVRPKVGMTTKGVESYFN 477

Db 1331 IGFSYKNLPHYLKPCFLYFGGLQKDIHVSKMTKLWVAESGFQVANNKEGQEDTAQGLD 1390

Qy 478 ELINRSMIQRSRVGIAGIKTCRIHDIIRDITVSIHQENFVLLPMGDSGLVQENTR-- 535

Db 1391 DLIGRNVVMAMEKRPNTKVTICRIHLLHKCEKAKQEDF--LLQINSGEVGFPERLEEY 1449

Qy 536 HIAFHGSMCKTGLD-W-----SIIRSLAIFGDRPKSLAHAVCPDOL-----R 577

Db 1450 RLFBH---SYQDEIDLWRPSRSNRSU-----LFNAIDPDNLWPRDISFESPK 1497

Qy 578 MLRVLDLEDVTLITQKDFDRIALLCHLKYSISYSSSIYSLPRSIGKQLQLOT-----631

Db 1498 LVKVLDE--SFNIGGTFPEIYQVLIQMKYFAA--QTDANSIPSSIAKLENLETFVVRGL 1553

Qy 632 ---LNPSTYIAALPSEISKLOCLTLRCIGQPHYDNFSLNHPMKCTINTICLPKVTPL 688

Db 1554 GGEMILFCSLL-----KMVKLRHIVNDRV-----SFGHLHNDVLTGNSQLPNLET-- 1600

; ORGANISM: Lycopersicon var.
US-09-803-286A-2

[illegible]

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Db      1150  CLGDITFHKLLKLLVKLNLISRWDSVEESFPLLETLVIKKCIDLSBIPLSFADIPTELEQI 1200
QY      909  EI 910
Db      1210  KL 1211

RESULT 14
US-09-245-928A-19
; Sequence 19, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245,928A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF2 encoded
; OTHER INFORMATION: polypeptide
US-09-245-928A-19

Query Match      10.6%; Score 557; DB 4; Length 1206;
Best Local Similarity 25.1%; Pred. No. 9,2e-40;
Matches 239; Conservative 173; Mismatches 365; Indels 174; Gaps 41;

QY      34  VEKDIWYIKDELKTMQAPL-RAAELMKKKDELLKVAEQIRDLSDYIEDSLDEFKVHIES 92
Db      361  IKEEIELVQSELEFIRSPFGDAAEQGLYD----IWA-RVLDVAYEAKDVID--SIIVRD 413
QY      93  QTLFROLVKLRHRIAIRHNLKSRVEVSSRNTRYSLVKPISSGTEIDMDSYAEIDRN 152
Db      414  NGLLHLIFSL-----PITIKKIKLKEBISALDENI----PKDRGL-IWVNSPKKPV 462
QY      153  QSARNVDEAELVCFSDSKRLEEMDTNANDGPA--KVICVGMGSLGKLTALSRKIFESE 210
Db      463  KSL--TTDKIIVGFEETNLIIRKL-----TSGPADLDVVISITGMPGSGKTTLAYKYV--ND 515
QY      211  EDIRKNPFCNAVITTSQSFRIELKMDIRQLLGPSSLDQLLQELQGVVQVHLSYVL 270
Db      516  KVSRRHFDLRANCTVDGQYDDKKLLDTIFSQVSGDS--NLSENID-----VADKL 564
QY      271  IBELEKEKRYFVVLDDLLWLHDMWNINEIAPP-KNNKKGSRIVITTRNVDLA--EKCATAS 327
Db      565  RKQLFCRYLIVLDDVW---DTTTLDELTPPPEAKKGSRIILTTREKEVALHGKLTNDP 621
QY      328  LVYHLDPLQWDAITLLLRKTNKHEDMESNKKMQQKQVRIYVVKCGRPLPLAITICAVLA 387
Db      622  L--DLRLRPDSWELLEKRTTFGNESCPCDELDDVGK---EIAENCKGLPLVADLIAGVIA 676
QY      388  --TKQVSEKCFVEHLPSPSELNPSLEALRRVMVTLGYNHLPSHLKPCFLVLSIFPDPDEI 445
Db      677  GREKKGSLVLEQSSLSSTFI-LNSEVEVM-KVIELSYDHLPHHLKPCLLHPASWPXDTPL 734
QY      446  KRNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELNRSMIQRSRVGIAGKIYCTRIHDI 505
Db      735  TIYLLTVYLGAGFGFTEKTEMKIGIEVVKIYMDLISLSLV--ICFNEIGDILNFQIHDLV 792
QY      506  RDIIVSISQEN-FULLPMGDSGLV-----QENTRIAFHSGM--SCKTGLDWSII 554
Db      793  HPCFLIKAKENLNFIRSSAPSDLLPROITIDYEEBEHFGNLFVFNDSNKKRHSKGHL 852

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Qy 555 RSLAIFGDR-PKSLAHAVCPDQLRMLRVLDLEDVTFELITQKDFRIALLCHLKYSIGYS 613
Db 853 YSLAINGDQLDDSVDAFHLRLRLRVLDLEPSLIMWDSLLNEICMLNHLRLI--R 910
Qy 614 SSIYSLPRSIGKLOGLQTL--NMPSTYIAALPS--EISKLOCLHLTRCIGQFHYDNFSLN 669
Db 911 TVQKYLFPFNSLNWLESFLVSNKGSILVLLPRILDLVKRLV-----SVGACSPFDMAD 966
Qy 670 HPMKCIINTICLPKVFTPLVSRDDRARAQIAELHMAKSCWSESIGVKVPKIGIKLRDLQV 729
Db 967 ESI-----LIAKDTKLENLRILGELLISYKDTWNI-----FKRPPNLQV 1006
Qy 730 LEYVDIRRTSSRAIKELQSLKRLKLGVTNGSTKECKKILYAAIEKLSISQSLHVAAG 789
Db 1007 LQF-----ELKESWDYSTEQHW-----FPKLDCLTELETLCVG 1039
Qy 790 ISDGGTLECLDSISSPPPLRLTLVLDGILEMPNW--IEQLTHLKKIYLLRSKLKEGKTM 848
Db 1040 FKSNTNHCSSVATNRP-----WDFHPSNLKELLLYDPPL--TSDLS 1082
Qy 849 ILGALPNLMVHLRYNAY-----LGEKLVFKTGAFPNLRTLWIYELDQLEIRPEDGSS 902
Db 1083 TIARLPNLENLSLYDTTIOGEEWNGEEDTFENLKFLNLRLLTSLKWEVGEE-----SF 1136
Qy 903 PLEKIEIGECRLSESGITGIIHLPKLKEIPIRYGS-----KVAGLGQLE 946
Db 1137 PNLEKCLKQEC-----GKLEIPSPGDIYSLKFIKIVKSPQLE 1175

RESULT 15
US-09-245-928A-17
; Sequence 17, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245, 928A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1243
; TYPE: PPT
; ORGANISM: Mi resistance gene deduced amino acid
US-09-245-928A-17

Query Match 10.6%; Score 557; DB 4; Length 1243;
Best Local Similarity 25.1%; Pred. No. 9,7e-40;
Matches 239; Conservative 173; Mismatches 365; Indels 174; Gaps 41;

Qy 34 VEKDIWIYKDELTWQAF--RAAEIMKKKDELLKVAEQIRDLSDYIEDSLDEPKVHIES 92
Db 398 IKEBIEVLVSQELFIRSPFGDAAEQGLYK----IWA-RVLDDVAYEAKDVID--SIIVRD 450
Qy 93 QTLFROLVKLRHRIARIHNLKSRVEEVSRRNTRYSLVKPISGTEIDMDSYAEIRN 152
Db 451 NGLHLIFSL-----PITIKKIKLKEIBISALDENI----PKORGL-IVVNSPKKPV 499
Qy 153 QSARNVDAEVLVGFSDSKRLLEIMDITNANDGPA--KVICVGMGGLGKTALSRRKIFESE 210
Db 500 KSL--TTDKIIVGEEETNLILRKL-----TSGPADLDVISITGMPGSKTTLAYKVY-ND 552
Qy 211 EDIRKNFCNAWITVQSFRHIELLKOMIRQLLGPSSLDQLLQELQGVVQVHHLSEYL 270
Db 553 KSVSRHFDLRAWCTVDQYDDKCLJDTTIFSVSGSDS--NLSENID-----VADKL 601
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Qy 271 IEELKEKRYFVVLDDDLWLHLDWMNINEIAPP--KNNKKSRIVITTRNVDLA--EKCATAS 327
Db 602 RKQLFGKRYLVLDDVW---DTTLDLDELTRFPPEAKKGSRIILLTTRKEVALHGLKNTDP 658
Qy 328 LVTHDLFLQWDAITLLLRKTNKHEDMESKQMKQKVERIVNKGRLPLAILTIGAVLA 387
Db 659 L--DLRLLRDPDESWELEKRTFGNESCPDELLDVGK---EIAENCKGLPLVADLIAGVIA 713
Qy 388 --TKQVSEWKFEYHLPSELEINPSLEALRRMTVLGYNHLPShLKPFLYLSIFPEPEI 445
Db 714 GREKRSVWLEVOSSLSFT--LNSEVEM--KVIELSYDHLPHLKLPCLLHFASPKPTPL 771
Qy 446 KRRLVGRWIAEGFVRPKVGMTTKDVGESYFENELINRSMIORSRVGIAGIKTKRIHDI 505
Db 772 TIYLLTVYLGAEFGFVKTEMKGIEEVVKIYMDLLISSLV--ICFNEIGDILNFQIHDLV 829
Qy 506 RDTVTSISROEN--FVLLPMGDGSDLV-----QENTRIHAFHGS--SCKTGLDWSII 554
Db 830 HDFCLIKARENLFDRIRSSAPSDLLPRQITIDYDEEEHFGLNFVNFDSNKKRHSKHL 889
Qy 555 RSLAIFGDR-PKSLAHAVCPDQLRMLRVLDLEDVTFELITQKDFRIALLCHLKYSIGYS 613
Db 890 YSLKINGDQLDDSVDAFHLRLRLRVLDLEPSLIMWDSLLNEICMLNHLRLI--R 947
Qy 614 SSIYSLPRSIGKLOGLQTL--NMPSTYIAALPS--EISKLOCLHLTRCIGQFHYDNFSLN 669
Db 948 TVQKYLFPFNSLNWLESFLVSNKGSILVLLPRILDLVKRLV-----SVGACSPFDMAD 1003
Qy 670 HPMKCIINTICLPKVFTPLVSRDDRARAQIAELHMAKSCWSESIGVKVPKIGIKLRDLQV 729
Db 1004 ESI-----LIAKDTKLENLRILGELLISYKDTWNI-----FKRPPNLQV 1043
Qy 730 LEYVDIRRTSSRAIKELQSLKRLKLGVTNGSTKECKKILYAAIEKLSISQSLHVAAG 789
Db 1044 LQF-----ELKESWDYSTEQHW-----FPKLDCLTELETLCVG 1076
Qy 790 ISDGGTLECLDSISSPPPLRLTLVLDGILEMPNW--IEQLTHLKKIYLLRSKLKEGKTM 848
Db 1077 FKSNTNHCSSVATNRP-----WDFHPSNLKELLLYDPPL--TSDLS 1119
Qy 849 ILGALPNLMVHLRYNAY-----LGEKLVFKTGAFPNLRTLWIYELDQLEIRPEDGSS 902
Db 1120 TIARLPNLENLSLYDTTIOGEEWNGEEDTFENLKFLNLRLLTSLKWEVGEE-----SF 1173
Qy 903 PLEKIEIGECRLSESGITGIIHLPKLKEIPIRYGS-----KVAGLGQLE 946
Db 1174 PNLEKCLKQEC-----GKLEIPSPGDIYSLKFIKIVKSPQLE 1212
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Search completed: February 9, 2005, 08:56:16

Job time : 36.2998 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:53:28 ; Search time 94.0327 Seconds
(without alignments)
3574.555 Million cell updates/sec

Title: US-10-656-394A-8
Perfect score: 5268
Sequence: 1 MAETVLSMARSLVGSALSKA.....SQVTLTNDSEIGTHAQAG 1032

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4942.5	93.8	1091	15	US-10-352-179-93
2	4925	93.5	1031	15	US-10-352-179-89
3	4397.5	83.5	1531	16	US-10-437-963-139799
4	3664.5	69.6	993	16	US-10-437-963-104966
5	3068.5	58.2	974	16	US-10-437-963-143499
6	3083.5	58.2	979	15	US-10-352-179-85
7	2769	52.6	862	16	US-10-437-963-141086
8	2575	48.9	993	15	US-10-352-179-87
9	2539	48.2	1007	16	US-10-437-963-110261
10	2484.5	47.2	1163	16	US-10-437-963-151916
11	2367	44.9	1054	15	US-10-352-179-91
12	1905	36.2	926	16	US-10-437-963-171923
13	1878.5	35.7	812	16	US-10-437-963-177336

14	1384	26.3	451	15	US-10-352-179-95	Sequence 95, Appl
15	1238.5	23.5	978	16	US-10-437-963-197236	Sequence 197236,
16	1210	23.0	981	16	US-10-437-963-149503	Sequence 149503,
17	1209.5	23.0	1226	16	US-10-437-963-135087	Sequence 135087,
18	1209	22.9	975	16	US-10-437-963-178601	Sequence 178601,
19	1204	22.9	1251	16	US-10-437-963-156608	Sequence 156608,
20	1187.5	22.5	1485	16	US-10-437-963-157799	Sequence 157799,
21	1135	21.5	1011	16	US-10-437-963-134127	Sequence 134127,
22	1101	20.9	1205	16	US-10-437-963-190992	Sequence 190992,
23	1085.5	20.6	774	16	US-10-437-963-135395	Sequence 135395,
24	1078	20.5	932	16	US-10-437-963-190783	Sequence 190783,
25	1077.5	20.5	947	16	US-10-437-963-114679	Sequence 114679,
26	1062.5	20.2	953	9	US-09-354-453-36	Sequence 36, Appl
27	1062.5	20.2	953	14	US-10-267-718-36	Sequence 36, Appl
28	1048	19.9	1025	16	US-10-437-963-170107	Sequence 170107,
29	1017	19.3	869	16	US-10-437-963-120106	Sequence 120106,
30	1016.5	19.3	970	16	US-10-437-963-120373	Sequence 120373,
31	1015.5	19.3	1662	16	US-10-437-963-125137	Sequence 125137,
32	1010	19.2	1003	16	US-10-437-963-181404	Sequence 181404,
33	1000.5	19.0	936	16	US-10-437-963-185358	Sequence 185358,
34	996.5	18.9	916	16	US-10-437-963-167102	Sequence 167102,
35	993	18.8	859	16	US-10-437-963-181820	Sequence 181820,
36	992.5	18.8	996	16	US-10-437-963-187715	Sequence 187715,
37	991	18.8	870	16	US-10-437-963-184762	Sequence 184762,
38	988	18.8	911	16	US-10-437-963-198474	Sequence 198474,
39	984	18.7	993	16	US-10-437-963-201464	Sequence 201464,
40	982.5	18.7	960	16	US-10-437-963-178460	Sequence 178460,
41	982.5	18.7	976	16	US-10-437-963-172739	Sequence 172739,
42	975.5	18.5	770	16	US-10-437-963-137267	Sequence 137267,
43	953.5	18.1	961	16	US-10-437-963-190153	Sequence 190153,
44	945	17.9	994	16	US-10-437-963-119823	Sequence 119823,
45	941	17.9	948	15	US-10-425-114-63389	Sequence 63389, A

ALIGNMENTS

RESULT 1

US-10-352-179-93
; Sequence 93, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-93

Query Match	93.8%	Score 4942.5	DB 15	Length 1091
Best Local Similarity	90.5%	Pred. No. 0		
Matches 987	Conservative 14	Mismatches 31	Indels 59	Gaps 1
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Qy	40	-----	-----	-----
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Qy	62	DELLKVAEQIRDLVYDIEDSLDEPKVHVESQTLFRQYIKDELKIMQAPLRAAEVKK	121	
Db	121	DELLKVAEQIRDLVYDIEDSLDEPKVHVESQTLFRQYIKDELKIMQAPLRAAEVKK	180	

QY 122 VSSNTRYSLVKPISSTGTEIDMSYAEDIRNOSARNVDAAELVGFSDSKRLLEMDTNA 181
DB 181 VSSNTRYSLVKPISSTGTEIDMSYAEDIRNOSARNVDAAELVGFSDSKRLLEMDTNA 240
QY 182 NDGPAAKVICVVMGGLGKTALSRKIFESSEDIRKNPCNAWITVSQSFHRIELKDMIRQ 241
DB 241 NDGPAAKVICVVMGGLGKTALSRKIFESSEDIRKNPCNAWITVSQSFHRIELKDMIRQ 300
QY 242 LIGPSSLDLLOELQOGKVQVHHLSYLLIEELKEKRYFVVLDLWILHDWNWINEIAPP 301
DB 301 LIGPSSLDLLOELQOGKVQVHHLSYLLIEELKEKRYFVVLDLWILHDWNWINEIAPP 360
QY 302 KNNKKGSRIVITTRNVDLAEKATASLVYHLDLQMDNDAILLLRKTNNKHEDMESKNM 361
DB 361 KNNKKGSRIVITTRNVDLAEKATASLVYHLDLQMDNDAILLLRKTNNKHEDMESKNM 420
QY 362 QKWVERIVNKGGRPLAILITIGAVLATKHVSEWEKRYEQLPSELEINPSLEALRMMVTLG 421
DB 421 QKWVERIVNKGGRPLAILITIGAVLATKHVSEWEKRYEQLPSELEINPSLEALRMMVTLG 480
QY 422 YNHLPSHLKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNELIN 481
DB 481 YNHLPSHLKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNELIN 540
QY 482 RSMIORSRVGIAGKIKTCRIHDIIRDITVSIHQENFVLLPMGDSGLVQENTRHIAFHG 541
DB 541 RSMIORSRVGIAGKIKTCRIHDIIRDITVSIHQENFVLLPMGDSGLVQENTRHIAFHG 600
QY 542 SMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLQDFRIAL 601
DB 601 SMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLQDFRIAL 660
QY 602 LCHLKYSIGYSSSIYSLPRSIGKLOGLQTLNMESTYIAALPSEISKLOCLHTLRCTGQF 661
DB 661 LCHLKYSIGYSSSIYSLPRSIGKLOGLQTLNMESTYIAALPSEISKLOCLHTLRCTGQF 720
QY 662 HYDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSEBSIGVKVPKGI 721
DB 721 HYDNFSLNHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSEBSIGVKVPKGI 780
QY 722 GKLRDLQVLEYVDIRRTSSRAIKELGQSLKRLKGLVTTNGSTKCKKILYAAIEKLSLQ 781
DB 781 GKLRDLQVLEYVDIRRTSSRAIKELGQSLKRLKGLVTTNGSTKCKKILYAAIEKLSLQ 840
QY 782 SLHVDAAIGSDGTTLECLDSISSPPPLRLTLVGLIEMENWIEQLTHLKKIYLLRSKL 841
DB 782 SLHVDAAIGSDGTTLECLDSISSPPPLRLTLVGLIEMENWIEQLTHLKKIYLLRSKL 900
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DB 783 SLVYNAALLSDIETLECLDSISSPPPLRLTLVGLIEMENWIEQLTHLKKIYLLRSKL 960
QY 784 KEGKTMILGALPNIMVLYHLYRNAYLGEKLVFKGAFPNLRTLWIELDQREIRFEEDGS 961
DB 784 KEGKTMILGALPNIMVLYHLYRNAYLGEKLVFKGAFPNLRTLWIELDQREIRFEEDGS 1020
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DB 785 SPLEKIEBIGCRLESIGITIIHLPKLEIPIRYGSKVAGLQGEVNAHPNRPVLIMY 1021
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DB 786 SDRYHDLGABAGSSISVQADPVPDAEGSVTVAAVEATDPLPEQBGSSQSQVITLTN 1080
QY 787 DSEETGTAQAG 1032
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RESULT 2
US-10-352-179-89
; Sequence 89, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 1031
; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-89

Query Match 93.5%; Score 4925; DB 15; Length 1031;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 976; Conservative 14; Mismatches 32; Indels 0; Gaps 0;

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DB 61 KDELKLVASQIRDLSDIEDSLDEFKVVHIESQTLFROLVKLRERHRIAIRHNLKSRVE 120
QY 121 EVSSNTRYSLVKPISSTGTEIDMSYAEDIRNOSARNVDAAELVGFSDSKRLLEMDTNA 180
DB 121 EVSSNTRYSLVKPISSTGTEIDMSYAEDIRNOSARNVDAAELVGFSDSKRLLEMDTNA 180
QY 181 ANDGPAKVICVVMGGLGKTALSRKIFESSEDIRKNPCNAWITVSQSFHRIELKDMIR 240
DB 181 ANDGPAKVICVVMGGLGKTALSRKIFESSEDIRKNPCNAWITVSQSFHRIELKDMIR 240
QY 241 QLLGPSSLDLLOELQOGKVQVHHLSYLLIEELKEKRYFVVLDLWILHDWNWINEIAPP 300
DB 241 QLLGPSSLDLLOELQOGKVQVHHLSYLLIEELKEKRYFVVLDLWILHDWNWINEIAPP 300
QY 301 PKNNKKGSRIVITTRNVDLAEKATASLVYHLDLQMDNDAILLLRKTNNKHEDMESKN 360
DB 301 PKNNKKGSRIVITTRNVDLAEKATASLVYHLDLQMDNDAILLLRKTNNKHEDMESKN 360
QY 361 MQKMWIRIVNKGGRPLAILITIGAVLATKHVSEWEKRYEQLPSELEINPSLEALRMMVTL 420
DB 361 MQKMWIRIVNKGGRPLAILITIGAVLATKHVSEWEKRYEQLPSELEINPSLEALRMMVTL 420
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DB 421 GYNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 480
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DB 601 LCHLKYSIGYSSSIYSLPRSIGKLOGLQTLNMESTYIAALPSEISKLOCLHTLRCTGQ 660
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DB 661 PHYNFSLNHPMKCITNTICLPKVFTPLVSRDDRAKQIAELHMATKSCWSEBSIGVKVPK 720
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DB 721 IGKLRDLQVLEYVDIRRTSSRAIKELGQSLKRLKGLVTTNGSTKCKKILYAAIEKLSL 780
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DB 781 QSLHVDAAIGSDGTTLECLDSISSPPPLRLTLVGLIEMENWIEQLTHLKKIYLLRSKL 840

Qy 841 LKEGKTMILGALPNLMVLYHLYRNAYLGEKLVFKTGAPPNLRTRLTWIYELDQLREIRFEDG 900
Db 841 LKEGKTMILGALPNLMVLYHLYRNAYLGEKLVFKTGAPPNLRTRLTWIYELDQLREIRFEDG 900
Qy 901 SSPLEKEIEGECRLSITGI IHLPLKKEIPRYGSKVAGLGQLEGVNAHPNRPVLJM 960
Db 901 SSPLEKEIEGECRLSITGI IHLPLKKEIPRYGSKVAGLGQLEGVNAHPNRPVLJM 960
Qy 961 YSDRRYHDLGAEAGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGSSQSQVITLTT 1020
Db 961 DSDRRHDLGAEAGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGSSQSQVITLTT 1020
Qy 1021 ND 1022
Db 1021 ND 1022

RESULT 3

US-10-437-963-139799
; Sequence 139799, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139799
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1.pep
US-10-437-963-139799

Query Match 83.5%; Score 4397.5; DB 16; Length 1531;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 862; Conservative 11; Mismatches 17; Indels 7; Gaps 3;
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Db 2 VASGNQSLAIDSVAEDIRNQSARNVDEAEVLGFSDSKKRLLEMDITNANDGPAKVICW 61
Qy 193 GMGGLGKTALSRKIFESEDIRKPPCNAMITVQSFPRIELDKMDIRQLGPSLQDLL 252
Db 62 GMGGLGKTALSRKIFESEDIRKPPCNAMITVQSFPRIELDKMDIRQLGPSLQDLL 121
Qy 253 QELQGVVVQVHHSEYLIELKERYFVVLDDLLWILDMNWNINEIAPPKNKKGSRIVI 312
Db 122 QELQGVVVQVHHSEYLIELKERYFVVLDDLLWILDMNWNINEIAPPKNKKGSRIVI 181
Qy 313 TTRNVDLAEKATASLVYHLDPLQWDAITLLLRKTNKHEDMESNKMQRQVRIYVNC 372
Db 182 TTRNVDLAEKATASLVYHLDPLQWDAITLLLRKTNKHEDMESNKMQRQVRIYVNC 241
Qy 373 GRPLAIIITIGAVLATKQVSEWEKRYEHLPSLEINPSLEALRRMTLGYNHLPSHLKPC 432
Db 242 GRPLAIIITIGAVLATKQVSEWEKRYEHLPSLEINPSLEALRRMTLGYNHLPSHLKPC 301
Qy 433 FLYLSIFPEDFEIKENRLVGRWIAEGFVRPKVGMTTKDVGESYNELINRSMIORSRGI 492
Db 302 FLYLSIFPEDFEIKENRLVGRWIAEGFVRPKVGMTTKDVGESYNELINRSMIORSRGI 361

Qy 493 AGKIKTCRIHDIIRDITVSISROENFVLLPMGDSGLVOENTRIHAFHGSMSCKTGLDWS 552
Db 362 AGKIKTCRIHDIIRDITVSISROENFVLLPMGDSGLVOENTRIHAFHGSMSCKTGLDWS 421
Qy 553 IIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLBDVTFLITQKDFRIALLCHLKVLSIGY 612
Db 422 IIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLBDVTFLITQKDFRIALLCHLKVLSIGY 481
Qy 613 SSSYISLPRSIGLQGLQTLNMPSTYIAALPSEISKLQCLHLTRLCIGQHYDNFSLNHPM 672
Db 482 SSSYISLPRSIGLQGLQTLNMPSTYIAALPSEISKLQCLHLTRLCIGQHYDNFSLNHPM 541
Qy 673 KCIITNTICLPKVPFPLVSRDRRAKQIAELHMAWTSCHSESGVGVKPGIGKRLQVLE 732
Db 542 KCIITNTICLPKVPFPLVSRDRRAKQIAELHMAWTSCHSESGVGVKPGIGKRLQVLE 601
Qy 733 VDIRTSSRAIKELGQSLKRLKLVTTNGSTKCKILYAAIEKLSLSQSLHVD---AG 789
Db 602 VDIRTSSRAIKELGQSLKRLKLVTTNGSTKCKILYAAIEKLSLSQSLHVDVLP 661
Qy 790 ISDGTLECLDSISSPPPLRLTLVDGILBEMPNIQLTHLKKIYLLRSKLKGGKTM 849
Db 662 II--GTLECLDSISSPPPLRLTLRLNGSLBEMPNIQLTHLKKIYLLRSKLKGGKTM 719
Qy 850 LGALPNLMVLYHLYRNAYLGEKLVFKTGAPPNLRTRLTWIYELDQLREIRFEDGSSPLLEKIE 909
Db 720 LGALPNLMVLYHLYRNAYLGEKLVFKTGAPPNLRTRLTWIYELDQLREIRFEDGSSPLLEKIE 779
Qy 910 IGECLRESGITGIHLPKLEIPRYGSKVAGLGQLEGVNAHPNRPVLLMYSDRRYHDL 969
Db 780 IGECLRESGITGIHLPKLEIPRYGSKVAGLGQLEGVNAHPNRPVLLMYSDRRYHDL 839
Qy 970 GAEAGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGSSQSQVITLTTNDSEEI 1026
Db 840 GAEAGSSIEVQTADPVPDAEGSVTVAVEATDPLPEQEGSSQSQVITLTTNDNRNL 896

RESULT 4

US-10-437-963-104966
; Sequence 104966, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 104966
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102251C.1.pep
US-10-437-963-104966

Query Match 69.6%; Score 3664.5; DB 16; Length 993;
Best Local Similarity 73.9%; Pred. No. 5e-266;
Matches 733; Conservative 76; Mismatches 122; Indels 61; Gaps 2;
Qy 1 MAETVLSMAKSLVGSALSKAASAADETSLLLGVKDIWIYKDELKTMQAPLRAELMKK 60
Db 60 MAETVLSMAKSLVGSALSKAASAADETSLLLGVKDIWIYKDELKTMQAPLRAELMKK 119
Qy 61 KDLELLKWAEBQIRLDSYDIEDSLDEFKVIHIESQTLFRQLVKLRERHRIATRIHNLKSRVE 120

Db 120 KDELKVAEQIRDSLYDIEDCLDEFKVHIESQNLFYQWVKLRKRHLIATQIRNLKSRVE 179
Qy 121 EVSSNTRYSLAVKPISSGTEIDMSYAEDIRNQSARNVDEALVGFSDSKRLLLEMDTN 180
Db 180 EVSSRNRYNLVVKPISSNEDMDCYAEDIRNQSTSNVDETELVGFSDSK----- 229
Qy 181 ANDGPAKVICVVGMGGLGKTALSARKIFESBEDIRKNPFCNAWITVSQSFHRIELKDMIR 240
Db 230 -----IRIELLKDMIR 240
Qy 241 QLLGPSSLDQLLOLQELQKVVVQVHHLSEYLIIEELKEKRYFVVLDDMLHDDWNNWINEIAP 300
Db 241 QFLGNSLSDQVLQELQKRVVQIPIHLSLYLKRKLKEKRYFVVLDDMLSLDAWNNWINDIAF 300
Qy 301 PKNNKGSRIIVITRNVDLAECATASLVYHDLFQWMDAITALLRKNKHEDMESNKN 360
Db 301 PKNNKGSRIIVITRDVGLAEKCTTSLVYHLEHLOWNDAITLLLRKTNRTHEDMGTNKN 360
Qy 361 MOKMVERIVNKCGRPLAAILTIGAVLATKQVSEWEKPYEHLPSLEINPSEALRRMVTL 420
Db 361 MOKIVEQV 420
Qy 421 GYNHLPKPCFYLKSIFFPEDFBIKRNRLVGRWIAEGFVRKPYGMMTKOVGESYFNELI 480
Db 421 GYNHLPKPCFYLKSIFFPEDFBIKRNRLVGRWIAEGFVRKPYGMMTKOVGESYFNELI 480
Qy 481 NRSMIQSRVGIAGKIKTCRIHDIIRDTIVSISIQENFVLLPMGDSGLVQENTRHIAFH 540
Db 481 NRSMIQSRVGIAGKIKTCRIHDIIRDTIVSISIQENFVLLPMGDSGLVQENTRHIAFH 540
Qy 541 GSKMCKTGLDWSIIRSLAIFGDRPKSLAHVCPQDLRMLRVLDLEDVTLTKQDFDRIA 600
Db 541 GSKMCKTGLDWSIIRSLAIFGDRPNLAHTTCSNKFMLRVLDLEDVTLTKQDFDRIA 600
Qy 601 LLCHLKYLSIG--YSSSTIYSLPRSIGLQGLQTLNMPSTYIAALPSEISKLOCLHLTRCI 658
Db 601 LLRLKYLKSGRIFSSCIYITLPRSIGLQGLQTLNMPSTYIAALPSEISKLOCLHLTRCT 660
Qy 659 GQFYHVNPSLNHPMKCINTTCLPKVFTPLVSRDDRAKQIAELHMATKSCWSESIGVKVP 718
Db 661 RVSNNNFNSINHPVKCLTNTMKNIFTNPSVSDNRAKQIAELHMATKSCWSESYKVP 720
Qy 719 KGIGKRLDQVLEVDIRRTSSRAIKELGQSLKRLGLVTNGSTKECKILYAAIEKLS 778
Db 721 KGIGKRLDQVLEVDIRRTSSRAIKELGQSLKRLGLVTNGSTKECKILYAAIEKLS 780
Qy 779 SLQSLHVDAAIGSDGTLCELDSSPPPLRLTLVLDGILEMPNWIQPLHLKXILYLR 838
Db 781 SLQSLHVDAAIGSDGTLCELDSSPPPLRLTLVLDGILEMPNWIQPLHLKXILYLR 840
Qy 839 SKLKEGKTMILGALPNLMVHLRYNAYLGEKLVKTCGAPFNLRITLWIELDQLEIRFE 898
Db 841 SKLKEGKTMILGALPNLMVHLRYNAYLGEKLVKTCGAPFNLRITLWIELDQLEIRFE 900
Qy 899 DGSSPLLEKIEIGRLESIGTGIHLPKLEIPIRYGSKVAGIQLGEVYNAHPNRPVL 958
Db 901 NDSSPLLEKIEIGRLESIGTGIHLPKLEIPIRYGSKVAGIQLGEVYNAHPNRPVL 960
Qy 959 LMYSDDRRYHDLGAEGSIEVQTDADVPDAE 990
Db 961 RMEEDRSCHDLRDGKGSVAWEATEPLPEPE 992

RESULT 5

US-10-437-963-143499
; Sequence 143499, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 143499
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1.pap
US-10-437-963-143499

Query Match 58.2%; Score 3068.5; DB 16; Length 974;
Best Local Similarity 62.9%; Pred. No. 3e-221;
Matches 611; Conservative 139; Mismatches 218; Indels 3; Gaps 3;

Qy 2 AETVLSWARSILVSAISKAASAAADETSLLIGVEKDIWYIKDELKTMQAFRAAELMKKK 61
Db 3 AETVSWMSVILGSAVGAASAAADEATLLGIGKEIWIYIKDELKTIQAFRAAAEVTCKK 62
Qy 62 DELLKWAEOIRDLSDYDIEDSLDEFKVHIESQTLFROLVKLRERHRIAIRIHNLSRVVE 121
Db 63 DDLKWAEOIRDLSDYDIEDSLDEFKVHIESQTLFROLVKLRERHRIAIRIHNLSRVVE 122
Qy 122 VSSRNTSYLVKPISS--GTEIDMSYAEDIRNQSARNVDEALVGFSDSKRLLLEMDTN 180
Db 123 VSNRNTSYLVKPISSITTEDRSDYLEDARNQSGSNTDESELVGFAKTKDELKLDVN 182
Qy 181 ANDGPAKVICVVGMGGLGKTALSARKIFESBEDIRKNPFCNAWITVSQSFHRIELKDMIR 240
Db 183 TNDGPAKVICVVGMGGLGKTTLARKAYENKHM-KNFSCCA WITVSQSFDRKEILKQVIR 241
Qy 241 QLLGPSSLDQLLOLQELQKVVVQVHHLSEYLIIEELKEKRYFVVLDDMLHDDWNNWINEIAP 300
Db 242 QLLGADSLDKLKEFSEKLVVQVHLDHVLVEGLKEKRYFVVLDDMLTIDAWNWIHDIAP 301
Qy 301 PKNNKGSRIIVITRNVDLAECATASLVYHDLFQWMDAITALLRKNKHEDMESNKN 360
Db 302 PKNNRGSRIIITRDAGLAGRCTSESIIYHLEPHLDDAIHLLAKTNIRLEDMDENED 361
Qy 361 MOKMVERIVNKCGRPLAAILTIGAVLATKQVSEWEKPYEHLPSLEINPSEALRRMVTL 420
Db 362 LGSIVTKLVKRCGYLPLAAILTIGGILATKIMWKGKPYRELPSLESNPSLEAMRRMVTL 421
Qy 421 GYNHLPKPCFYLKSIFFPEDFBIKRNRLVGRWIAEGFVRKPYGMMTKOVGESYFNELI 480
Db 422 SYNHLPSHLKPCFYLKSIFFPEDFBIQGRVLVDRWIAEGFVRATGVNIEDVGNSHFNELI 481
Qy 481 NRSMIQSRVGIAGKIKTCRIHDIIRDTIVSISIQENFVLLPMGDSGLVQENTRHIAFH 540
Db 482 NRSLIQPSKSVSTDGVVKRCRIHDIIMRDIIVSISREENFVLLTREKITVVAESIRHLAFH 541
Qy 541 GSKMCKTGLDWSIIRSLAIFGDRPKSLAHVCPQDLRMLRVLDLEDVTLTKQDFDRIA 600
Db 542 GSKCKIKLENNHLRSVTLFGDREVGRTPALCSQPFRLRLVLDLEDVTLTKQDFDRIA 601
Qy 601 LLCHLKYLSIGYSSSIYSLPRSIGLQGLQTLNMPSTYIAALPSEISKLOCLHLTRCIQ 660
Db 602 LLRHMKYLNFASTIITLPRSIGLQGLQTLNMPSTYIAALPSEISKLOCLHLTRCISR 661
Qy 661 FHYDNFS-LNHPMKCINTTCLPKVFTPLVSRDDRAKQIAELHMATKSCWSESIGVKVP 719
Db 662 SGSGYFSIIDNPKECLMITMCLPMVFLTSINFSRDKLIPICWCSCTRSWSDTKGVRVPR 721
Qy 720 GIGKRLDQVLEVDIRRTSSRAIKELGQSLKRLGLVTNGSTKECKILYAAIEKLS 779
Db 722 GIDNLKELQILEVVDINRTSRKAIEELGELIQLKLSVTTKGATNKKYQIFCAAIKELSS 781

Best Local Similarity 52.8%; Pred. No. 3.1e-177; Matches 520; Conservative 165; Mismatches 262; Indels 37; Gaps 12;	
Qy	40 YIKDELTKMOAFLRAAEIMKKKDELLKVAQIIRDLSDYDIEDSLDEPKVHIESOTLFRQL 99
Db	5 YIKDELTKMAFLRAAEVTEKDELBKVAQVDRDLAYDIECDUEFTIIRVHGQSLRQL 64
Qy	100 VKLRRHRIAIRIHNLSRVEVSRRTRYSLVKPISSGTEIDMSYAEIDRNSARNVD 159
Db	65 MKLRRHRIAVQIRSLRVQEVSNRNRYNFIKSAPSREMDDFSTNMWTRYQAAHYVD 124
Qy	160 EAEUVGSDSKRLLEMDITNANDGPAKVICVGMGGLGKTALSRKIFESEEDIRKNPPC 219
Db	125 EAKLVGDPGPKKILKMI-SGSEDEVQTIWIVGAGGLGKTTLAKKVYES-SNITSMFPC 182
Qy	220 NAWITVSQSHRIELLKMDITROLGSPSLDOLLOELQGVVQVHLSYIELIEELKEKRY 279
Db	183 RAWITVSQSFVMDLLKMDIKQLLGKESLDNLFYK-EVKIKENLUTDHLKELRNKRY 241
Qy	280 FVLVDDLWILHDMNWIENIAFPKNNKKGSRIVITTRNVDLAEKCATASLVVHLDLQWMD 339
Db	242 FLVLDDLKSTKANDCLKPTLW-GNNREGSRLVVTTRNDRDAEG-SSGPLVYPLQTLHRED 299
Qy	340 AITLLLRKTNKHEDMESNKNQKVRIRVKNKGRPLAILITIGAVLATKOVSEWEKPYE 399
Db	300 ATKLLAKTNKSLCDINKD-GMNETFEKILKKGGLPLAITITIGLLAAKQDVKEWDGLYA 358
Qy	400 HLPSELEINPSLEALRMVTLGYNHLPSHLKPCPLYLISIPPEDEFEIKRNLVGRWIAEGP 459
Db	359 QIPSELENNPFEVMRQALSYKPLPSHLKPCPLYLISIPPEDEFEIQRKRLVYRWIAEGF 418
Qy	460 VRPKVGTTKDVGSSYFNELINRMIORSRVGIAGKIKTKRHHDIIRDITVTSIRQENFV 519
Db	419 IRADGVSIVDVAKYFNDLINRSLMQPSRVNMEGTIKSCRVHDIIRDIMISIRBEKEFV 478
Qy	520 LLPMGSDSLVQENRTHIAFHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRML 579
Db	479 CRIDDKETCLMEENIHVAFYNSNSEIAMDINQVRSILTVGERHKELTPLLCSPQVRML 538
Qy	580 RVLDEDTVFLITOKDFDRIALLCILKYLST-----GYSSSIYSLPRSTCKLOGL 629
Db	539 RVLDFQGVRFQMTQKMDHIMVSLHLKYMNRICDYNLPNSSGY-SKIYRIPRSTCKLOGL 597
Qy	630 QTLNMPSTYIAALPSEISKLOLTCIGOFHYDNFSLNHPMKITNTICLPKVFPTLV 689
Db	598 RVLDSINTCITSLTEICELRSLNILRCTRKEYEFPDPSPKIQCLFALSCIP-VTWALA 656
Qy	690 SRDRAKQIAELHMATKSCWSESIGVKVPKGIGKRLDLQVLEYVDIIRTSRAIKELGOL 749
Db	657 DSDQRHEITAEHLMACSTRWPTCGVRVPMRIGNLKLQELGYVDIRLTSKAVKELGEL 716
Qy	750 SKLRKLGVTNTGSTKECKILYIAIEKLSSLOSLHVDAAAGISDGGTLECLDSISSPBL 809
Db	717 SOLKKRLRINGATQRCVKVLEAKIEKLSSLOSLRINAFDVSLLRNLEWLHYTSSPPFL 776
Qy	810 RTLVDGTLBEMPNWIEQTLHKYILLRSLKSGKTMILGALPNLMVLHLYRNAYLGE 869
Db	777 KNLTLEGCKEI-DWLRFEFTHLVKHLFGSKLKGKTVQILGELPNLMVLQLRWAGVGV 835
Qy	870 KLVFKTGAPPNLRLTWIYELDQLREIRPEDGSSPLLEKIEIGECRLSESGITGIHLPKLK 929
Db	836 KLLFRAEAFPKRLKLEIRFLEDREMRFEERTSPQMETIEISHCRLESSGIIGIKHLPKLK 895
Qy	930 EIPTRYGSKVAGLQLEGEVNAHNPVRVLLMYSDRRVHDLGAEABGSSIEVQTADPVDDA 989
Db	896 EISLRWNCVEARLQGLLEEVKANPNRPVLLLYNDPSKHDLGDTQEGSG----- 943
Qy	990 EGSVTVAEATDPLPEQEGESSQS 1013
Db	944 -----TPVEANEP-PKNVGESSQS 961

US-10-352-179-91 ; Sequence 91, Application US/10352179 ; Publication No. US20040006788A1 ; GENERAL INFORMATION: ; APPLICANT: Wang, Guo-liang ; APPLICANT: Liu, Guifu ; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Plant ; FILE REFERENCES: 22727/04108 ; CURRENT FILING DATE: 2003-01-27 ; PRIOR APPLICATION NUMBER: 60/352,179 ; PRIOR FILING DATE: 2002-01-25 ; NUMBER OF SEQ ID NOS: 97 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 91 ; LENGTH: 1054 ; TYPE: PRT ; ORGANISM: Oryza minuta US-10-352-179-91	
Query Match 44.9%; Score 2367; DB 15; Length 1054; Best Local Similarity 50.3%; Pred. No. 1.8e-168; Matches 516; Conservative 149; Mismatches 266; Indels 94; Gaps 22;	
Qy	1 MAETVLSMARSLVGSIAISKAASAAADETSLLLGVEKDIIWIKDELTKMQAFLRAEALMKK 60
Db	1 MADTVLSIAKSLVGSVSKVASVAADKMIILGLVQKEIWFIKDELQTIQAFLIAAE-ASK 59
Qy	61 KDELKVAQIIRDLSDYDIEDSLDEPKVHIESOTLFRQLVKLRRHRIAIRIHNLSERVE 120
Db	60 KSTLLKVVQVQVRDLSDYDIEDCLDEFTVHVGSQNLKMLKDRHRIAIQIRNLRTIE 119
Qy	121 EVSSRNTRYSLVK-PISSGTEIDMSYAEIDRINQSRARNVDEAEUVGSDSKRLLEMDIT 179
Db	120 EVSTRNRYNLIENDLTCTTTDERNLFMEDIRNQ-ANNIEADLVGSGPKRELLDLIDV 178
Qy	180 NANDGPAKVICVVMGGLGKTALSRKIFESEEDIRKNFPCNVAMITVSQSHRIELLKDMI 239
Db	179 HANDGPTKVVVGMGGLGKTTIARKIYESKEDIKKNFSCCAWITVSQSFVRVELLKDL 238
Qy	240 RQLLGPSLLDQLLOELQGVVQVHLSYELIEBELKEKRYFVLDLWILHDMNWIENIA 299
Db	239 VKLFGEEVLKKRLRELEGK-VPQVDDLASYLRTLNERRYFVLDNVMSTDSWKWINSIA 297
Qy	300 FP-KNNKKGSRIVITTRNVDLAEKCATASLVVHLDLQWMDAITLLLRKTNKHEDMESN 358
Db	298 FPRNNKNGSRVITTRDVGTLKETSSELIYQLPLEINYAKELLRKANKAIGDNESD 357
Qy	359 KNNQKVRIRVKNKGRPLAILITIGAVLATKQVSEWEKPYEHLPSLEINPSLEALRMV 418
Db	358 K-MSDITTKIKKCGYLPLAILITIGVLTSTKEIREWETFYSQIPSELESNPNLEAMRRIV 416
Qy	419 TLGVNHLPSHLKPCFLYLISIPPEDEFEIKRNLVGRWIAEGFVRPKVCMWTYKDVCESYNE 478
Db	417 TLSYNLPSHLKQCFLYLSIPPEDEFEINRNLNVRNMAEGFIKARTNMTTIEDVGSYFKE 476
Qy	479 LIRNSMIQRSGVIGAKIKTKRHHDIIRDITVTSIROENFVLLPMGSDSLVQENRTHIA 538
Db	477 LIRNSMIQPSRAGIRGDFKRCRVHDIRDITIISIREENFTLLPDGTDYDVVHGNTRHIE 536
Qy	539 FHGSMSC-KTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDELTFFLTOKDFD 597
Db	537 FHGSKYCSFSLDWSIIRSLTMFGERSVELEHSVCCSSQLRMLRVLDTDAQFSITQNDVD 596
Qy	598 RIALLCHLKLYLSTG-----YSSSIYSLPRS-----ICKLQGLQTLNMPSTYIAALPS 644
Db	597 NIVLLCHLKLYLCIKIQQIPFTIYLTFTSTIHSTAWSADIGLGSVDHFNTAN--SDY----- 648
Qy	645 EISKLOCLHTLCIGQPHYDNFSLNHPMKITNTICLPKVFPTPLVSRDDRAKQIAELHMA 704
Db	649 -----LRSRLRCMKWEYFSSSLFTT-----LTNTLCULPMIFTFPVSTSDRSETTAKUHMA 699
Qy	705 TKSCWSESIGVKVPKGI-----GKLRDLQVLEYVDIRTSRAIKELQGLSKRLKLGVTTN 760

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 177336

; LENGTH: 812

; TYPE: PR1

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_74999C.1.pap

US-10-437-963-177336

Query Match 35.7%; Score 1878.5; DB 16; Length 812;

Best Local Similarity 45.2%; Pred. No. 6.1e-132; Indels 265; Gaps 20;

Matches 450; Conservative 88; Mismatches 193; Indels 265; Gaps 20;

Qy 48 MQAFRAAELMKKDELKQWAEQIRLSYDIEDSLDEFKVHIESQTLFROLVKLRERHR 107

Db 1 MQAFRAAEVMMKKDELK-----LVKLRERHR 28

Qy 108 IAIIRHNLKSRVEEVSRRNTRYSLVKPISSCTEIDMSYAEIDRQSNRVDEALVGFS 167

Db 29 IAIIRHNLKSRVEEVSRRNTRYNLVEPISSCTEDDMSYAEIDRQSNRVDEALVGFS 88

Qy 168 DSKRRLLEMDITNANDGPAKVICVVGGLGKTALSRKIFESBEDIRKNFPCNAWITVSQ 227

Db 89 DSKRRLLEMDITNANDGPAKVICVVGGLGKTALSRKIFESBEDIRKNFPCNAWITVSQ 148

Qy 228 SFHRIELKDMIRQLGSSLDQLLQELQGVVQVHLSYLLIEELKEKRYF-VVLDDL 286

Db 149 SFHRIELKDMIRQLGSSLDQLLQELQGVVQVHLSYLLIEELKEKRNFSVVGRL 208

Qy 287 WILDHWNINIAEPKNNKSGSRVITTRVNDLAEKATASL-----VHLD----- 333

Db 209 IHFRFOQLSTVSLPLDLPALPPKLTGVCAAAARTSATGRLELGIITGIHLPRLKEISL 268

Qy 334 -----FLQWDAI-----TLLLRKTNKHEDMESKNM-----QKQVERIVNKKCR- 374

Db 269 EYRSKVAPFAQLEGEVCAHPKHPVLOMEDRSYRDLGRHSSWFQVIISSSIGISGRP 328

Qy 375 -LPLAI-----LTIGAVLATKQVSEWEKFEYHLPSELEINPS 410

Db 329 WLPASVAPSGADLRRLHPLFSIASQLPAPRMSEACVHGREDIEWEILLYAQLPSELGCPNS 388

Qy 411 LEALRWMTLYGNHLPKHLKCFLYLSIFPDEFKRNRLVGRWIAEGFVPPKVGMTYKD 470

Db 389 LAAMKVVVALSYNLPKSHVKPCFLYLCIFPDEFQVQKRLVHRWIAEGFVRAK----- 441

Qy 471 VGESYFENELINRSMIQRSRVGIAGIKTKCRTHDIIRDITVSIQRQENFVLLPMGDSDLV 530

Db 442 GGEFWND-----

Qy 531 QENTRHIAFHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFL 590

Db 453 -----

Qy 591 ITQKDFDRIALLCHLYLSIGYSSSIYSLPRSIGKLGLOTLNMPSTVIAALPSEISKLQ 650

Db 453 -----LRKELPPFQ 461

Qy 651 CLHTLRCITGQHYDNFSLNHPMKCTNTICLPKVTPLVSRDRRAKQIAELHMAKCSWS 710

Db 462 YLGRDRRGSY-YLDDTNRKERVILS-CIPLIMA-LSDSDNHRRLITDLHTGCSSHHW 518

Qy 711 E-SIGVKVPKIGIKRLDQVLEYVDIRRTSSRAIKELQGLSKRLKGLVYTTNGSTKECKI 769

Db 519 RIKDGRVPRGIGNLRLKVLVEIVDIAVTDKSAIQELGELNQLRKLSVMTKGSNNKKCKI 578

Qy 770 LYAAIEKUSSLOSLHVA-AGISDGGTLECLDSSPPPLRLTLVLDGILEMNPWIBQL 828

Db 579 LCAAIEKLTSPKSYVDGDHGYSLDGTLECLDSISHPPS-LKSLRLKGCIKETPNWFREL 637

Qy 829 THLKKIYLLRSKLLKEGKTMILGALPNLMVLHLRYNAYLGEKLVFKTGAFPNLRLTWIYE 888

Db 638 KHLVKIYLYKSHL-NGDTMEILGELHNLMDLHFRWYAYVGEKLVFIEGAFQNLRLKLVVET 696

Qy 889 LDQLREIRFEDGSSPLEKTEIGECRLSEGTGIIHLPKLKEIPRYGSKVAGLGQLEGE 948

Db 697 EDKLRVRFEBGTSPOQEWIEICHCELISGIVGVKHLPRLKEIGLK-SAKVARLGQLEGE 755

Qy 949 VNAHNPRLVLLMYSRRYHDLGAEAGSGSEVQTAD 984

Db 756 VDTNPRLILRLSEKRSYHDLG-ETHVSVEVEVAD 790

RESULT 14

US-10-352-179-95

; Sequence 95, Application US/10352179

; Publication No. US20040006788A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Guo-liang

; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla

; CURRENT APPLICATION NUMBER: US/10/352,179

; PRIOR FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/352,106

; PRIOR FILING DATE: 2002-01-25

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 95

; LENGTH: 451

; TYPE: PR1

; ORGANISM: Oryza minuta

US-10-352-179-95

Query Match 26.3%; Score 1384; DB 15; Length 451;

Best Local Similarity 51.6%; Pred. No. 3.5e-95;

Matches 281; Conservative 73; Mismatches 93; Indels 98; Gaps 3;

Qy 1 MAETVLSMARSLSGSAISKAAADETSLLLGYEKDIWIYKDELKTMQAFRAAELMKK 60

Db 1 MADTVLSIAKSLGSAISKVASVAADKMLLLGVQKINFIKDELOTIOAFPLMAE-ASK 59

Qy 61 KDELKQWAEQIRLSYDIEDSLDEFKVHIESQTLFROLVKLRERHRIATRIHNLKGRVE 120

Db 60 KSILLKVVQVQVRLSYDIEDCLOEFTVHVSQTLRQLMKLKDHRHIAVQIRNLRTIE 119

Qy 121 EVSSRNTYSLVKPISSCTEIDMSYAEIDRQSNRVDEALVGFSDKRLEMDITN 180

Db 120 EVSSRNTYSLNIENDLTSTTGERNFIMEDIRNESANNIEAEALVGFSGPKRELLDLIDVH 179

Qy 181 ANDGPAKVICVVGGLGKTALSRKIFESBEDIRKNFPCNAWITVSQSFHRIELKDMIR 240

Db 180 AKOGFTKVCVVGGLGKTALSRKIFESBEDIRKNFPCNAWITVSQSFVRLLELLKDLV 239

Qy 241 QLLGFSLDQLLQELQGVVQVHLSYLLIEELKEKRYFVVLDDLTLHDDWNWINEIAP 300

Db 240 KLFEEVLYKKELRELECK-VQVDDLASYLATLERNERRYFVLLDDVWSTDSWKWINSIAF 298

Qy 301 PKNKKGSRVITTRVNDLAEKATASLVYHLDLQWMDAITLLLRKTNKHEDMESKN 360

Db 299 PRNNKSGSRVITTRVNDLAEKATASLVYHLDLQWMDAITLLLRKTNKHEDMESKN 358

Qy 361 MQKQVERIVNKKCGRLPLAILTIGAVLATKQVSEWEKFEYHLPSELEINPSLEALRRMVTL 420

Db 359 MSDIITKIVKCGVLPAILTIGAVLATK----- 387

Qy 421 GYNHLPKPCFLYLSIFPDEFKRNRLVGRWIAEGFVPRKVGMTTKDVGESYFENLI 480

Db 388 ----- 387

Qy 481 NRSMIQSRVGIAGIKTKCRTHDIIRDITVSIQRQENFVLLPMGDSGLVQENTRHIAFH 540

Db 388 -----DPSRAGVRGEFKSCRIHDIRDIAISIREENFIILPEGTDYDVVHGNTRHIAFH 442

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 22:05:35 ; Search time 8457.77 Seconds
(without alignments)
17170.053 Million cell updates/sec

Title: US-10-656-394A-11
Perfect score: 2997
Sequence: 1 atggcgagacggtgctgag.....tgctactggtccagcatga 2997

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgc.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2655	88.6	138870	8 AP005659	Oryza sat
2	1495.2	49.9	3890	8 AK067966	Oryza sat
3	1403.6	46.8	122193	2 AP006053	Oryza sat
4	1225.2	40.9	3231	8 AK121397	Oryza sat
5	1040.8	34.7	3457	8 HVU507094	Hordeum v
6	987.6	33.0	147363	8 AP003487	Oryza sat
7	986	32.9	4326	8 AK120452	Oryza sat
8	946.6	31.6	176979	8 AP001168	Oryza sat
9	696.6	23.2	4248	8 AK070885	Oryza sat
10	405.4	13.5	2015	8 AK071029	Oryza sat
11	250.8	8.4	564	8 HVU506137	Hordeum v
12	202.2	6.7	4001	8 AB013451	Oryza sat
13	202.2	6.7	4030	8 AK065693	Oryza sat
14	196.6	6.6	4949	8 AK101823	Oryza sat
15	196.4	6.6	2294	8 AK065372	Oryza sat
16	191	6.4	145018	8 AP005828	Oryza sat
17	191	6.4	146775	8 AP007223	Oryza sat
18	177.2	5.9	95612	2 AP003862	Oryza sat
19	177.2	5.9	150761	8 AP004592	Oryza sat

20	176.6	5.9	543	8 AF186640	Sorghum b
21	175.4	5.9	164819	8 AC114983	Oryza sat
22	175	5.8	149697	8 AC109832	Oryza sat
23	174.8	5.8	3819	8 AK073612	Oryza sat
24	174.4	5.8	3329	8 AK103886	Oryza sat
25	169	5.6	3353	8 AK065775	Oryza sat
26	168.2	5.6	117860	8 AP004648	Oryza sat
27	167.8	5.6	149400	8 AC121327	Oryza sat
28	167.8	5.6	168063	8 CNS07YQ8	Oryza sat
29	167.4	5.6	2576	8 AK073176	Oryza sat
30	166.2	5.5	3255	8 AK119293	Oryza sat
31	166	5.5	2947	8 AK101707	Oryza sat
32	163	5.4	168063	8 CNS07YQ8	Oryza sat
33	161.8	5.4	3185	8 AK064889	Oryza sat
34	161.2	5.4	386	8 TVE249947	Aegilops
35	161	5.4	106970	2 AC124968	Medicago
36	160.2	5.3	4001	8 AK066020	Oryza sat
37	157.6	5.3	183990	8 AF114171	Sorghum b
38	156.4	5.2	144207	2 AC120530	Oryza sat
39	156.4	5.2	180999	8 AC137924	Oryza sat
40	156.4	5.2	197516	8 AC146948	Oryza sat
41	156.2	5.2	100294	8 AP003840	Oryza sat
42	155.8	5.2	170228	8 AP005829	Oryza sat
43	155.6	5.2	123847	8 AC138002	Oryza sat
44	154	5.1	3378	8 AK066779	Oryza sat
45	154	5.1	3534	8 AK103311	Oryza sat

ALIGNMENTS

RESULT 1
LOCUS AP005659 138870 bp DNA linear PLN 09-APR-2004
DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6, PAC clone:P0649C11, complete sequence.
ACCESSION AP005659
VERSION AP005659.2 GI:46309315
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0649C11
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 138870)
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
COMMENT (E-mail:tsasaaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Apr 8, 2004 this sequence version replaced gi:22415844.
The orientation of the sequence is from SP6 to T7 of the PAC clone.
FEATURES
source
Location/Qualifiers
1. 138870
/organism="Oryza sativa (japonica cultivar-group)"
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/cultur="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
/clone="P0649C11"

ORIGIN

Query Match 88.6% Score 2655; DB 8; Length 138870;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 2853; Conservative 0; Mismatches 10; Indels 172; Gaps 2;

Db	58211	TACTTATTGAGGACCAACTAAAGGAGTTAAACCATGCTGATCTTGGGGCATTCGCC	58270
Qy	2338	AACCTCATGGTCTTGATCTTTATTCGGAAGCTTACCTTGGGGGAAGCTAGTATTCAAA	2397
Db	58271	AACCTCATGGTCTTGATCTTTATTCGGAAGCTTACCTTGGGGGAAGCTAGTATTCAAA	58330
Qy	2398	ACAGGAGCATTCGCCAAATCTTAGACACTTTTCGATTTCAGATTTCGGATCAGCTAAGAG	2457
Db	58331	ACAGGAGCATTCGCCAAATCTTAGACACTTTTCGATTTCAGATTTCGGATCAGCTAAGAG	58390
Qy	2458	ATTAGATTGAGGACGCGAGCTCGCCCGAGTTGGAAAGATAGAAATCAGATTCTGCAGG	2517
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Qy	2518	TTGGAATCAGGATATTATGGTATTATTCACCTTCCAGGCTCAAGGAGATTCTCTGGA	2577
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Qy	2578	TACGAAAGTAAAGTGGCGCTTGCTCAGCTGGAGGAGAGTGGCCACACACCCCAAT	2637
Db	58511	TACGAAAGTAAAGTGGCGCTTGCTCAGCTGGAGGAGAGTGGCCACACACCCCAAT	58570
Qy	2638	CACCCCGTCTGCGAAAGAGGAGGACCGAAGTGTATCACGACCTTGCTTGTGAGCGCCGA	2697
Db	58571	CACCCCGTCTGCGAATGAGGAGGACCGAAGTGTATCACGACCTTGCTTGTGAGCGCCGA	58630
Qy	2698	GGATCCCTGTTGAAGTGAAGCAACGGATCCCTCCAGAGCAGGAGGAGAGCTCG	2757
Db	58631	GGATCCCTGTTGAAGTGAAGCAACGGATCCCTCCAGAGCAGGAGGAGAGCTCG	58690
Qy	2758	-----	2757
Db	58691	CAGGTGATCAGTTGACGTGCAACAACAGGTCAGTCACTCCCTATATGCGCAGCTTAATTA	58750
Qy	2758	-----	2757
Db	58751	ACTTGTTCAAATATCTTTTGTTCAGTATTAGGATCGGGTATATCGATGATTCAAA	58810
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Qy	2783	GCTGGTTTATCAAGTATGATCTCTCTCCATTCGATTCGATTCGCTGCTCTCTCTCT	2842
Db	58871	GCTGGTTTATCAAGTATGATCTCTCTCCATTCGATTCGATTCGCTGCTCTCTCTCT	58930
Qy	2843	CGCGCTGGCACACTCGCTGTTCCGAGAGGGGTGCTGATCTAAGGAGGCTTCCACTTT	2902
Db	58931	CGCGCTGGCACACTCGCTGTTCCGAGAGGGGTGCTGATCTAAGGAGGCTTCCACTTT	58990
Qy	2903	CTTCAATTGCGTCTCAGCTCTCGATTCTTCCCTCTCGGGTATGAATTGTTTCAATCTGA	2962
Db	58991	CTTCAATTGCGTCTCAGCTCTCGATTCTTCCCTCTCGGGTATGAATTGTTTCAATCTGA	59050
Qy	2963	CTTTTCTCGTATGCTACTGTTTCAGCATGA	2997
Db	59051	CTTTTCTCGTATGCTACTGTTTCAGCATGA	59085
RESULT 2			
AK067966			
LOCUS	AK067966	3890 bp	linear
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:J013122117, full insert sequence.		
ACCESSION	AK067966		
VERSION	AK067966.1	GI:32977984	
KEYWORDS	FLI_CDNA; CAP trapper.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
REFERENCE	1		

AUTHORS

The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narioka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Kikuchi, T., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kuwamori, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

TITLE

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
22752273
12869764

REFERENCE

AUTHORS

2 (bases 1 to 3890)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kobayashi, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuura, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narioka, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Oka, Y., Otono, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

TITLE

JOURNAL

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp)
Tel:81-29-838-7007, Fax:81-29-838-7007
This clone is one of the 28K full-length cDNA clones from japonica rice.

COMMENT

URL : <http://cdna01.dna.affrc.go.jp/cdna/>
NTAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.
FAIS Genome Sequencing & Analysis Group: Otono, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narioka, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hiraoka, T., Hori, P., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,

Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.		Location/Qualifiers	
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Matches 1985; Conservative		0; Mismatches 678; Indels 33; Gaps 5;	
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Db	684	TGGGTTTTCTTGGACCCAAAAGAGAGTTGCTTGATCTTATAGATGTCCATGCCAATATCG	743
Qy	326	GTCCGGCCAAAGGTAATCTGTGTTCTTGGGATGGGTGTTTAGGCAAGACAGCTCTTTTCGA	385
Db	744	GACCTACAGAAAGTCGTATGTGTGCGTATGGGTGGTGGGTGAAGACTACTATTTCGAA	803
Qy	386	GGAAAGATCTTTGAAAGCGAAGAACATTAAGGAAGAACTTCCCTTGCATCTTGGATTA	445
Db	804	GGAAAAATTTATGAAGCAAGAGGACATTCGAAAGAAATTTTCTGTGCTGTTGGATTA	863
Qy	446	CAGTGTCACAAATCTTTACAGGATGAGCTACTTAAAGATATGATAGCCCACTTCTTG	505
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Qy	506	GCCCCAGTTCTCGGATCAACTCTTCGAAAGATTCGAAAGGAGGTGGTGGTCAAGTAC	565
Db	924	GAGAGGAAGTACTGAGAGCGAGATGAGAGAACTCGAAGGGAA---GGTCCACAGTAG	980
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Db	981	ACGACCTCGCAGCTACCTCAGGACAGATTAATGAAGAGGAGTACTTTGTTGTGCTTG	1040
Qy	626	ATGATCTATGGAATTTTACATGATGGAATGGATTAATGAAATTCGCAATTTCCCTAAGAACA	685
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Qy	1583	GCCACTTGAATACTCTGAGTATTGGAT-----ATTGTCATTCATTAATTAATCACTTC	1633
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Qy	1634	CCAGATCCATTTGTAAACTACAGGGCTTACAAACTTTTGAACATGCCGAGACATACATATG	1693
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Db	2181	ATAATGATTTTCTTCTTT-----CACAAATGTTTAACTGACACATTTGT	2225
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Db	2286	ACTTGCACTTGGCCACCAAGCTTCGTTTCAAAATCAAAATGGCGGTCAAGGTACCAAAAG	2345
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Qy	866	TGGTTGAACGAATTGTATAAATAAATGTGTGTCGTCTACCAATTAGCAATACTTACAATTAGGAG	925
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Qy	926	CTGTGCTTGCAACTAAACAGAGTGTGAGAAATGGGAGAAATTTCTATGAAACACCTTCCTTCAG	985
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Qy	986	AACTAGAAATAAACCAGCTGGAAGCTTTTGAGGAGAAATGCTGAGCAATCTAGTTCACAACC	1045
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Qy	1046	ACCTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTCTCGAGGATTTTG	1105
Db	107963	ACTTGCCATCTCATCTTAAGCAATGCTTTTGTATCTAAGCATACTTCTCGAGGATTTTG	107904
Qy	1106	AAATCAAAAGAAATGCTCTAGTAGATGATGATAGCAGAGAGGGTTGTTAGACCAAGG	1165
Db	107903	AAATTAATAGGAACCGTCTGGTAAATAGATGATGAGAGGGGTTTATTAAGCTAGG	107844
Qy	1166	TTGGGATGACCACTAAGGATGTCGAGAGAAAGTTACTTTAATGAGCTAATCAACCGAAGTA	1225
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Qy	1226	TGATTCACCACTCAAGAGTGGGCATGACGAGGAAATTAAGACTTGTGCAATTCATGATA	1285
Db	107783	TGATTCAGCCATCAAGACGGGTGTACGAGGAGAGTTTATAGATTGTGAGTCCATGATA	107724
Qy	1286	TCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATTTGTTACCAATGG	1345
Db	107723	TAAATGCGTGATTAACAATTTTCTGATTTCTAGAGAGGAAAAATTTGTATTTCTTACCTAGG	107664
Qy	1346	GAGATGGCTCTGATTTAGTTTTCAGGAAACACCTCGCCACATAGCATTTCCATGGGAGTAGT	1405
Db	107663	GCATCGACTATGAAGCAGTACAGGGGAACACTCGGCCACATAGCATTTTTCAGGGAGTAGT	107604
Qy	1406	CCTGC---AAAACAGGATTTGAGTTGGAGCATTTATTCGATCATTTAGCTATTTTGTGTCACA	1462
Db	107603	ATTGCTCTAAGATAAGCTTTGACTGGAGCATTTATACGGTCATTAATATGTTTGGCCGAGA	107544
Qy	1463	GACCCAGAGTCTAGACATGCAAGTTGTCAGATCAATTTGAGGATGTTACGGGCTCTGG	1522
Db	107543	GGCCGTTAGAACTAGAGCAATTCAGTTGTTCTATCTCAGTTGAGGATGTTACGGGCTCTGG	107484
Qy	1523	ATCTTGAAGATGTGACATTTCTAATCATCTCAAAAAGATTTTCGACCGTATTCGATTTGTTGT	1582
Db	107483	ATCTTAAGAGATGCAAAATTTACTATCACACAAAATGATGTCAACAAATATAGTGTCTTGT	107424
Qy	1583	GCCACTTGAATACTTTGAGTATTTGGA-----TATTTGTCATCCATATATTCACATTC	1633
Db	107423	GCCACTTGAATACTTAGCATTTGCAGATACAAATATGTCATCATATTTACTCACATTC	107364
Qy	1634	CCAGATCCATTTGGTAAACTACAGGGCTTACAACTTTGAACATGCGGACGACATACATG	1693
Db	107363	CAAAATCCATAGGAAGACTGGATGCTGCGACATTTGGACTTTGGATTTCGACGAAACATTT	107304
Qy	1694	CAGCACTACCAAGTGAGATCAGTAAACCTCCAATGTCGTGCACTACTCTTCGTTGTAGTAGNA	1753
Db	107303	CAACACTGCCAACTCAGATTAATCTAAGCTTCGAGGCTCTCGGAGCCCTTAGTCATGAAGC	107244
Qy	1754	AGTTTGTTCGACAACTTTTATGCTTAACCCCAATGAAGTGATCACTAACAACAATAT	1813
Db	107243	AATATGATTTTCTTCTTCAC-----AACATGTTTAACTGACATATGTT	107199
Qy	1814	GCCTGCCCTAAAGTATTTCAACCTTTAGTTAGTCGCGATGATCGTGCAATACAAATTCGCTG	1873
Db	107198	GCCTGCCCATGATATTCAACCTTCGGTTAGTACCTCTGATCGTCTGAAGAAAAATTCCTA	107139
Qy	1874	AATTGCACATGGCCACCAAAAGTTGCTCGGTATAAATCAATTCGGTGTGAAGGTACCCAAAG	1933
Db	107138	ACTTGCATTCGGCCACCAAAAGCTTTCGGTTCAAAATCGCCGTCAAGGTACCAAAAG	107079

Qy	1334	GAATAGGTAACTTGGGAGACCTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCAAGTA	1993
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Qy	1994	GTAGAGCAATCAAAGAGCTGGGCGAGTTAAAGCAAGCTCAGGAAAATTAGGTGTGATGACAA	2053
Db	107018	GTAGAGTATATAAAGAGTTTGGGCGAGTTTAGCAAGCTGAGGNACTATATGTGTGTAAANA	106959
Qy	2054	ATGGCTCGACAAAGGAAAATGTAAAGATATCTTTGTGACCCATTTGAGAAGCTCTCTTCCC	2113
Db	106958	AGGCACTCTACAAAGTTTAAATGTGAGATCTATACAGCCATCCAGAAGCTCTATTCCC	106899
Qy	2114	TCCAAATATCTATGTGAATCTCTCAGAAATCTCAGATGGTGGAAACATTTGAGTGCCTAG	2173
Db	106898	TACAAATCTCTCCATATGGATCTGTGGGATGGCAGAGTATTGGAAACATTTGAGTGCCTAG	106839
Qy	2174	ATTCATATTCCTCTCTCTCCCTACTCTGAGGACACTCGTGTGTGATGGAAGTCTTTGAAG	2233
Db	106838	ATTCGTGTTTCATCGCCTCTCTCCCTATTGAGGACACTCAGGTTGAAATGGAAGTCTTTGAAG	106779
Qy	2234	AGATGCCCTAACTGGAAATGAGCAGCTCACTCACTGAAGAAGATCTACTATTTTGAGGAGCA	2293
Db	106778	AGTTGCCCTAACTGGAAATGAGCGGCTCACTCACTGAGGAAATTTCTACTATTTTGAGGACCA	106719
Qy	2294	AACTAAAGGAGGTAAACCAATGCTGATCTTTGGGGCAATGCCCCAACCTCATGCTTCTTC	106559
Db	106718	AACTAAAGGAGGTAAACCAATGCTGATCTTTGGGGCAATGCCCCAACCTCATGCTTCTTC	106599
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Db	106658	ATTTTGTGCACAATGCTTACCTCTGGGGAGAAAGTTAGTATTCAAAAACAGGAGCAATCCCAA	106599
Qy	2414	ATCTTAGAACACTTTTCGATTTTACGATTTGGATCATCTAAGAGAGATTTAGATTTGAGGAGC	2473
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Qy	2474	GCAGCTGCCCCAGTTTGGAAAGATAGAAATCAGATTTCTGACAGTTTGGAAATCAGGGAATTA	2533
Db	106538	GCAGCTACCCCAATTTGGAAAGATAGAAATAGGCAGGTGCAGATTTGGAAATCAGGGAATTA	106479
Qy	2534	TTGGTATPATCCACTTCCAAAGGCTCAAGGAGATTTCACTTGGATACGAAAGTAAAGTGG	2593
Db	106478	TTGGTATCATTTCACTTCCAAAGGCTCAAGGAGATTTCACTTGGTGAATACAAAGTAAAGTGG	106419
Qy	2594	CTGGGCTTGCTCAGCTGGAGGGAGAGTGCACACACCCCAAAATCACCCCGTCTGCGAA	2653
Db	106418	CGATGCTTGCTCAGCTGGAGGGAGAGTGAACGCACACCCCAAAATGTCCTCGTCTGCGAA	106359
Qy	2654	AGAGGGAGGACCGAAGTGATCACGACCTTGCTTGTTGAGCGCGGAAGGATCCCCCTGTTGAAG	2713
Db	106358	TGGCAATGGACCGAAGTGATCACGATCTTGCTGGCAACGCCCAAGGATCTCCTCCCTAAG	106299
Qy	2714	TGGAAG	2719
Db	106298	CAGGAG	106293

RESULT 4	
AK121397	
LOCUS	3231 bp mRNA linear PLN 29-OCT-2003
DEFINITION	<i>Oryza sativa</i> (japonica cultivar-group) cDNA clone.J02313G18, full insert sequence.
ACCESSION	AK121397
VERSION	AK121397.1 GI:37991020
KEYWORDS	FLI_CDNA; CAP trapper.
SOURCE	<i>Oryza sativa</i> (japonica cultivar-group)
ORGANISM	<i>Oryza sativa</i> (japonica cultivar-group)
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
	Ehrhartoideae; Oryzeae; <i>Oryza</i> .
REFERENCE	1
AUTHORS	The Rice Full-Length cDNA Consortium, National Institute of
	Agrrobiological Sciences Rice Full-Length cDNA Project Team;

Qy	984	AGA - ACTAGAAATAAACCCAAAGCCTCGGAAGCTTTGAGGAGAATGGTGACCCCTAGGTTACA	1042
Db	1257	AGAGGCTTGAGAGCAATCCAAAGCCTAGAACCATGAGGAGGATGGTGACCTAAGCTACA	1316
Qy	1043	ACACCTACCATCCCATCTGAACCATGCTTTTGTATCTAAGTATCTTTCTCTGAGGATT	1102
Db	1317	ATCACTTACCATTCTCATCTTAAACCAATGCTTTCTTTTACCTTAAGTATTTTCCCTGAAGATT	1376
Qy	1103	TTGAAATCAAAAGGAATCGTCTAGTAGTAGATGATAGCAGAGGGTGTGTTAGACCAA	1162
Db	1377	TTGAAATTCAAAGAGGGCGCTGGTAGATAGATGGATAGCAGAGGGTTTGTGAGAGCCA	1436
Qy	1163	AGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGCTAATCAACCGAA	1222
Db	1437	CAGATGGGTGAACATTGAGGATGTTGGAATAGTCACTTTAATGAGCTTATCAACAGAA	1496
Qy	1223	GTATGATTCACCGATCAAGAGTGGGCATAGCAGGAAAAATTAAGACTTGTGCAATTTCATG	1282
Db	1497	GTCTGATTCAGCCCTCAAAGATTAGTACAGATGGAGTGTGTTAAGAGATGTCGAATCCATG	1556
Qy	1283	ATATCATCCGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTTATTGTTACCAA	1342
Db	1557	ATATCATGCGTGATATCATAGTTTCAATTTCTAGAGAGGAAAAATTTTGTGCTGTTGACTA	1616
Qy	1343	TGGGAGATGGCTCTGATTTAGTTTTCAGGAAAAACACTCGCCACATAGCATTCATCGGGAGTA	1402
Db	1617	GGGAGAAGATCATGTTGTAGCGGAGAGAGCATCCGCCATCTAGCANTTTCATGGGAGCA	1676
Qy	1403	TGTCCTGCAAAACAGGATTCGATTTGGAGCAATTAATCGATCA - TTAGCTATTTTGGTGA	1460
Db	1677	AATGCTCAAAGATATGCTTGGAGTGGAAACCATCTGCGCTCAAGTAACTTTGTTGGCGAC	1736
Qy	1461	CAGACCCAGAGTCTAGCACATGCACTTTGTTGCCAGAT - CAATTGAGAGATGTTAGCGGTCT	1519
Db	1737	AAGACCTGTGGGGCGAACA CTGCACTTTGTTTCAACTTACAAATTTAGGATGCTGAGAGTGT	1796
Qy	1520	TGGATCTTGAAGATGTCACATTCCTTAATCACTCAAAAAGATTTTCGACCGTATTGTCATTGT	1579
Db	1797	TGGNTC - TGGAGATGCAAAATTCGAAATTCACAAAAATGATATCAGGAATATAGGGTTGT	1855
Qy	1580	TGTGCCACTTGAATACTTTGAGTATTCGATATTCGTCATCCATATATTCACCTTCCAGAT	1639
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Db	1916	CCATAGGAAAAATTTGCAGTGCTTGCAAAATTTTGAACATGAGGAGGCAAAATATCTCAGCAC	1975
Qy	1700	TACCAAGTGAGATCAGTAAACTCCAATGCTGTCATACTCTTGGTTGTAGTAGAAAGTTTG	1759
Db	1976	TAAACA CTGAGGTGACTAAACTCGAATCTCCGATGCTCCGATGCGATGAGGAGGTCTG	2035
Qy	1760	TTTTCTGACAACTTTAGTCTTAA - - - ACCACCCAATGAAGTGATAACTAAACACAATATGCC	1816
Db	2036	GTTCGTGTTACTTTAGCATAAATAGATAATCCAGGAATGCTTGATGATCACCATGTGCT	2095
Qy	1817	TGCGTAAAGTATTACACCTTTAGTTAGTGGGATGATGCTGTCAAATACAAATTTGCTGAAT	1876
Db	2096	TACCGATGGTTTTCTTAACCTTCAATAAATTTTCACTGACCGGTGTGAAGTTTAATTTCTTGAGA	2155
Qy	1877	TGCACTGCGCCACCAAAAGTTGCTGTTAATAACTCATTTCCGTGTGCAAGGTACCCAAAGGAA	1936
Db	2156	TATGCATGTCTATGTTCTTACCGTTTGGTCTGATACAAAGGGTGTGAGGGTGCCAAAGAGAA	2215
Qy	1937	TAGTAAAGTTTCCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCAAGTAGTA	1996
Db	2216	TTGACACCTTAAAGAGTTACAGATTTCTAGAGTCTGTGGACATCAACAGAACTAGTAGGA	2275
Qy	1997	GAGCAATCAAAGAGCTGGGCGATTAGCAAGCTGAGGAAATTAAGTGTGATGACAAATG	2056
Db	2276	AGGCGATTGAAGAGCTGGGGAGCTAATTCAGTTTAAAGAAATTAAGGCGTGACAAACAAAG	2335

QY	2057	GCTGCACAAAGAAAATGTAAGATCTTTGTGTGCAGCCATGTGAGAAGCTCTCTCCCTCC	2111
Db	2336	GCGCCACAAATGAAGATATCAGATATATTTGTGTGCAGCGATTTGAAGAAGCTCTCTCTCTCGC	2395
QY	2117	AATATCTCTATGTAAGTCTGCAGGAATCTCAGATGTGTGGAACACTTTGAGTGGCTCAGATT	2176
Db	2396	AATCTCTCCGTGTGGATGCTGAGGGAATCTCAGATCTCGAATCTGGAACACTTTGAGTGGCTCAATT	2455
QY	2177	CTATTTCTCTCTCCCTCCCTACTCAGGAGACACTCTGTGTGTATGGAAGTCTTTGAAGAGA	2236
Db	2456	CGATTGATGTCCTCTCCATCTTGAAGAGACTCAAGTTGAATGGATCTCTTCGCAGATA	2515
QY	2237	TGCCTAATCGATTGACAGCTCACTCACTGAAGAAGATCTACTTATTTAGGAGAGCAAAAC	2296
Db	2516	CACCAAACTGGTTTGGGAACCTTAAGCAGCTGGTGAAGATGTGCTTATCCAGATGTGGGC	2575
QY	2297	TAAAGGAAGGTAAAACCATGCTGATCTCTGGGGCATTTGCCCACTCATGGTCTCTTGATC	2356
Db	2576	TAAAGATGTGTAACACTATGGAGATACTTGGGGCACTGCCCAACCTTATGGTCTCTCGTC	2635
QY	2357	TTTATCGAAAGCTTACCTTTGGGGAGAAGCTAGTATTCAAAAACAGGAGCAATCCCAATC	2416
Db	2636	TTTATCGAACGATATGCTGACGAGAAATGACATTCAGAAGGGGAACATTTCCCAATC	2695
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QY	2657	GGGAGGACCGAAGTGATCAGACTTTCCTTGT	2688
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RESULT 5			
HVU507094			
LOCUS			
DEFINITION	HVU507094	3457 bp	linear
ACCESSION			PLN 29-APR-2003
VERSION	AJ507094.1		
KEYWORDS			
SOURCE			
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LOCUS
DEFINITION
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BAC clone:OSJNBa0007020, complete sequence.
ACCESSION
AP003487
VERSION
AP003487.1 GI:13548703
KEYWORDS
HTG.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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1
REFERENCE
AUTHORS
Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
clone:OSJNBa0007020
JOURNAL
Published Only in Database (2001)
REFERENCE
2 (bases 1 to 147363)
AUTHORS
Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE
Direct Submission
JOURNAL
Submitted (04-APR-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(8-mail:tsasak@abrc.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT
The orientation of the sequence is from M13rev to -21M13 of the BAC
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RESULT 8

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LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
clone:P0425F02.
ACCESSION AP001168
VERSION AP001168.1 GI:6983854
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
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REFERENCE
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone:P0425F02
JOURNAL Published Only in Database (2000)
REFERENCE 2 (bases 1 to 176979)
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2000) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

COMMENT
Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from SP6 to T7 of the PAC clone.
Genes were predicted from the integrated results of the following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October1998 version). The genomic sequence was searched against the non-redundant database NRP(PIR,SWISSPROT, GENPEPT, PDB) from MAFF DNAbank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no. and RGP clone ID.
Detailed information on assemble quality together with annotation of this entry at <http://www.dna.affrc.go.jp:82/genomicdata/Genomef1nished.html>.

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LTR

CDS

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CDS

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internal region (AB014741)"
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LTR

CDS

/note="ESTs AU077636(E30684),AU064227(E20182),
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hypothetical protein"

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complement(join(54820..57727,58608..58723))

CDS

Db 55800 AC GTTGGCCATG CCGCTTGATGTTGACACCAATTA GTTGGTCTTCG CAGCAGCGCAATTA TACT 55741
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Db 55740 ATTGCTGAGCTACACAGGCGCTACTCTAGCCATTTGGT CAGAGACACAGGCGTGAGGGTT 55681
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Db 55680 CCAACAGGAATACGCAAACTAAAGAGTTG CAGGTTTAGAGGTTGTAGACCTTTAAACTA 55621
Qy 1987 ACCAGTAGTAGCAATCAAGAGCTGGGCGAGTTTAGCAAGCTGAGGAAATTAGTGTG 2046
Db 55620 ACTAAAAGCAAGCAATTTGAAGCTGGTGAACCTTCGCTGCTACAAAATTTACGGGTG 55561
Qy 2047 ATGCAAAATGCTCGACAAAGGAAAATGTAAGATAC TTTCTGCGAGCCATTGACGAAGCTC 2106
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Qy 2749 GAGAGCTCGCA 2759
Db 54849 GAGAGCTCGCA 54839

RESULT 9
AK070885
LOCUS AK070885 4248 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023064A19, full
insert sequence.
ACCESSION AK070885

VERSION
KEYWORDS
SOURCE
ORGANISM

AK070885.1 GI:32980908
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS

The Rice Full-length cDNA Consortium, National Institute of
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Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Hotta,I.,
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Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
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Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Iehii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Oato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE

2 (bases 1 to 4248)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
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Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
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Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Oato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
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Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
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Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
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This clone is one of the 28K full-length cDNA clones from japonica
rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

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Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center

Query Match		13.5%;	Score 405.4;	DB 8;	Length 2015;
Best Local Similarity		64.1%;	Pred. No. 4.4e-95;		
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Qy	205	GATTCCTATGAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAGCTT	264		
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Qy	325	GSTCGGCGCAAGGTAATCTGTCTGCGATGGTGGTGTAGGCAAGACAGCTCTTTCG	384		
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Qy	445	ACAGTGTCAATATCTTTACAGGATGAGCTACTTAAAGATATGATACGCCAATCTTCT	504		
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Qy	505	GGCCCCACTTCTCGATCAACTCTTGCAGNAATTGCAAG---GAAGGTGGTGTGCAA	561		
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Db	1346	GTGGNAGACTCTGGGAAGACTTGNAGCAAGTCTTAAAGAGAAAGGACTCTTTGTGTT	1405		
Qy	622	CTAGATGATCTATGGATTTTACATGATTTGGAATGGATTAATGAATTTCTTAAG	681		
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Qy	682	AACATAGAAGGCGAGTCAATAGTATATACCACTTGGATTTGATCTTGGCGAGAG	741		
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Qy	922	GGAGCTGTGCTTGCAACTTAAACAGGTGTACAGATGGGAGAAATCTATGAACACTTCT	981		
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Qy	1162	AAGGTGTGGATGACCACTCAAGGATTCGAGAAAGTTACTTTAATGAGCTAATCAACCGA	1221		
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Qy	1222	AGTATGATTTCAAC	1234		

Db	2002	AGCATGATTTCAAC	2014		
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LOCUS	HVU506137	564 bp	DNA	linear	PLN 28-APR-2003
DEFINITION	Hordeum vulgare partial rga S-9202 gene for NBS-LRR disease resistance protein homologue.				
ACCESSION	AJ506137				
VERSION	AJ506137.1	GI:28555849			
KEYWORDS	NBS-LRR disease resistance protein homologue; rga S-9202 gene.				
SOURCE	Hordeum vulgare				
ORGANISM	Hordeum vulgare				
REFERENCE	1	Madsen, L.H., Collins, N.C., Rakwalaka, M., Backes, G., Sandal, N., Krussell, B., Jensen, J., Waterman, E.H., Jahoor, A., Pryor, A.J., Langridge, P., Schulze-Lefert, P. and Stougaard, J.			
AUTHORS	Barley disease resistance gene analogs of the NBS-LRR class: identification and mapping				
TITLE	Mol. Genet. Genomics 269 (1), 150-161 (2003)				
JOURNAL	22600637				
MEDLINE	12715163				
PUBMED	2	(bases 1 to 564)			
REFERENCE	Madsen, L.H.				
AUTHORS	Direct Submission				
TITLE	Submitted (22-AUG-2002) Madsen L.H., Department of Molecular Biology, Aarhus University, Gustav Wieds Vej 10, DK-8000 C, DENMARK				
JOURNAL	Location/Qualifiers				
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Query Match	8.4%;	Score 250.8;	DB 8;	Length 564;	
Best Local Similarity	66.4%;	Pred. No. 2e-54;			
Matches	376;	Conservative 0;	Mismatches 187;	Indels 3;	Gaps 1;
Qy	352	GGGATGGGTGGTTAGGCAAGACAGCTCTTTTCGAGGAGAGATCTTTTGAAGCAAGAGAC	411		
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Qy	412	ATTAGGAAGAACTTCCCTTGCATGCTTGGATTACAGTGTCAATCATTTTCACAGGATT	471		
Db	61	ATTGTGAATAAATTTGCAATGTTGTGCTTGGATCACCGTCTCACAGTCAATTTTCCAAATA	120		
Qy	472	GAGCTACTTAAAGATATGATAGCCAACTTCTTGCCCCAGTCTCTCGATCAACTCTTG	531		
Db	121	GAGATGCTCAAGGAGATGATAGACAGCTTTTGGGTACCGAGTTGCTGAGGCAATGCTTG	180		
Qy	532	CAAGAATTGCAAGGAAAGGTGGTGGTCAAGTACATCATCTTCTGAGTACCTGATAGAA	591		
Db	181	AAAGAACTTGAAGAGAA---GGCTGTGCACGTAGAGGATCTTGCAGCTACCTCAGAGAA	237		
Qy	592	GAGCTCAAGGAGAAAGGATCTTTGTTGTTCTTAGATGATCTATGGATTTTACATGATTGG	651		

Db	238	AAGCTAGAGACATGAGATACCTTTATTGTTCTTGATGACTTGTGGACCATAGATGCTTGG	297
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Qy	772	GATTTCTTGCAGATGAACGATGCCATACAACTGCTACTTGAGAAAAACAATAAAAAATCAT	831
Db	418	AAGCACCTCGCAATAGAGGATGCCACAAATTTGCTACTAAGAAAGAGTAGGAAAACATGG	477
Qy	832	GAAGACATGGAAATCAAAATAAAAAATATGCAAAAAGATGGTTGAACGAATTTGTAATAAATGT	891
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Qy	892	GGTGCTCTACCATTAGCAATACTTAC	917
Db	538	GGTGTGCTCCCTTCGCCCTCATCAC	563
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AB013451			
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DEFINITION	Oryza sativa PibH8	mRNA, complete cds.	
ACCESSION	AB013451		
VERSION	AB013451.1	GI:7415940	
KEYWORDS	NBS-LRR type resistance gene.		
SOURCE	Oryza sativa		
ORGANISM	Oryza sativa		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
REFERENCE	1	Wang, Z. X., Yano, M., Yamanouchi, U., Iwamoto, M., Monna, L., Hayasaka, H., Katayose, Y. and Sasaki, T.	
AUTHORS	The Pib gene for rice blast resistance belongs to the nucleotide binding and leucine-rich repeat class of plant disease resistance genes		
TITLE	Plant J. 19 (1), 55-64 (1999)		
JOURNAL	Plant J. 19 (1), 55-64 (1999)		
MEDLINE	99348180		
PUBMED	10417726		
REFERENCE	2	Wang, Z. X., Yamanouchi, U., Katayose, Y., Sasaki, T. and Yano, M.	
AUTHORS	Expression of the Pib rice-blast-resistance gene family is up-regulated by environmental conditions favouring infection and by chemical signals that trigger secondary plant defences		
TITLE	Plant Mol. Biol. 47 (5), 653-661 (2001)		
JOURNAL	Plant Mol. Biol. 47 (5), 653-661 (2001)		
MEDLINE	21582385		
PUBMED	11725950		
REFERENCE	3	(bases 1 to 4001)	
AUTHORS	Sasaki, T. and Yano, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-APR-1998) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan		
(E-mail: tsasaki@agr.affrc.go.jp, Tel:0298-38-7441, Fax:0298-38-7468)			
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ORIGIN				
	Query Match	6.7%;	Score 202.2; DB 8; Length 4001;	
	Best Local Similarity	46.5%;	Pred. No. 1.7e-41;	
	Matches 1023; Conservative	0;	Mismatches 1118; Indels 60; Gaps 9;	
Qy	335	AGGTAATCTGTGTTGGGATGGGTGGTTAGGCAAGACAGCTCTTTGAGGGAAGATCT	394	
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Qy	395	TTGAAACGGAAGAGACATTTAGGAAGAACTTCCTCTTGCATGCTTGGATTACACGTGTCAC	454	
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Qy	455	AATCATTTTCAGGATTGAGCTACTTAAAGATATGATAC-----GCCAACTTCTTGGC	507	
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Qy	508	CCAGTCTCTGATCAACTCTTGCAAGAAATTCGACGGGAAGGTGGTGGTGCAGATACAT	567	
Db	1609	CTGGAAGAAAGGTAGAAATCTATACAGGACTTGCAGAGGAGTGGTTTAAAGCACGATGGGAT	1668	
Qy	568	C-----ATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTACTTGTGTCTTC	622	
Db	1669	CTGAAGAAATTAATTGACAGTTGAGCAAGATTTAACTGGGAAGAGTACTCATTTGTC	1728	
Qy	623	TAGATGATCTATGGATTTTACATGATTGGAATTTGGATAAATGAAATTTGCAATTTCTTAAGA	682	
Db	1729	TTGATGACCTATCGACTACTGAGTGGGATTCAATAA---TAAGAAACTTGCTATAA	1785	
Qy	683	ACATAAGAGGCGCAGTCAAAATAGTAATAACCACTTGGAAATGTTGATCTTTGGCGGAGAAGT	742	
Db	1786	ACAACAATGGTAGCCGGATCATACTGACTACAAGATTTAAACTTTGTTGGCGCAACATTTGTT	1845	
Qy	743	GTGCCACAGCCTCACTGGTGTACCACTTGATTTCTTTCGAGATGAACGATGCCATAACAT	802	
Db	1846	CCAAGAAAGAAATGAACATGCACAAATTGAAGGTCTTAACAGACGGAGATGCTCTTGAGC	1905	
Qy	803	TGCTACTGAGAAAAACAATAAATAATCATCAAGACATCGGAATCAAAATAAATAATGCAAA	862	
Db	1906	TATTCTTAATAGGTACGATGGTGAATCAATCAGAAATTTGAAACCTGACTTGAAGG	1965	
Qy	863	AGATGGTTGAACGAATTGTAATAAATGATGGTCTGTACCAATTAGCAATACTTACAATAG	922	
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Qy	923	GAGCTGCTTGC-----AACTAAA	CAGGTTGCAGAAATGGAGAAATTTCTATGAACACC	976	
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Qy	977	TTCCCTTCAGAACTAGAAATAAACCAAGCC	TGGAGCTTTTCAGAGAGAAATGGTGNACCCCTAG	1036	
Db	2086	TCAGTGAAGAAATTTGATAACCAACCAAGCT	TTGAGATGATAAAGAAATAACTTTGCATCAA	2145	
Qy	1037	GTTCACAAACCACCTACCACTCCCATCTGAAAC	CATCTCTTTTGTATCTAAGTATCTTTCCCTG	1096	
Db	2146	GCTATGAGGGTTTAACTTACCACTTGAAATCT	TGCTTCCATATATGTGCAATTTTCCCTG	2205	
Qy	1097	AGGAATTTTGAATCAAAAGGAATCGTCTAGT	PAGTAGATGGATAGCAGAAGGTTTGTGTA	1156	
Db	2206	AAGACTCTGACATCAGATATAGACGATATATT	TGAGCGGATGCACTGCAGAGGTTACTCAA	2265	
Qy	1157	GACCAAAAGGTTGGGATCAGCACTAAGGAT	GTGCGAGAAAGTTACTTTAAATGAGCTAATCA	1216	
Db	2266	GAGCAACGAGAAACAGGAGCAACAGAGAAAG	TGGCAGAGAACAGTTTCACAGCTCTTCTCA	2325	
Qy	1217	ACCGAAAGTATGATTCAACAGATCAAGAGT	TGGGCATAGCAGGAGAAATTAAGACTTGTGCA	1276	
Db	2326	ACAAGAGTATGATCCAAACATCAAAAACGAT	TGCCAGTGGAGAGCAGGTTTCTGCCAAG	2385	
Qy	1277	TTCATGATATCATCCGTGATATCA	CAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTGT	1336	
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Qy	1397	GGAGTATGTCTGCAAAACAGGATTGGAT	TGGAGCATTTTCGATCAATTAGCTATTTTTCG	1456	
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Qy	1457	GTGACAGACCAAGAGCTTAGCA	CATCGAGTTTGTCCAGATCAATTGAGGATGTTACGGG	1516	
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Qy	1517	TCTTGGATCTTGAAGATGTGCATCTTTA	ACTCACTCAAAAAGATTTGCACCGTATGTCAT	1576	
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Qy	1577	TGTTGTGCGCACTTGAATACTTTGAGTAT	TGATATTCGTATCCATATATTCCTACTTCCCA	1636	
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Qy	1637	GATCCATTGGTAAACTACAGGGCCTCA	AAACTTTTGAACATGCGGAGCACAATATGTCAG	1696	
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Qy	1817	TGCGTAAAGTATTCA	CACCTTTTAGTTAGTGGCGATGATCGTGC	1876	
Db	2905	AGTTTCAGATCAATCCGAGAGAGAT	GGGAACCAAGTTTCGCTGTATCATATCATGTTGT	2964	
Qy	1877	TGCACTGGGCCACAAAAGTTTGTGGT	ATAAATCATTTCCGTTGTGAAGGTAACCCAAAGGAA	1936	
Db	2965	TCATCACCGCTTGGTTAAGAAA	CTGTGAT--GTATGTGTGTTAAAGTGCCAAAGGGA	3021	
Qy	1937	TAGGTAAGTTGCGAGACTTACAGGTTCT	TAGAGTATGTAGATATCAGCGGACCAAGTAGTA	1996	
Db	3022	TTGACCGGTTGAGGTC	CAATTCACACACTGAGCATCGTGAACATTTGCA	CGGG--GAAAGG	3078

Qy	1997	GAGCAATCAAGAAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTAAGTGTGATGACAAATG	205
Db	3079	CTTTGGTCTAAAAAAGCTCAAAAGAGCTACCCAACTGTGTAAACTAGTGTG-----ACTG	3132
Qy	2057	GCTCGACAAAGGAAAATGTAAGATCTTTTGTGCAGCCTATGAGAGCTCTCTTCCCTCC	2116
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Qy	2117	AATATCTCTATGTGAATGCTGCGAGGAATCTCAGATGGTGGAAACACTTTGAGTGGCTAGATT	2176
Db	3193	AGTCCTTTACTTGGCGGACAGGGTA-----ATGCTGGGTTAGAGGTTGTTGGATA	3246
Qy	2177	CTATTTCTCTCTCTCTCCCTACTAGGACACTCTGTGTTGTATGGAAGTCTTTGAAGAGA	2236
Db	3247	ACATGTCCCGAGCTCTCTAAAGAGCTTTAAAGAGCTTCCAGTTGTATCGGCAATCTCGTGA	3306
Qy	2237	TGCTTAACCTGGATTGAGAGCTCACTCACCTGAAGAGATCTACTTTATTGAGGAGCAAC	2296
Db	3307	TACCAGAATGGATTAAAGATCTTTAAATTTCTACAAAGCTGAGCCTTCGCGAACCAATC	3366
Qy	2297	TAAAGGAAGGTAAAAACCATCTGATCTTGGGGCATTTGCCCAACCTCATGGTCTCTTGATC	2356
Db	3367	TGAAGGCAGATCTACCATGGAGTGTCTGGAAACCTACCAATGCTAGCAATCTTCTCGT	3426
Qy	2357	TTTATCGGAAAGTTTACCTTTGGGGAGAGCTAGTATTTCAAAACAGGAGCAATCCCAATC	2416
Db	3427	TCCAGGACAATCGTGTGAGGAGGAAGACTCTGTTTCGGTCCGAGCGTTTTCACAGGTC	3486
Qy	2417	TTAGACACTTTTCGATTACGATTTGGATTCAGTCTAGAGAGATAGATTGAGGACGGCA	2476
Db	3487	TGACGTCATTGGAGCTTCTCAATTTGGGAGAGCCTCAAGTCGGTGGAAATTTGAACGAGG	3546
Qy	2477	GCTCGCCCCAGTTGGAAAAGATAGAAATCAGATTCTGCAGG	2517
Db	3547	CTACTCTAACTGAAGTGCTACTGCTGCACACTGTTGG	3587

RESULT 13	AK065693	4030 bp	mRNA	linear	PLN 24-JUL-2003
LOCUS	Oryza sativa (japonica cultivar-group)	cdna clone:J013043101	full		
DEFINITION	Oryza sativa (japonica cultivar-group)	insert sequence.			
ACCESSION	AK065693	1	GI:32975711		
VERSION	AK065693.1				
KEYWORDS	FLU CDNA; CAP trapper.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
REFERENCE	1				
AUTHORS	The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project team, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,N., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group., Otono,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narioka,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nishikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsumura,K., RIKEN, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kawaga,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.				
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice				
JOURNAL	Science	301	(5631),	376-379	(2003)
MEDLINE	22752273				
PUBMED	12869764				

Db 2580 CTCTGACAGTCTTTGGGAGTGGAAATCAATTTTTCCTTTCTTAAAGATGAGGATGCTTC 2639
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Db 2859 ACGTCCATGCCGATCTTTAGATGATGAGGATGATCAGCCGATATTAATACTACTGCATC 2918
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Db 2919 AGTTCAGATCAATCCGAGAAGATGGGAACAGGTTCGCTGTATCATATATCATGTTGT 2978
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Qy 1937 TAGTAAAGTTCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGGACCACTAGTA 1996
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Db 3147 GCATCAACAGAAATACGCAAGAGCTCTGTTCTGCCATTTGCCAGCATCGCCGCTTGC 3206
Qy 2117 AATATCTCTATGTGAATGCTGAGAAATCTCAGATGTGTGGAACACTTGAGTGCCCTAGATT 2176
Db 3207 AGTCTTTATTACTGCGGCGCAGAGGTA-----ATGCTGGGTAGAAGGTTGTTTGGATA 3260
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Db 3261 ACATGTCCAGCCCTCTTAAAGACCTTAAAGACCTTAAAGACCTTAAAGACCTTAAAGACCTT 3320
Qy 2237 TGCCTAACTGGATTGAGCAGCTCACTCACTGGAAGAGATCTACTTATTGAGGAGCAAAAC 2296
Db 3321 TACCAGATGATTAAGATCTTAAATCTTCAAAAGCTGAGCTTCGCGAACACCAATC 3380
Qy 2297 TAAAGGAAGTAAACCACTGCTGATCTGTTGGGCACTTGCACCACTCATGCTCTTGCATC 2356
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Qy 2477 GCTGCCCGGAGTTGGAAAAGATAGAAATCAGATTTCTGCAGG 2517
Db 3561 CTACTCTCTAACTGAAGTGTCTACTGCTGCACACTACTGTTGG 3601

AK101823
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:J033067K01, full insert sequence.
ACCESSION
AK101823
VERSION
AK101823.1 GI:32987032
KEYWORDS
FLU_CDNA; CAP trapper.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ohtsuki,Y., Tsunoda,Y.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
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Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

TITLE
japonica rice

JOURNAL
MEDLINE
23752273

PUBMED
12869764

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AUTHORS

2 (bases 1 to 4949)
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Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
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Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
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Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
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305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp).
Tel:81-29-838-7007, Fax:81-29-838-7007

TITLE
JOURNAL

This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Ohtsuki,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,

COMMENT

Query Match	6.6%;	Score 196.6;	DB 8;	Length 4949;
Best Local Similarity	55.7%;	Pred. No. 5.2e-40;		
Matches 467;	Conservative 0;	Mismatches 354;	Indels 18;	Gaps 4;
Qy	539	TGCAAGGGAAGGTGGTGGTCAAGTACATCATCTTTCTGAGTACCTCATAGAGAGCTCA	598	
Db	2534	TGGATGGAATGGAAGATGGGAAGTTGGCAGTCTGGCTGAAAAGTTAGGCAGTATTTC	2593	
Qy	599	AGGAGAAGAGGTACTTTTGTGTTCAGATGATCTATGGATTTTACATGATTTGGAATTTGGA	658	
Db	2594	TAGACAAAAGGTATATTGTCACTTTTGACGACATATGACCATATCAGTTGGGAGAGTA	2653	
Qy	659	TAAATGAATTCATTTCTTAAGAACAAATAAGAAGGGCAGTCAAAATAGTATATACCACTT	718	
Db	2654	TCA---GATGTGCATTGCGCT---GACAAATAGAAGGGCAGCAGTAGTAATTATATACCA	2707	
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Qy	896	GTCTACCAATTAGCAATACTTACAATAGAGCTGTGCTTG-----CAACTAAACAGG	946	
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Qy	1007	TGGAGCTTTTGAGAGAAATGGTGAACCTTAGGTTACAACCACTTACCATCCGATCTGAAAC	1066	
Db	3008	TGGAAGTTGCAAGCAAGTGTAAACCTTGAGCTATAATGATCTACCTTACCATCTGAAGG	3067	
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Qy	1127	TAGTAGATGGATAGCAAGAGGGTTTGTGTAGACCAAAAGGTTGGGATGACCACTAAGGATG	1186	

TITLE
JOURNAL
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
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COMMENT

Accession number: F020300, Eukaryote: 29-030-000, taxid: 290300, this clone is one of the 28K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariikawa, R., Niihara, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tanoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Haashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

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FEATURES
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ORIGIN

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Matches 909; Conservative 0; Mismatches 991; Indels 48; Gaps 7;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2395.2	79.9	99090	12	Adm72250 O. minuta
5	2393.6	79.9	3099	12	Adm72244 O. minuta
6	2377.6	79.3	3276	12	Adi57175 Oryza min
7	2359.8	78.7	3099	12	Adm72240 O. minuta
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9	1354.2	45.2	2422	12	Adm72252 O. minuta
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25	125.4	4.2	2739	3	Aaz50262 Coding re
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ALIGNMENTS

RESULT 1
ADM72248
ID ADM72248 standard; cDNA; 2997 BP.
XX
AC ADM72248;
XX
DT 03-JUN-2004 (first entry)
XX
XX O. minuta NBS6 polypeptide encoding cDNA.
XX
KW Pi2; NBS6; plant protectant; gene therapy; rice; disease resistance;
KW gene; ss.
XX
OS Oryza minuta.
XX
XX Key Location/Qualifiers
FT CDS 1..2997
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XX WO2004022715-A2.
XX
PD 18-MAR-2004.
XX
XX 08-SEP-2003; 2003WO-US027913.
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XX 09-SEP-2002; 2002US-0409216P.
PR 18-MAR-2003; 2003US-0455713P.
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XX
XX (OHIS) UNIV OHIO STATE.
XX
XX Wang G;
XX
XX WPI; 2004-257576/24.
DR P-PSDB; ADM72249.
XX
XX New rice Pi2-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX
XX Claim 1; SEQ ID NO 11; 120pp; English.
XX

CC The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA
CC encoding a rice NBS6 polypeptide.

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2997; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	967	TGTGCCACAGCCTCAGCTGGTGTACCACTTGATTTCTTGACAGTGAACGATGCCATAACA	1026
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RESULT 3

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Qy	1942	AAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCACTAGTAGAGCA	2001
Db	2167	AAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACCACTAGTAGAGCA	2226
Qy	2002	ATCAAAGAGCTGGGGCAGTTAAAGCAAGCTGAGGAAATTTAGGTGTGATGACAAAATGGCTCG	2061
Db	2227	ATCAAAGAGCTGGGGCAGTTAAAGCAAGCTGAGGAAATTTAGGTGTGATGACAAAATGGCTCG	2286
Qy	2062	ACAAAGGAAAAATGTAAAGATACCTTTGTGCGAGCCATTGAGAAAGCTCTCTTCCTCCAATAT	2121
Db	2287	ACAAAGGAAAAATGTAAAGATACCTTTGTGCGAGCCATTGAGAAAGCTCTCTTCCTCCAATAT	2346
Qy	2122	CTCTATGTGATGCTGCGAGGATCTCAGATGGTGGAACTTTGAGTGCCTAGATCTTATTT	2181
Db	2347	CTCTATGTGATGCTGCGAGGATCTCAGATGGTGGAACTTTGAGTGCCTAGATCTTATTT	2406
Qy	2182	TCCTCTCCTCCTCCCTACTGAGGACACTCGTGTGTATGGAAGCTTTGAAAGAGATGCCT	2241
Db	2407	TCATCTCCTCCTCCCTACTGAGGACACTCGGTTGTAATGGAGTCTTTGAAGAGATGCCT	2466
Qy	2242	AACCTGGATTGAGCAGCTCACTCACTGAAAGAGATCTATTTATTTGAGGAGCAAACTAAAG	2301
Db	2467	AACCTGGATTGAGCAGCTCACTCACTGAAAGAGATCTATTTATTTGAGGAGCAAACTAAAG	2526
Qy	2302	GAAGTTAAACCACTGCTGATACTTTGGGGCATTCGCCAACCTCATGCTCTTATTTAT	2361
Db	2527	GAAGTTAAACCACTGCTGATACTTTGGGGCATTCGCCAACCTCATGCTCTTATTTAT	2586
Qy	2362	CGGAAAGCTTACCTTTGGGGAGAGCTAGTATTTCAAAAACAGGAGCATTTCCCAAATCTTAGA	2421
Db	2587	TGGNAATGCTTACCTTTGGGGAGAGCTAGTATTTCAAAACGGGAGCATTTCCCAAATCTTAGA	2646
Qy	2422	ACACTTTCGATTTACGATTTTGGATCAGCTAAGAGAGATTTAGATTTTGGAGCGGAGCTCG	2481
Db	2647	ACACTTTCGATTTACGATTTTGGATCAGCTAAGAGAGATTTAGATTTTGGAGCGGAGCTCG	2706
Qy	2482	CCCCAGTTGGAAAAGATAGAAATCAGATTTCTGCGAGTTGGNAATCAGGGATTTATTTGTTAT	2541
Db	2707	CCCCAGTTGGAAAAGATAGAAATCAGATTTCTGCGAGTTGGNAATCAGGGATTTATTTGTTAT	2766
Qy	2542	ATCCACCTTCCAGGCTCAAGGAGATTTTCACTTCGATACGAAAGTAAAGTGGCTGGGCTT	2601
Db	2767	ATTCACTTCCAGGCTCAAGGAGATTTTCACTTCGATACGAAAGTAAAGTGGCTGGGCTT	2826
Qy	2602	GCTCAGCTGGAAGGAGGAGTGCACACACCAAAATCAACCCCGTGTGCGAAAAGGAGAG	2661
Db	2827	GCTCAGCTGGAAGGAGGAGTGCACACACCAAAATCAACCCCGTGTGCGAAAAGGAGAG	2886
Qy	2662	GACCGAAGTATCAGACCTTGTGTTGACGCCGGAAGATCCCTGTTGAAGTGGAGCA	2721
Db	2887	GACCGAAGTATCAGACCTTGTGTTGACGCCGGAAGATCCCTGTTGAAGTGGAGCA	2946
Qy	2722	ACGATCTCCCTCCAGAGCAGGAGGGA	2748
Db	2947	GCAGATCTGTTCTGATGCGGAAGGA	2973

Qy	2717	AAGCAACGGATCCCTCCAGAGCAGGAGGA	2748	Qy	377	CTCTTCGAGGAAGATCTTTGAAAGCGAAGACATTTAGAAAGAACTTCCTCTTGCATG	436
Db	80459	AAACAGCAGATCCTGTTCTCTGATGCCGAAGGA	80490	Db	602	CTCTTCGAGGAAGATCTTTGAAAGCGAAGACATTTAGAAAGAACTTCCTCTTGCATG	661
RESULT 5							
ADM72244							
ID	ADM72244	standard; cDNA; 3099 BP.		Qy	437	CTTGGATTACAGTGTCAATCATTTTCA CAGGATTGAGCTACTTTAAAGATATGATACGCC	496
AC	ADM72244;			Db	662	CTTGGATTACAGTGTCAATCATTTTCA CAGGATTGAGCTACTTTAAAGATATGATACGCC	721
XX	03-JUN-2004	(first entry)		Qy	497	AACTTCTTGGCCCCAGTTCTCTGGATCAACTCTTTGCAAGAAATTCGAAGGAAAGTGTGTGG	556
DT				Db	722	AACTTCTTGGCCCCAGTTCTCTGGATCAACTCTTTGCAAGAAATTCGAAGGAAAGTGTGTGG	781
XX	O. minuta	NBS4 polypeptide encoding cDNA.		Qy	557	TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGAGAGAGAGAGTACTTTTG	616
DE	Pi2; NBS4;	plant protectant; gene therapy; rice; disease resistance;		Db	782	TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGAGAGAGAGTACTTTTG	841
KW	gene; SB.			Qy	617	TGTGTTCTAGATGATCTATGGATTTTACATGATTTGGATTTGGATTAATGAAATTCGATTTTC	676
XX	Oryza minuta.			Db	842	TGTGTTCTAGATGATCTATGGATTTTACATGATTTGGATTTGGATTAATGAAATTCGATTTTC	901
OS	Key	Location/Qualifiers		Qy	677	CTAAGAACAAATAAGAAGGCGAGTCAAAATAGTAATAACCACTTCGGAATGTTGATCTTTGCCG	736
FH	CDS	1..3099		Db	902	CTAAGAACAAATAAGAAGGCGAGTCAAAATAGTAATAACCACTTCGGAATGTTGATCTTTGCCG	961
FT		/*tag= a		Qy	737	AGAAAGTGTGCCACAGCTCTACTGGGTACCACTTGATTTCTTTCGAGATGAACAGATGCCA	796
FT		/product= "NBS4"		Db	962	AGAAAGTGTGCCACAGCTCTACTGGGTACCACTTGATTTCTTTCGAGATGAACAGATGCCA	1021
XX	WO2004022715-A2.			Qy	797	TAACATTTGCTACTGAGAAAACAATAAATAATCATGAGACATGGAATCAAAATARAANAATA	856
XX	18-MAR-2004.			Db	1022	TAACATTTGCTACTGAGAAAACAATAAATAATCATGAGACATGGAATCAAAATARAANAATA	1081
XX	08-SEP-2003; 2003WO-US027913.			Qy	857	TGCAAAAGATGTTTGAACGAATTTGTAATAATAATGTTGTTGCTCTACCAATAGCAATACTTA	916
PR	09-SEP-2002; 2002US-0409216P.			Db	1082	TGCAAAAGATGTTTGAACGAATTTGTAATAATAATGTTGTTGCTCTACCAATAGCAATACTTA	1141
PR	18-MAR-2003; 2003US-0455713P.			Qy	917	CAATAGGAGCTGTGCTTTGCAACTAAACAGAGTGTGAGAAATGGGAGAAATTTCTATGAACACC	976
XX	05-SEP-2003; 2003US-00656394.			Db	1142	CAATAGGAGCTGTGCTTTGCAACTAAACAGAGTGTGAGAAATGGGAGAAATTTCTATGAACACC	1201
XX	(OHIS) UNIV OHIO STATE.			Qy	977	TTCCTTCAGAACTAGAAAATAAACCCAGAGCTTGGAGCTTTGAGAGAAATGGTGACCCCTAG	1036
PI	Wang G;			Db	1202	TTCCTTCAGAACTAGAAAATAAACCCAGAGCTTGGAGCTTTGAGAGAAATGGTGACCCCTAG	1261
XX	WPI; 2004-257576/24.			Qy	1037	GTTTACAACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTTAAGTATCTTTCTCTG	1096
DR	P-PSDB; ADM72245.			Db	1262	GTTTACAACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTTAAGTATCTTTCTCTG	1321
XX	New rice Pi2-like disease resistance nucleic acid molecule that confers			Qy	1097	AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATGGATAGCAGAGAGGTTTGTTA	1156
PT	disease resistance in plants, useful for creating or enhancing disease			Db	1322	AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATGGATAGCAGAGAGGTTTGTTA	1381
PT	resistance in plants.			Qy	1157	GACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGCTAATCA	1216
XX	Claim 1; SEQ ID NO 7; 120pp; English.			Db	1382	GACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGCTAATCA	1441
PS	The invention relates to novel broad-spectrum resistance gene pi2 and the			Qy	1217	ACCGAAGTATGATTCACAGATCAAGAGTGGGCATAGCAGGAAAAATTTAAGACTTGTGCA	1276
CC	NBS(1-6) genes present in the pi2 gene cluster region. The rice pi2-like			Db	1442	ACCGAAGTATGATTCACAGATCAAGAGTGGGCATAGCAGGAAAAATTTAAGACTTGTGCA	1501
CC	disease resistance nucleic acid molecules are useful for enhancing			Qy	1277	TTCATGATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATGT	1336
CC	disease resistance in plants. The present sequence represents a cDNA			Db	1502	TTCATGATATCATCCGCTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTGTATGT	1561
XX	encoding a rice NBS4 polypeptide.			Qy	1337	TACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACTCTCGCCACATAGCATTCCATG	1396
XX	Sequence 3099 BP; 954 A; 613 C; 743 G; 789 T; 0 U; 0 Other;			Db	1562	TACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAACTCTCGCCACATAGCATTCCATG	1621
Qy	Query Match	79.9%; Score 2393.6; DB 12; Length 3099;		Qy	1397	GGAGTATGTCCTGCAAAACAGGATTTGGATTTGGAGCAATTTATTCATCATTTAGCTATTTT	1456
Db	Best Local Similarity	96.1%; Pred. No. 0;		Db	1622	GGAGTATGTCCTGCAAAACCTGGATTTGGATTTGGAGCAATTTATTCATCATTTAGCTATTTT	1681
	Matches 2453; Conservative	0; Mismatches 99; Indels 0; Gaps 0;		Qy	1457	GTGACAGACCCCAAGAGTCTAGCACATCGAGTTTGTCCAGATCAATTTGAGGATGTTCAGGG	1516
Qy	197	TAGCAATAGATTCTCTATGCGAAGACATTCGAATCAATCAGCTCGAAATGTGGATCAAG	256				
Db	422	TTGACATGATGATTCCTATGCGAAGACATTCGTAATCAGTCACTGCGCAATGTGGATGAGG	481				
Qy	257	CTGAGCTGTGGGTGTTTCTGACTCCAGAAAAAGGCTGCTTGAATGATGATACCAATG	316				
Db	482	CTGAGCTGTGGGTGTTTCTGACTCCAGAAAAAGGCTGCTTGAATGATGATACCAATG	541				
Qy	317	CTAATGATGTCGGGCCAAGGTAAATCTGTGTTGTTGGATGGGTGTTTGGCAAGACAG	376				
Db	542	CTAATGATGTCGGGCCAAGGTAAATCTGTGTTGTTGGATGGGTGTTTGGCAAGACAG	601				

Db 1682 GTGACAGACCCAGAGTCTAGACATGCGATGTTTGTCCAGATCAATTGAGGATGTTACGGG 1741
Qy 1517 TCTTGGATCTTGAAGATGTGACATCTTAAATCACTCAAAAAGATTTCGACCGTATTGCAT 1576
Db 1742 TCTTGGATCTTGAAGATGTGACATCTTAAATCACTCAAAAAGATTTCGACCGTATTGCAT 1801
Qy 1577 TGTGTGCCACTTGAATACTTGTAGTATTGATGATTTGTCATCCATATATTCACTTCCCA 1636
Db 1802 TGTGTGCCACTTGAATACTTGTAGTATTGATGATTTGTCATCCATATATTCACTTCCCA 1861
Qy 1637 GATCATTGTGTAACTACAGGCGCTACAAACTTTGAACTCCGAGCACATACATTTGCAG 1696
Db 1862 GATCATTGTGTAACTACAGGCGCTACAAACTTTGAACTCCGAGCACATACATTTGCAG 1921
Qy 1697 CACTACCAAGTGAGATCAGTAAATCTCCAAATGTCTGCATATCTTCTGTTGTAGTAGAAAGT 1756
Db 1922 CACTACCAAGTGAGATCAGTAAATCTCCAAATGTCTGCATATCTTCTGTTGTAGTAGCAAGT 1981
Qy 1757 TTGTTTCTGCAACCTTTAGTCTTAAACCCCAATGAAGTGCATTAACCTAACATATATGCC 1816
Db 1982 TTTCAATATGACAACCTTTAGTCTTAAACCCCAATGAAGTGCATTAACCTAACATATATGCC 2041
Qy 1817 TGCCTAAAGTATTCACACCTTTAGTCTGCGATGATCGTCAATACAAATTTGCTGAAT 1876
Db 2042 TGCCTAAAGTATTCACACCTTTAGTCTGCGATGATCGTCAAAACAAATTTGCTGAAT 2101
Qy 1877 TGCAATGGCCACCAAAAGTTGCTGGTATAAATCAATTCGGTGTGAAGGTACCCAAAGGAA 1936
Db 2102 TGCAATGGCCACCAAAAGTTGCTGGTCTGAATCAATCGGTGTGAAGGTACCCAAAGGAA 2161
Qy 1937 TAGTAAAGTTCGAGACCTTACAGGTTTACAGATGATGATAGATATCAGGCGGACCATGATGA 1996
Db 2162 TAGTAAAGTTCGAGACCTTACAGGTTTACAGATGATGATAGATATCAGGCGGACCATGATGA 2221
Qy 1997 GAGCAATCAAGAGCTGGGCGAGTTTACAGAGCTGAGGAATTAAGTGTGATGACAAATG 2056
Db 2222 GAGCAATCAAGAGCTGGGCGAGTTTACAGAGCTGAGGAATTAAGTGTGATGACAAACG 2281
Qy 2057 GCTCGACAAAGGAAAAATGTAAGATACCTTTGTGAGCCATTTGAGAAGCTCTCTTCCCTCC 2116
Db 2282 GGTGACAAAGGAAAAATGTAAGATACCTTTGTGAGCCATTTGAGAGCTCTCTTCCCTCC 2341
Qy 2117 AATATCTATGTGAATGCTCGAGGAATCTCAGATGTTGGAACACCTTGAGTGCCTAGATT 2176
Db 2342 AATCTCTCATGTGGATGCTCGAGGAATCTCAGATGTTGGAACACCTTGAGTGCCTAGATT 2401
Qy 2177 CTATTTCT 2236
Db 2402 CTATTTCT 2461
Qy 2237 TGCTTAATCTGATTTGAGCAGCTCACTCACTGAAAGAGATCTACTTATTGAGGAGCAAAAC 2296
Db 2462 TGCTTAATCTGATTTGAGCAGCTCACTCACTGAAAGAGATCTACTTATTGAGGAGCAAAAC 2521
Qy 2297 TAAAGGAAGTAAACCACTGTATCTGATCTGGGCAATGCCCCAATCTCATGCTCTTGCATC 2356
Db 2522 TAAAGGAAGTAAACCACTGTATCTGATCTGGGCAATGCCCCAATCTCATGCTCTTGCATC 2581
Qy 2357 TTTATCGGAAGCTTACCTTGGGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAATC 2416
Db 2582 TTTATCGGAATGCTTACCTTGGGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAATC 2641
Qy 2417 TTAGAACACTTTTCGATTTTACGATTCAGCTTAAGAGAGATTTAGATTTCGAGGACGCA 2476
Db 2642 TTAGAACACTTTTCGATTTTACGATTCAGCTTAAGAGAGATTCGATTTTCGAGGACGCA 2701
Qy 2477 GCTCGCCCCAGTTGGAAAAGATAGAAATCAGATCTTCGAGGTTGGAATTCAGGGATTTATG 2536
Db 2702 GCTCACCCCTGTTGGAAAAGATAGAAATTCGAGGTTGGAATTCGAGGATTTACTG 2761
Qy 2537 GTATTATCCACCTTCCAAAGGCTCAAGGAGATTTTCACTTGGATACGAAAGTAAAGTGGCTG 2596

Db 2762 GTATCATTTACCTTCCAAAGCTCAAGGAGATTTCCAAATTAGATACGAGTAAGATGGCTG 2821
Qy 2597 GGCTTGTCTAGCTCGAGGAGAGATGCGCACACACCCAAATCACTCCCTGCTGCGAAAGA 2656
Db 2822 GGCTTGTCTAGCTCGAGGAGAGATGAAACGACACCCAAATCGCCCGCTGCTCTAAATGT 2881
Qy 2657 GGGAGGACCGAAGTATCATCAGACCTTCTTGTGACGCGGAGGATCCCTCTTGAAGTGG 2716
Db 2882 ACAGTGACCGAAGTATCATCAGACCTTGGGGCTGAAGCGGAAAGGATCTTCTATAGAAGTGC 2941
Qy 2717 AAGCAACGGATCCCTCCAGAGCAGGAGGCA 2748
Db 2942 AAACAGCAGATCTCTGTTCTCTGATCCCGAAGCA 2973

RESULT 6
ADI57175
ID ADI57175 standard; DNA; 3276 BP.
XX
AC ADI57175;
XX
DT 22-APR-2004 (first entry)
XX
DB Oryza minuta P19 locus nucleotide binding site (NBS) gene #5.
XX
KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; gene; ds.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JAN-2003; 2003US-00352179.
XX
PR 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX
PA (WANG/) WANG G.
PA (LIU/) LIU G.
PI Wang G, Liu G;
XX
DR WPI; 2004-121064/12.
DR P-PSDB; ADI57176.
XX
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
PS Claim 3; SEQ ID NO 92; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents an NBS gene from
CC the Oryza minuta P19 locus.
XX
SQ Sequence 3276 BP; 1028 A; 631 C; 770 G; 847 T; 0 U; 0 Other;
Query Match 79.3%; Score 2377.6; DB 12; Length 3276;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 2443; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
Qy 197 TAGCAATAGATTCTCTATGCGAGAGACATTCGCAATCAATCAGCTCGAAATGTGATGAAG 256
Db 599 TTGACATGGATTCTATGTCAGAGACATTCGTAATCAGTCAGCTCGCAATGTGATGAAG 658
Qy 257 CTGAGCTTGTGGGTTTTCTGACTCCAGAAAGGCTGCTTGAATGATCGATACCAATG 316
Db 659 CTGAGCTTGTGGGTTTTCTGACTCCAGAAAGGTTGCTTGAATGATCGATACCAATG 718

Qy 317 CTAATGATGGTCCGGCCAAAGTAATCTGTGTTGTTGGGATGGGTGGTTTAGGCAAGACAG 376
Db |||||
Qy 719 CTAATGATGGTCCGGCCAAAGTAATCTGTGTTGTTGGGATGGGTGGTTTAGGCAAGACAG 778
Db |||||
Qy 377 CTCTTTGCGAAGAGATCTTTGAAAGCGAAGAGACATTAAGGAAGAACTTCCTCTGCAATG 436
Db |||||
Qy 779 CTCTTTGCGAAGAGATCTTTGAAAGCGAAGAGACATTAAGGAAGAACTTCCTCTGCAATG 838
Qy 437 CTTGGATTAAGTGTCAATCATTTTCAAGGATTTGAGCTCTTAAGAGATATGATACGCC 496
Db |||||
Qy 839 CTTGGATTAAGTGTCAATCATTTTCAAGGATTTGAGCTCTTAAGAGATATGATACGCC 898
Qy 497 AACTTTCTGGCCCCAGTTCTCTGATCAACTCTTTCGAAGAAATTCGAAGGGAAGGTGGTG 556
Db |||||
Qy 899 AACTTCTAGTCCCAATCTCTGAAAACAATCTTTCGAAGAAATTCGAAGGGAAGGTGGTG 958
Qy 557 TCGAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTACTTTTG 616
Db |||||
Qy 959 TCGAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTACTTTTG 1018
Qy 617 TTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGATAAATGCAATTTTC 676
Db |||||
Qy 1019 TTATTTCTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGATAAATGCAATTTTC 1078
Qy 677 CTAAGAAACAATAAGAAAGGCGAGTCAAAATAGTAATAAACCACTTTGGAATGTTGATCTTGCGG 736
Db |||||
Qy 1079 CTAAGAAACAATAAGAAAGGCGAGTCAAAATAGTAATAAACCACTCTCGGAATGTTGATCTAGGG 1138
Qy 737 AGAAGTGTGCCACAGCCTCACTGTGTACCACTTTGATTTCTTCAGATGAACGATGCCA 796
Db |||||
Qy 1139 AGAAGTGTGCCACAGCCTCACTGTGTACCACTTTGATTTCTTCAGATGAACGATGCCA 1198
Qy 797 TAACAATTTGCTACTGAGAAAACAATAAATCATGAAGACATGGATCAAAATAAAATA 856
Db |||||
Qy 1199 TAAATTTGCTACTAAGAAAACAATAAATCAATCAATGAAGACATGGAAATCAAAATAAAATA 1258
Qy 857 TGCAAAAAGATGGTTGAAGCAATTTGTAATAAATGTTGTTGCTACCACTTACCAATAGCAATACTTA 916
Db |||||
Qy 1259 TGCAAAAAGATGGTTGAAGCAATTTGTAATAAATGTTGTTGCTCTACCAATAGCAATACTTA 1318
Qy 917 CAATPAGAGCTGTCTTTGCCAACTAAACAGAGTGTGAGAAATGGGAGAAATTTCTATGAACACC 976
Db |||||
Qy 1319 CAATPAGAGCTGTCTTTGCCAACTAAACAGTGTGAGAAATGGGAGAAATTTCTATGAACAGC 1378
Qy 977 TTCTTTCAGAACTAGAAATAAACCCAGCCTGGAGCTTTTCAGAGAAATGGTGAACCCCTAG 1036
Db |||||
Qy 1379 TTCTTTCAGAACTAGAAATAAACCCAGCCTGGAGCTTTTCAGAGAAATGGTGAACCCCTAG 1438
Qy 1037 GTTACAACCACTACCACTCCCATCTGAACCCATCGCTTTTGTATCTAAGTATCTTTCTCTG 1096
Db |||||
Qy 1439 GTTACAACCACTACCACTCCCATCTGAACCCATCGCTTTTGTATCTAAGTATCTTTCTCTG 1498
Qy 1097 AGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAAGAGGTTTGTTA 1156
Db |||||
Qy 1499 AGGATTTTGAATCAAAAGGAATCGTCTGTAGGTAGATGGATAGCAAGAGGTTTGTTA 1558
Qy 1157 GACCAAGGTTGGATGACGACTAAGGATTCGAGAGAAAGTTACTTTAATGAGCTAATCA 1216
Db |||||
Qy 1559 GACCGCAGGTTGGGATGACGACTAAGGATTCGAGAGAAAGTTACTTTAATGAGCTAATCA 1618
Qy 1217 ACCGAAGTATGATTTCAAGCATCAAGAGTGGGCAATAGCAGGAAAAATTAAGACTTTGTCGAA 1276
Db |||||
Qy 1619 GCCGAAGTATGATTTCAAGCATCAAGAGTGGGCAATAGCAGGAAAAATTAAGACTTTGTCGAA 1678
Qy 1277 TTCTATGATATCATCCGTGATATCAGTTTCAATCTTCGAGACAGGAAAAATTTGTAATGT 1336
Db |||||
Qy 1679 TCCATGATATCATCCGTGATATCAGTTTCAATCTTCGAGACAGGAAAAATTTGTAATGT 1738
Qy 1337 TACCAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAAAACATCGGCCACATAGCATTTCCATG 1396
Db |||||
Qy 1739 TACCAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAAAACATCGGCCACATAGCATTTCCATG 1798

Qy 1397 GGAATATGTCTCTGCAAAACAGGATTTGGATTTGGAGCATTAATTCGATCAATAGCTATTTTGT 1456
Db |||||
Qy 1799 GGAATATGTCTCTGCAAAACAGGATTTGGATTTGGAGCATTAATTCGATCAATAGCTATTTTGT 1858
Qy 1457 GTGACAGACCAGAGCTTAGCACATGCACTTTGTCCAGATCAATTCAGAGATGTTACGGG 1516
Db |||||
Qy 1859 GTGACAGACCAGAGCTTAGCACATGCACTTTGTCTAGATCAATTCAGAGATGTTACGGG 1918
Qy 1517 TCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCAT 1576
Db |||||
Qy 1919 TCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCAT 1978
Qy 1577 TGTGTGCCACTTTGAAATACCTTGAATATTGGATATTCTGTCAATCAATATTCCTCTCCCA 1636
Db |||||
Qy 1979 TGTGTGCCACTTTGAAATACCTTGAATATTGGATATTCTGTCAATCAATATTCCTCTCCCA 2038
Qy 1637 GATCCATTTGTTAAACTACAGGGCCTACAAAATTTTGAACATGCTGAGAAACATACATTCGAG 1696
Db |||||
Qy 2039 GATCCATTTGTTAAACTACAGGGCCTACAAAATTTTGAACATGCTGAGAAACATACATTCGAG 2098
Qy 1697 CACTTACCAAGTGTAGATCAGTAAACTCTCCAATGTCTGCATACTCTTCGTTGTAGTAGAAAGT 1756
Db |||||
Qy 2099 CACTTACCAAGTGTAGATCAGTAAACTCTCCAATGTCTGCATACTCTTCGTTGTAGTAGAAAGT 2158
Qy 1757 TTGTTTCTGACAACTTTTGTCTAAACCAACCAATGAAAGTGCATAACTAAACAATATGCCC 1816
Db |||||
Qy 2159 TTGTTTATGACAACTTTTGTCTAAACCAACCAATGAAAGTGCATAACTAAACAATATGCCC 2218
Qy 1817 TGCTTAAAGTATTTCAACACTTTTGTAGTTCGAGATGATCGTGCATTAACAATTTGCTGAAT 1876
Db |||||
Qy 2219 TGCTTAAAGTATTTCAACACTTTTGTAGTTCGAGATGATCGTGCATTAACAATTTGCTGAAT 2278
Qy 1877 TGCAATGTGCCACCAAAAGTTTGTGTATAAACTCATTTCCGTTGTGAAGGTACCCAAAAGAA 1936
Db |||||
Qy 2279 TGCAATGTGCCACCAAAAGTTTGTGTCTGAATCATTTCCGTTGTGAAGGTACCCAAAAGAA 2338
Qy 1937 TAGTAAAGTTGCGAGACTTACAGTCTTAGAGTATGTAGATATCAGCGGACCACTAGTA 1996
Db |||||
Qy 2339 TAGTAAAGTTGCGAGACTTACAGTCTTAGAGTATGTAGATATCAGCGGACCACTAGTA 2398
Qy 1997 GAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTTGAGGAAATTTAGGTGTGATGCAATG 2056
Db |||||
Qy 2399 GAGCAATCAAGAGCTGGGCGAGTTAAGCAAGTTGAGGAAATTTAGGTGTGATGCAATG 2458
Qy 2057 GCTCGACAAAAGGAAAAATGTAAGATACTTTGTGCGAGCAATTTGAGAAAGCTCTCTTCCCTCC 2116
Db |||||
Qy 2459 GCTCGACAAAAGGAAAAATGTAAGATACTTTTATGCGGCCATTTGAGAAAGCTCTCTTCCCTCC 2518
Qy 2117 AATATCTCTATGTGAATGTCTGCAAGGAATCTCAGATGGTGGAAACACTTTGAGTGCCTAGATT 2176
Db |||||
Qy 2519 AATCTCTCTATGTGAATGTCTGCGTTATTTATCAGATATTTGAAACACTTTGAGTGCCTAGATT 2578
Qy 2177 CTATTTCTCTCTCTCTCTCTCTACTAGGACACTCGTGTGTTGTATGGAAGCTTTGGAAGAGA 2236
Db |||||
Qy 2579 CTATTTCTCTCTCTCTCTCTCTACTAGGACACTCGCGGTTGGAATGGAAGCTTTGGAAGAGA 2638
Qy 2237 TGCTTAATCTGATTTGAGCAGCTCACTCACCTGAAGAGATCTACTTATTTAGGAGGACAAAC 2296
Db |||||
Qy 2639 TGCTTAATCTGATTTGAGCAGCTCACTCACCTGAAGAGATCTACTTATTTAGGAGGACAAAC 2698
Qy 2297 TAAAGGAAGGTAAACCAATCTGATACTTTGGGCAATTTGCCAACCTCATGTCTTGTATC 2356
Db |||||
Qy 2699 TAAAGGAAGGTAAACCAATCTGATACTTTGGGCAATTTGCCAACCTCATGTCTTGTATC 2758
Qy 2357 TTTATTCGGAAGCTTACTTTGGGAGAGAGCTAGTATTTCAAAAACAGGAGCATTTCCCAATC 2416
Db |||||
Qy 2759 TTTATTCGGAATGCTTACTTTGGGAGAGAGCTAGTATTTCAAAAACGGAAGCATTTCCCAATC 2818
Qy 2417 TTAGAACACTTTTCGATTTTTCGATTTGATCAGCTTAAGAGAGATTTAGATTTTCGAGGACGCA 2476
Db |||||
Qy 2819 TTAGAACACTTTTCGATTTTTCGATTTGATCAGCTTAAGAGAGATTTAGATTTTCGAGGATGCA 2878
Qy 2477 GCTCGCCCCAGTTGGAAAAAGATAGAAATCAGATTTCTCGAGGTTGGAATTCAGGGATTTATTG 2536


```
Qy 1282 GATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTGTTACCA 1341
Db |||||
Qy 1507 GATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTATACCA 1566
Db |||||
Qy 1342 ATGGGAGATGCTCTGATTTAGTTTCAAGAAACACATCGCCACATAGCATNTCCATGGGAGT 1401
Db |||||
Qy 1567 ATGGGAGATGCTCTGATTTAGTTTCAAGAAACACATCGCCACATAGCATNTCCATGGGAGT 1626
Db |||||
Qy 1402 ATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTATTCGATCATTTAGCTATTTTGGTGAC 1461
Db |||||
Qy 1627 ATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTATTCGATCATTTAGCTATTTTGGTGAC 1686
Db |||||
Qy 1462 AGACCCAAAGAGTCTAGCACATGTCAGTTTGTCCAGATCAATTTAGAGATGTTTACGGGCTTTG 1521
Db |||||
Qy 1687 AGACCCAAAGAGTCTAGCACATGTCAGTTTGTCCAGATCAATTTAGAGATGTTTACGGGCTTTG 1746
Db |||||
Qy 1522 GATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTTCGATTTGTTG 1581
Db |||||
Qy 1747 GATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTTCGATTTGTTG 1806
Db |||||
Qy 1582 TGCCACTTTGAATTTAGTATTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTG 1641
Db |||||
Qy 1807 TGCCACTTTGAATTTAGTATTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTG 1866
Db |||||
Qy 1642 ATTGCTAAACTACAGGGGCTACAAACTTTGAAACATGCCGAGCACATACATTTGCAGCACTA 1701
Db |||||
Qy 1867 ATTGCTAAACTACAGGGGCTACAGACTTTGAAACATGTCAAGCACATACATTTGCAGCACTA 1926
Db |||||
Qy 1702 CCAAGTGAGATCAGTAACTCTCAATGTCTGATATCTCTTCGTTGTAGTAGAAAGTTGTTT 1761
Db |||||
Qy 1927 CCAAGTGAGATCAGTAACTCTCAATGTCTGATATCTCTTCGTTGTAGTAGAAAGTTGTTT 1986
Db |||||
Qy 1762 TCTGACAACTTTAGTCTAAACCCCAATGAGTGCATATCACTAATATGCTGCCT 1821
Db |||||
Qy 1987 TTTGACAACTTTAGTCTAAATCACCCCAATGAGTGCATATCACTAATATGCTGCCT 2046
Db |||||
Qy 1822 AAAGTATTTCACACCTTTAGTTAGTTCGGATCATCTGTCGAATACAAATTTGCTGAATTTGCAC 1881
Db |||||
Qy 2047 AAAGTATTTCACACCTTTAGTTAGTTCGGATCATCTGTCGAATACAAATTTGCTGAATTTGCAC 2106
Db |||||
Qy 1882 ATGCCCAACCAAAAGTTGCTGTATATAATTCATTCGGTGTGAAGGTACCCAAAGGAATAGGT 1941
Db |||||
Qy 2107 ATGCCCAACCAAAAGTTTCTGTCTGAATCATTCGGTGTGAAGGTACCCAAAGGAATAGGT 2166
Db |||||
Qy 1942 AAGTTGGAGACTTACAGGTTCTAGATATGTAGATATCAGGCGGACACAGTAGTAGGCA 2001
Db |||||
Qy 2167 AAGTTGGAGACTTACAGGTTCTAGATATGTAGATATCAGGCGGACACAGTAGTAGGCA 2226
Db |||||
Qy 2002 ATCAAAGAGCTGGGCGCAGTTAAGCAAGCTGAGGAAATTTAGGTGTGATGACAAAATGGCTCG 2061
Db |||||
Qy 2227 ATCAAAGAGCTGGGCGCAGTTAAGCAAGTTGAGGAAATTTAGGTGTGATGACAAAAGGCTCG 2286
Db |||||
Qy 2062 ACAAGGAAAAATGTAAGATATCTTTGTGCGCCATTTGAGAGAGCTCTCTTCCTCCCAATAT 2121
Db |||||
Qy 2287 ACAAGGAAAAATGTAAGATATCTTTGCGCCATTTGAGAGAGCTCTCTTCCTCCCAATCT 2346
Db |||||
Qy 2122 CTCTATGTGAATGTGCGAGGAATCTCAGATGGTGGAAACACTTTGAGTGCTTAGATTTCTATT 2181
Db |||||
Qy 2347 CTCTATATGAATGTGCGCTTTATATCAGATATTTGAAACACTTTGAGTGCTTAGATTTCTATT 2406
Db |||||
Qy 2182 TCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2241
Db |||||
Qy 2407 TCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2466
Db |||||
Qy 2242 AACTGGATTGAGCAGCTCACTCACTGAAAGAGATCTACTTTATTGAGGAGCAAACTAAAG 2301
Db |||||
Qy 2467 AACTGGATTGAGCAGCTCACTCACTGAAAGATTTCACTTATGAGTAGTAACTAAAG 2526
Db |||||
Qy 2302 GAAGGTAACCATGTGATATCTTGGGGCATTTGCCAACCTCATGTGCTTGTATCTTTAT 2361
Db |||||
Qy 2527 GAAGGTAACCATGTGATATCTTGGGGCATTTGCCAACCTCATGTGCTTGTATCTTTAT 2586
Db |||||
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Qy 2362 CGGAAAGCTTACCTTGGGGAGAGCTAGTATTTCAAAAACAGGAGCAATTTCCAAAATCTTTAGA 2421
Db |||||
Qy 2587 CATAAATTTTATCTTTGGGGAGAGCTAGTATTTCAAAAACGGGAGCAATTTCCAAAATCTTTAGA 2646
Db |||||
Qy 2422 ACACCTTCGATTTACGATTTGGATCAGCTAAGAGAGATTTAGATTTGAGGACGGCAGCTCG 2481
Db |||||
Qy 2647 ACACCTTCGATTTTCAATTTTGGATCAGCTAAGAGAGATTTAGATTTGAGGACGGCAGCTCA 2706
Db |||||
Qy 2482 CCCAGTTCGAAAAAGATAGAAATCAGATTTCTGTCAGGTTTGGAAATCAGGAGATTTATTTGGTATT 2541
Db |||||
Qy 2707 CCCAGTTCGAAAAAGATAGAAATCTCTGTCAGGTTTGGAAATCAGGAGATTTATTTGGTATC 2766
Db |||||
Qy 2542 ATCCACCTTCCAAAGGCTCAAGGAGATTTCACTTGGATACGAAAGTAAAGTGGCTGGGCTT 2601
Db |||||
Qy 2767 ATTCACTTCCAAAGGCTCAAGGAGATTTCACTTGAATACAAAAGTAAAGTGGCTAGGCTT 2826
Db |||||
Qy 2602 GCTCAGCTGAGGAGGAGGAGTGGCGCACACCCAAATACACCCGTCGTCGCAAGAGGGAG 2661
Db |||||
Qy 2827 GGTGAGCTGAAGGGAGAGTGAACACACCCAAATCGCCCGTCTGCGAATGGACAGT 2886
Db |||||
Qy 2662 GACCGAAGTGATCAGCACTTTGCTTGTGACGCCGAAGGATCCCTGTTTGAAGTGGAGCA 2721
Db |||||
Qy 2887 GACCGAAGGATCAGCACTTGGGGGCTGAAGCCGAGAGATCTTCTATAGAAGTGCMAACA 2946
Db |||||
Qy 2722 ACGGATCCCTCCAGAGCAGGAGGGA 2748
Db |||||
Qy 2947 GCAGATCCTGTTCTCTGATGCCAAGGA 2973
Db |||||
```

RESULT 8

AD157173

ID AD157173 standard; DNA; 3220 BP.

XX AC AD157173;

XX DT 22-APR-2004 (first entry)

XX DE Oryza minuta Pi9 locus nucleotide binding site (NBS) gene #4.

XX KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;

XX OS plant breeding; transgenic plant; plant; gene; ds.

XX OS Oryza minuta.

XX PN US2004006788-A1.

XX PD 08-JAN-2004.

XX PF 27-JAN-2003; 2003US-00352179.

XX PR 25-JAN-2002; 2002US-0352106P.

XX PR 01-FEB-2002; 2002US-0353304P.

XX XX (WANG/) WANG G.

XX XX (LIU/) LIU G.

XX XX Wang G, Liu G;

XX XX WPI; 2004-121064/12.

XX XX P-PSDB; AD157174.

XX XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2

XX XX and NBS3, useful for producing plants resistant to Magnaporthe grisea

XX XX infection.

XX XX Claim 3; SEQ ID NO 90; 136pp; English.

XX XX The invention comprises the amino acid and coding sequences of nucleotide
XX XX binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
XX XX blight and rice blast resistance genes). The DNA sequences may be used as
XX XX markers for resistance to infection with Magnaporthe grisea in plant
XX XX breeding programs. The present DNA sequence represents an NBS gene from
XX XX the Oryza minuta Pi9 locus.

XX SQ Sequence 3220 BP; 990 A; 616 C; 747 G; 867 T; 0 U; 0 Other;
Query Match 47.1%; Score 1411; DB 12; Length 3220;
Best Local Similarity 74.1%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 620; Indels 40; Gaps 7;
Qy 206 ATTCTATGCGAAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAGCTTG 265
Db |||||
Qy 431 ATTTATTTATGGAAGACATTCGCAACCAATTAAGCTAAACATTTGAGGAAGCTGATCTTG 490
Db |||||
Qy 266 TTGGGTTTCTCGACTCAAGAAAGGCTGCTTGAATGATCGATACCAATGCTAATGATG 325
Db |||||
Qy 491 TGGGTTTTTCTGGACCCAAAGAGAGATGCTTGATCTTATAGATGTCATGCCAATGACG 550
Db |||||
Qy 326 GTCCGGCCAAAGTAACTCTGTGTTGGGATGGGTGGTTAGGCAAGACAGCTCTTTCGA 385
Db |||||
Qy 551 GACCTACAAAGTTGATGTGTTGCGTATGGGTGGTTGGGTAAGACTACTATTGCAA 610
Db |||||
Qy 386 GGAAGATCTTTGAAGCGAAGACATTAAGGAAGAACTTCCCTTGGCAATGCTTGGATTA 445
Db |||||
Qy 611 GGAATAATTTGAAGCAAGAGAGACATTTGCAAGAAATTTTTCTTGTGCTTGGATTA 670
Db |||||
Qy 446 CAGTGTCAACATCTTTCACAGGATTCAGCTACTTAAGATATCATCGCCCACTCTTG 505
Db |||||
Qy 671 CTGTTTCAACATCTCTTGTAGGGTGAACCTACTCAAGGATTTGATGGTGAACCTTTTG 730
Db |||||
Qy 506 GCCCCAGTTCTCTGGATCAACTCTTTCGAAGAAATTCGAAGGGAAGGTGGTGCAGTAC 565
Db |||||
Qy 731 GAGAGGAAGTACTGAAGAGCGGCTGAGAGAACTCGAAGGAA---GGTCCCAAGTAG 787
Db |||||
Qy 566 ATCATCTTTCGAGTACTGATAGAAGAGCTCAAGGAGAGAGAGTACTTTGTTGTTCTAG 625
Db |||||
Qy 788 ACGACCTCGCAGCTACTCTCAGGACAGAGTTAAATGAAAGGAGGTACTTTGTTGCTTG 847
Db |||||
Qy 626 ATGATCTATGGAATTTACATGATTTGGAATTTGGAATGAATTTGCAATTTCTTAAGACA 685
Db |||||
Qy 848 ATAACGTGTGGATACAGATTCATGGAATGGATTAATAGTATTTGCTTCCCTTGAATA 907
Db |||||
Qy 686 ATAGAAGGGCAGTCAAAATAGTAATAACCACTTGGATTTGATCTTGGGAGAGAGTGTG 745
Db |||||
Qy 908 ACAATAAGGGAGCGGGTGTAGTAAACAACAGAGATTTGGCTTAACTAAGAGGTGA 967
Db |||||
Qy 746 CCACAGCTCACTGGGTGACACCTTGATTTCTTTCGAGATGAACGATGCCATAACATTGC 805
Db |||||
Qy 968 CTTCTGAATTCCTTATCTACCAGCTTAAACCCCTAGAAATAAACTATGCAAAAGAGTTGC 1027
Db |||||
Qy 806 TACTGAGAAAAAATAAATAATCATGAGCATGGAAATCAATAAATAATATGCAAAAGA 865
Db |||||
Qy 1028 TTCTACGGAAGCAAAATAAGCAATAGGAGATATGGAAGGTGATAAAGATGAGTGACA 1087
Db |||||
Qy 866 TGGTTGAACGAATTTGTAATAATGTTGCTGCTTACCATTAGCAATATCTTACAAATAGGAG 925
Db |||||
Qy 1088 TTATACTAATAATAAAGAGTGTGCTATTTACCCTGGCTATATCTCAATAGAG 1147
Db |||||
Qy 926 CTGTGCTTGCACCTAAACAGGTGTGAGAAATTTCTATGAACACCTTCCCTTCAG 985
Db |||||
Qy 1148 GCGTGTCTTCCACCAAGAGATAAGAGAGTGGGAACTTTTTATAGTCAGATACCTTCAG 1207
Db |||||
Qy 986 AACTAGAAATAAACCCAGCTGGAAGCTTTGAGGAGATGGTGAACCTAGGTTTACAACC 1045
Db |||||
Qy 1208 AGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAGGATAGTGACCTTAAGTTTACAAC 1267
Db |||||
Qy 1046 ACCTACCATCCCATCTGAACCAATGCTTTTGTATCTAAGTATCTTTCTGAGGATTTTG 1105
Db |||||
Qy 1268 ACTTACGCTCTCATCTTAAGCAATGCTTTTTGTATCTAAGCAATATTTCTGAGGATTTTG 1327
Db |||||
Qy 1106 AAATCAAAAGGAATCGTCTAGTAGGTAGATGGATGAGAGAGGTTTGTAGACCAAGG 1165
Db |||||
Qy 1328 AAATTAATAGGAACCGTCTGTAAATAGATGATGGCAGAGGGTTTTATTAAAGCTAGGA 1387
Db |||||
Qy 1166 TTGGGATGACGACTAAGATGTCGGAGAAAGTTACTTTAATGAGCTAATCAACCGAAGTA 1225
Db |||||

Db 1388 CTAATATGACTATTGAAGATGTTGGGAAAGTTACTTTAAAGAACTTATCAACCGTAGCA 1447
Qy 1226 TGATTTCAACGATCAAGAGTGGGCATAGCAGGAAATAATTAAGACTTTGTGCAATTCATGATA 1285
Db |||||
Db 1448 TGATTCAGCCATCAAGAGCGGTATACAGGAGATTTTAAAGAGCTGTCGAGTCCACGACA 1507
Qy 1286 TCATCCGTGATATCAGAGTTTCAATCTCGAGACAGGAAATTTTGTATTTGTTTACCAATGG 1345
Db |||||
Db 1508 TCATCCGTGATATTACAAATTTGATTTTCTAGAGAGAAATTTTCACACTCTTTACCCGATG 1567
Qy 1346 GAGATGCTCTGATTTAGTTTTCAGGAAACACTCCGCCACATAGCAATTCATCGGAGTAGT 1405
Db |||||
Db 1568 GCACTGACTATGATGTAGTACATGGGAACACTCGGCACTAGAAATTTTTCACGGGAGTAGT 1627
Qy 1406 CCTGC---AAAAACAGGATTTGGATTGGAGCAATTAATTCGATCAATAGCTATTTTGGTGACA 1462
Db |||||
Db 1628 ATTGCTCTGAAAACAAGCTTGGACTGGAGCAATTAACGGTCAATTAACATATGTTGGTGAGA 1687
Qy 1463 GACCCAAAGTCTAGACATGCGAGTTTGTCCAGATCAATTTGAGGATGTTTACGGGTCTTGG 1522
Db |||||
Db 1688 GGTCCGTAGAACTAGAGCAATTCAGTTGTTTCTCAGTTGAGGATGTTTACGGGTCTTGG 1747
Qy 1523 ATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACGCTATTCGATTTGTTGT 1582
Db |||||
Db 1748 ATCTAACAGATGCAATTTTCTATCAACAAATGATGTGCAACAACATAGTCTCTTGT 1807
Qy 1583 GCCACTTGAATACTTCTGAGTATT-----GGATAATTCGTCTCATCATATTTCACTT 1632
Db |||||
Db 1808 GCCACTTGAATACTTCTGATGATTAAGATACAGATACCGTTTCAACATATATTTTCACTT 1867
Qy 1633 CCAGATCCATTTGGTAAACTACAGGGCTCAAACTTTTGAACATGCCGAGCACATACATT 1692
Db |||||
Db 1868 CCACAATCCATAGCTAGACTGCAATGTTCTGAGACATTTGGACTTTGGGTGACAGCTACATT 1927
Qy 1693 GCAGCACTACCAAGTGAATCAGTAAACTCCTCAATGCTGCTGCTACTCTTCTGTTGTAGTAGA 1752
Db |||||
Db 1928 TCAACACTGCCAATCTAGATTACT-AACTTGGAGTCTCCGTAGCTTTCGATGATGANA 1986
Qy 1753 AAGTTGTTTCTGACAACTTTAGTCTAAACCCCAATGAAGTGCATAACTAAACACATA 1812
Db |||||
Db 1987 GAATATTTTCTTCTTCTTT-----AACACATATTTTAACTAAACACATTA 2031
Qy 1913 TGCTGCTTAAAGTATTTCACACTTTAGTTAGTCGCGATGATTCGTGCATTAACAATTTGCT 1872
Db |||||
Db 2032 TGCTGCTCCATGATATTTCACACTTTCGTTAGTACCTCGGATCGTTCTGAAACAATTTGCT 2091
Qy 1873 GAATTCACATGCGCCCAAAAGTTGCTGTTAATAATCAATTCGCTGTTGAAGTACCACAA 1932
Db |||||
Db 2092 AAATTCACATGCGCCCAAAAGGCTTCCGTTCAAAATCAATGTTGTCAGGTTACCAANA 2151
Qy 1933 GGAATAGGT---AAGTTGCGAGACTTTACAGGTTTCTAGAGTATGTAGATATCAGCGCGAC 1988
Db |||||
Db 2152 GGAATATGTAATAAATAAATACTCGACTTCAAAATTTGGAGGTAGTGGATATTAGAGGAC 2211
Qy 1989 CAGTAGTAGCAATCAAGAGCTGGGGCAGTTTAAGCAAGCTGAGGAAATTTAGGTGTAT 2048
Db |||||
Db 2212 TAGCAGTAGAGCAATCAAGAGTTGGGGCAGTTAAGCAAGCTGAGGAAATTTATGTTGGT 2271
Qy 2049 GACAAATGCTCGACAAAGGAAATGTAAGATACTTTGTCAGCCATTTGAGAGCTCTC 2108
Db |||||
Db 2272 ACAAAGGGAATCCAAAGGAAATTTGAGATACTCTATACACTATCCAGAAAGCTCTG 2331
Qy 2109 TTCCCTCCAATATCTCTATGTGAATGCTGAGGAATCTCAGATGGTGGAAACACTTTGAGTG 2168
Db |||||
Db 2332 TTTCTACATCTCTCAATGTGAATGCTGTGGGATTTTCAGGTATTGGAACACTTCACTG 2391
Qy 2169 CCTAGATTTCT 2228
Db |||||
Db 2392 TATAGATTCTTATTTCT 2451
Qy 2229 TGAAGAGATCGCTAACTGGATTTGAGCAGCTCACTCACTGAGAGAGATCTACTTATTGAG 2288
Db |||||
Db 2452 TGAGGAGATGCTTAACCTGGATTTGAGCAGCTCACGCACTCTGATGAAGTTCACTTATGGAG 2511

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Qy 2289 GAGCAAACTAAGGAAGTAAACCATGCTGATCTTGGGGCATTTGCCAACCTCATGGT 2348
    |||||
Db 2512 GAGCAAACTAAGGAAGTAAACCATGCTGATCTTGGGGCATTTGCCAACCTCATGGT 2571
    |||||
Qy 2349 CCTTGATCTTTATCGGAAAGCTTACCTTTGGGGAGAGCTAGTATTCAAAAAGAGGCAAT 2408
    |||||
Db 2572 CCTTTATCTTCAATCCCAATGCTTACCATGGGGAGAGCTAGTATTCAAAAATGGGAGCAAT 2631
    |||||
Qy 2409 CCCAAATCTTAGACACTTTTCGATTTACGATTTTCGATTCGATTCGATTCGATTCGATTTGA 2468
    |||||
Db 2632 CCCAAATCTTAGACACTTTTCGATTTACGATTTTCGATTCGATTCGATTCGATTTGA 2691
    |||||
Qy 2469 GGACGGCAGCTCGCCCGAGTTGGAAAGATAGAAATCAGATTTCTGCAGGTTGGAAATCAGG 2528
    |||||
Db 2692 GGACGGCAGCTCAATCTTGTGGAAAGATAGAAAT----ATTGAGGTTGGAAATCAGG 2747
    |||||
Qy 2529 GATTATTTGGTATTATCCACTTCCCAAGCTCAAGGAGATTTCACTTGGATACGAAAGTAA 2588
    |||||
Db 2748 GATTGTTGGTATCATTCACCTTCCCAAGCTCAAGGAGATTTCACTTGGATACGAAAGTAA 2807
    |||||
Qy 2589 AGTGGCTGGGCTTCTCAGCTGGAGGGAGAGTGGGCACACACCAATCACCCCGTCT 2648
    |||||
Db 2808 AGTGGCTAGGCTTGGTCACTGGAGGGAGAGTGGGCACACACCAATCACCCCGTCT 2867
    |||||
Qy 2649 GCGAAAGAGGGAGGACCGAAGTGTACGACCTTGTGTCGCGCGAAGGATCCCCCTGT 2708
    |||||
Db 2868 GCGAATGAGGGAGGACCGAAGTGTACGACCTTGTGTCGCGCGAAGGATCCCCCTGT 2927
    |||||
Qy 2709 TGAAGTGAAGCAACGGATCCCTCCAGAGCA 2741
    |||||
Db 2928 TGAAGTGAAGCAACAGATCTCTGTGAGAGCTCA 2960
    |||||
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RESULT 9

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ADMT72252
ID ADM72252 standard; cDNA; 2422 BP.
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AC XX

XX XX

XX 03-JUN-2004 (first entry)

DT XX

DE XX O. minuta Pi2 region fragment cDNA-21.

KW XX Pi2; NBS1; plant protectant; gene therapy; rice; disease resistance;

KW XX Gene; ss.

XX Oryza minuta.

OS XX

XX WO2004022715-A2.

XX PN

XX 18-MAR-2004.

PD XX

XX 08-SEP-2003; 2003WO-US027913.

XX PF

XX 09-SEP-2002; 2002US-0409216P.

XX PR

XX 18-MAR-2003; 2003US-0455713P.

XX PR

XX 05-SEP-2003; 2003US-00656394.

XX XX

XX (OHIS) UNIV OHIO STATE.

XX PA

XX Wang G;

XX PI

XX WPI; 2004-257576/24.

XX DR

XX New rice Pi2-like disease resistance nucleic acid molecule that confers
XX disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.

XX XX

XX Example 6; SEQ ID NO 15; 120pp; English.

XX PS

XX The invention relates to novel broad-spectrum resistance gene Pi2 and the
XX NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like

XX CC

XX CC

CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA-21
CC fragment from the Pi2 region, that matched to NBS4.

XX
SQ Sequence 2422 BP; 718 A; 492 C; 561 G; 635 T; 0 U; 16 Other;

Query Match 45.2%; Score 1354.2; DB 12; Length 2422;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 1254 AGGAAAAATTAAAGACTTGTGCAATTCATGATATCATCCGTGATATCAGATTTCAATCTC 1313

Db 1 AGGAAAAATTAAAGACTTGTGCAATTCATGATATCATCCGTGATATCAGATTTCAATCTC 60

Qy 1314 GAGACAGAAAAATTTTCGATTTTACCAATGGGAGATGGCTCTGATTTAGTTTACAGAAAA 1373

Db 61 GAGACAGAAAAATTTTCGATTTTACCAATGGGAGATGGCTCTGATTTAGTTTACAGAAAA 120

Qy 1374 CACTCGCCACATAGCATTTCCATGGGAGTATGTCCTGCAAAACAGGATTTGGATTGGAGCAT 1433

Db 121 CACTCGCCACATAGCATTTCCATGGGAGTATGTCCTGCAAAACAGGATTTGGATTGGAGCAT 180

Qy 1434 TATTCGATCATTAGCTATTTTGGTGACAGACCAGAGCTAGCACATGCGAGTTTGTCC 1493

Db 181 TATTCGATCATTAGCTATTTTGGTGACAGACCAGAGCTAGCACATGCGAGTTTGTCC 240

Qy 1494 AGATCAATTGAGGATGTTTACGGGCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCA 1553

Db 241 AGATCAATTGAGGATGTTTACGGGCTTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCA 300

Qy 1554 AAAAGATTTCGACCGTATTGTCATTTGTCGCACCTTGAAATFACITTGAGTATFGGATATTC 1613

Db 301 AAAAGATTTCGACCGTATTGTCATTTGTCGCACCTTGAAATFACITTGAGTATFGGATATTC 360

Qy 1614 GTCATTCATATATTCACTTCCAGATCCATTTGGTAAACATACAGGCGCTACAAACTTTGAA 1673

Db 361 GTCATTCATATATTCACTTCCAGATCCATTTGGTAAACATACAGGCGCTACAAACTTTGAA 420

Qy 1674 CATGCCGAGCACATACATTCGACACTACCAAGTGAGATCAGTAAACTCCCAATCTCTGCA 1733

Db 421 CATGCCGAGCACATACATTCGACACTACCAAGTGAGATCAGTAAACTCCCAATCTCTGCA 480

Qy 1734 TACTCTTTCGTTGTAGTAGAAAAAGTTTGTTCGCACACTTTAGTCTAAACCAACCAATGAA 1793

Db 481 TACTCTTTCGTTGTAGTAGAAAAAGTTTGTTCGCACACTTTAGTCTAAACCAACCAATGAA 540

Qy 1794 GTGCATTAACATAACAATATGCTGCTTAAAGTATTACACCTTTAGTTAGTCGCGATGA 1853

Db 541 GTGCATTAACATAACAATATGCTGCTTAAAGTATTACACCTTTAGTTAGTCGCGATGA 600

Qy 1854 TCGTGAATACAAATTCCTGAATTTGCACATGGCCACCAAAAGTTGCTGGTATAAATCAAT 1913

Db 601 TCGTGAATACAAATTCCTGAATTTGCACATGGCCACCAAAAGTTGCTGGTATAAATCAAT 660

Qy 1914 CGGTGTGAAGGTACCCAAAGGAATAGGTAAAGTTTCGAGACTTTACAGSTTCTAGAGTATGT 1973

Db 661 CGGTGTGAAGGTACCCAAAGGAATAGGTAAAGTTTCGAGACTTTACAGSTTCTAGAGTATGT 720

Qy 1974 AGATATCAGCGGACACAGTAGTAGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAG 2033

Db 721 AGATATCAGCGGACACAGTAGTAGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAG 780

Qy 2034 GAAATTAGGTGTGATGACAAATGGCTCGACAAAGAAAAATGTAAGATACCTTTGTGCAGC 2093

Db 781 GAAATTAGGTGTGACAAACAAACCGGTTCGACAAAGAAAAATGTAAGATACCTTTGTGCAGC 840

Qy 2094 CATTGAGAAGCTCTCTTCCCTCCAATATCTCTATGTGAATGCTGCAGGAATCTCAGATGG 2153

Db 841 CATTGAGAAGCTCTCTTCCCTCCAATATCTCTATGTGAATGCTGCAGGAATCTCAGATGG 900

Qy 2154 TGGAAACCTTGAGTGCCTAGATTTCTATTTCTCTCTCCCTCTCCCTACTGAGGACACTCGT 2213

Db 901 TGGAAACCTTGAGTGCCTAGATTTCTATTTCTCTCTCCCTCTCCCTACTGAGGACACTCGT 960

Qy 2214 GTTGTATGGAAGTCTTGAAGAGATGCCCTAACTGGAATTGAGCAGCTCACTACCTGAAGAA 2273
|||
Db 961 GTTGGATGGAATCTTGAGGAGATGCCCTAACTGGAATTGAGCAGCTCACTACCTGAAGAA 1020
|||
Qy 2274 GATCTACTTATTGAGGAGCAACTAAAGGAGGTAAACCACTGCTGATCTACTTGGGGCAAT 2333
|||
Db 1021 GATCTACTTATTGAGGAGCAACTAAAGGAGGTAAACCACTGCTGATCTACTTGGGGCACT 1080
|||
Qy 2334 GCCCAACCTCATGGTCTCTTGATCTTTATCGGAAGCTTTACCTTGGGGAGAGCTAGTATT 2393
|||
Db 1081 GCCCAACCTCATGGTCTCTTGATCTTTATCGGAATGCTTTACCTTGGGGAGAGCTAGTATT 1140
|||
Qy 2394 CAAAACAGGAGCATCCCAAACTTTAGAA CACTTTTCGATTTACGATTTGGAATCAGCTAAG 2453
|||
Db 1141 CAAAACAGGAGCATCCCAAACTTTAGAA CACTTTTCGATTTTATGGAATTTGATCAGCTAAG 1200
|||
Qy 2454 AGAGATTAGATTTCAGGAGCGCAGCTCGCCAGTTCGGAAGAGATAGAAATCAGATTCTG 2513
|||
Db 1201 AGAGATCAGATTTCAGGAGCGCAGCTCACCCCTCTTGGAAAGAGATAGAAATAGCGAGTG 1260
|||
Qy 2514 CAGGTTGGAATCAGGAGTATTGTTGATTTATCCACCTTCCCAAGGCTCAAGGAGATTTCACT 2573
|||
Db 1261 CAGGTTGGAATCTGGGATTACTGTTATCACTTCCCAAGGCTCAAGGAGATTTCCAAAT 1320
|||
Qy 2574 TGGATACGAAGTAAAGTGGCTGGGCTTGTCTCAGCTGGAGGAGAAAGTGGCGCA CACACC 2633
|||
Db 1321 TAGATACGAAGTAAAGTGGCTGGGCTTGTCTCAGCTGGAGGAGAAAGTGAACGCA CACACC 1380
|||
Qy 2634 AAATCACCCTGCTGCGAAGAGGAGGAGCGGAGTGAATCAGCAGCTTGTCTTGAGCG 2693
|||
Db 1381 AAATCGCCCCGTGCTGCTAAATGTACAGTACCGAAGGTATCACGACCTGGGGGCTGAAGC 1440
|||
Qy 2694 CGAAGGATCCCTGTTGAAGTGGAGCAACGAGATCCCTCCAGCAGCAGGAGGGA 2748
|||
Db 1441 CGAAGGATCTCTATAGAAAGTGCAACAGCAGATCTGTTCTGTGATGCCGAGGA 1495
|||

RESULT 10
ADI57167

ID ADI57167 standard; DNA; 2940 BP.

XX AC ADI57167;

XX 22-APR-2004 (first entry)

XX Oryza minuta Pi9 locus nucleotide binding site (NBS) gene #1.

XX nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
XX plant breeding; transgenic plant; plant; gene; ds.

XX Oryza minuta.

XX US2004006788-A1.

XX 08-JAN-2004.

XX 27-JAN-2003; 2003US-00352179.

XX 25-JAN-2002; 2002US-0352106P.

XX 01-FEB-2002; 2002US-0353304P.

XX (WANG/) WANG G.

XX (LIU/) LIU G.

XX Wang G, Liu G;

XX WPI; 2004-121064/12.

XX P-PSDB; ADI57168.

XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection..

XX

PS Claim 3; SEQ ID NO 84; 136pp; English.

CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents an NBS gene from
CC the Oryza minuta Pi9 locus.

XX SQ Sequence 2940 BP; 915 A; 547 C; 717 G; 761 T; 0 U; 0 Other;

Query Match 43.2%; Score 1293.4; DB 12; Length 2940;

Best Local Similarity 70.6%; Pred. No. 0;

Matches 1755; Conservative 0; Mismatches 726; Indels 6; Gaps 2;

Qy 205 GATTCTCTATGCAGAAACATTCGCAATCAATCAGCTCGAATGTGGATGAAGCTGAGCTT 264
|||
Db 433 GATTCTCTATGCAGAAACATTCGCAATCGATCGATAGCAACACTGACGACTGAGACTT 492
|||
Qy 265 GTTGGGTTTTCTGACTCCAAGAAAGGCTGCTTGAATGATCGATACCAATGCTTAATGAT 324
|||
Db 493 GTGGGCTTTGCCAAGACTAAAGATGAGTTGCTTAACTGATAGATGTCAATACTAATGAC 552
|||
Qy 325 GGTCCGGCCAAAGTAACTGCTGTTGGGATGGGTGTTAGGCAAGACAGCTCTTTGCG 384
|||
Db 553 GGTCCAGCTAAAGTGATATGTGGTGGAAATGGGTGGATTTAGGCAAGACTACCTTTGCA 612
|||
Qy 385 AGGAAGATCTTTGAAAGCGAAGACATATTAGGAAGAACTTCCCTTGCAATGCTTGGATT 444
|||
Db 613 AGGAAGCATATGAAACAAGGAACACAT---GAAGAACTTCTCGTGTGCTTGGATC 669
|||
Qy 445 ACAGTGTCACAATCATTTTCAGGATTCAGCTACTTAAAGATATATACGCGCAACTTCTT 504
|||
Db 670 ACTGTGCTCAGTCATTTGACAGGAAGAAATTTCTGAAACAATGATCAGCAACTTCTG 729
|||
Qy 505 GGCCCCAGTCTCTGGATCAACTCTTGCAGAAATTCGAAGGAAAGTGGTGGTGAAGTA 564
|||
Db 730 GGTGCTGATTCATTAGACAACCTCTTGAAGAAATTTAGTGAAGATTTGCTGTCGAAGTC 789
|||
Qy 565 CATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGGAGAGAGGTACTTTGTTGTTCTA 624
|||
Db 790 CAGCATCTCGCTGATCACTTGGTTGAAGGGCTAAAGGAGAAAGGTACTTTGTTGCTCTT 849
|||
Qy 625 GATGATCTATGGATTTTACATGATTTGGAATTTGGATAAATGAAATTTGCAATTTCTTAAGAAC 684
|||
Db 850 GATGACCTATGGACCATAGATGATGCAATTTGGATTCATGATCTGCTTTTCCGAAGATT 909
|||
Qy 685 AATGAAGGGCAGCTCAATAGTAAATTAACCACTTGGAAATGTTGATCTTTCGGGAGAAAGTGT 744
|||
Db 910 AACAAACAGAGGTAGTCGCATAATAATAACAACGCGAGATGCTGGCTTAGCTGGAAGGTGT 969
|||
Qy 745 GCCACAGCTCAGTGGGTACCACTTGATTTCTTTCGAGATGAACGATGCCATTAACATTG 804
|||
Db 970 ACCTCTGAATCAGTTATTTACCCTTGAAACCGTTACATATAGATGATGCTATACACTTG 1029
|||
Qy 805 CTACTGAGAAAAACAAATAAAAAATCATGAAGACATGGAATCAAAATAAAAAATATGCAAAAG 864
|||
Db 1030 CTACTAGCAAAAGCAACAATAAGACTTGAAGACATGGAATAATGATGAGGACTTGGGCAGC 1089
|||
Qy 865 ATGGTTGAACGAATTTGAAATAAATGTTGGTGTCTCACTTATGCAATCTTACCAATAGGA 924
|||
Db 1090 ATAGTTACAAAATTTGGTAAAAAGGTGGTTATTTACCGCTGGCTACTACTACCAATAGGA 1149
|||
Qy 925 GCTGTGCTTCGCACTAAACAGGTGTGAGATGGGAGAAATTTCTATGACACCTTCCCTTCA 984
|||
Db 1150 GGCATTTCTGCTACTAAGAAAGATAATGGAATGGGGAAAAATTTTACAGGAACCTTCCCTTCA 1209
|||
Qy 985 GAACCTAGAAATAAACCCCAAGCTCGAAAGCTTTTGAAGGAGAAATGGTGACCTAGGTTTACAAC 1044
|||
Db 1210 GAGCTTGAGGCAATCCAGCCTAGAGCCATGAGGAGGATGGTGAACCTTAAGCTACAT 1269
|||
Qy 1045 CACCTACCATCCCATCTGAACCAATGCTTTTGTATCTTAAGTATCTTTTCTCTGAGGATTTT 1104
|||

1270	Db	 C A C T T A C C A T C T C A T C T T A A A C C A A T G C T T C T T A C C T A A G T A T T T T C C C T G A A G A T T T T T
1105	Qy	 G A A A T C A A A A G G A A T C G T C T A G T A G G T A G A T A G C A G A A G G G T T G T T A G A C C A A A G
1330	Db	 G A A A T T C A A A G A G G G C C C T G T A G A T A G A T T G A T A G C A G A G G G T T T T G T C A G A G C C A C A
1165	Qy	 G T T G G G A T G A C G A C T A A G G A T G T C G G A A A G T T A C T T A A T A G A G C T A A T C A A C C G A A G T
1390	Db	 G A T G G G G T G A A C A T T G A G G A T G T T G G A A A T A G T C A C T T T A A T A G A G C T T A T C A A C A G A A G T
1225	Qy	 A T G A T T C A A C G A T C A A G A G T G G G C A T A G C A G G A A A A A T T A A G A C T T G T C G A A T T C A T G A T
1450	Db	 C T G A T T C A G C C C T C A A A A G T T A G T A C A G A T G A G T T G T T A A G A G A T G T C G A A T C C A T G A T
1285	Qy	 A T C A T C G T G A T A T C A C A G T T T C A A T C T C G A G A C A G G A A A T T T T G T A T T G T T A C C A A T G
1510	Db	 A T C A T G C G T G A T A T C A T A G T T T C A A T T T C A G A G A G A A A T T T T G T G T T G T A C T A G G
1345	Qy	 G G A G A T G G C T C T G A T T T A G T T C A G A A A A C A C T C G C A C A P A G C A T T C C A T G G G A G A T G
1570	Db	 G A G A A G A T C A C T G T T G T A G C G G A G A G A T C C G C C A T C T A G C A T T T C A T G G G A G C A A A
1405	Qy	 T C C T G C A A A A C A G A A T T G G A T T G A G C A A T T A T T C G A T C A T T A G T A T T T T T G T G A C A G A
1630	Db	 T G C T C A A A G A T A T G C T T T G G A G T G A A C C A T C T G C G C T C A G T A A C T T T G T T G T G T G A C A G A
1465	Qy	 C C C A A G A G T C T A G C A C A T G C A G T T T G T C A G A T C A A T T G A G G A T G T T A C G G T C T C G A T
1690	Db	 C C T G C G G G G A A C A C C T G C A C T T T G T T C A C C A A T T A G A T G C T G A G A G T G T T G A T
1525	Qy	 C T T G A A G A T G A C A T T C T T A A T C A C T C A A A A A G A T T T C G A C C G A T T G C A T T G T T G T G T G C
1750	Db	 C T G A A G A T G C A A A A T T C A A A T T C A C A C A A A T G A T A T C A G G A T A T A G G G T T G T T G C G C
1585	Qy	 C A C T T G A A A T A C T T G A G T A T T G G A T A T T G G T C A T C C A T A T A T T C A C T T C C C A G A T C A A T T
1810	Db	 C A C A T G A A A T A T T T G A A T T T T G C A A G A G C C T C A A C T A T T T A T A C A C T T C C A A G G T C C A T A
1645	Qy	 G G T A A A C T A C A G G G C C T A C A A A C T T T C G A A T C C G A C A T A T A T T C A C A T T G C A G A C A T A C C A
1870	Db	 G G A A A A T T G C A G T C G T T G C A A A T T T T G A A C A T A G G G A G G C A A A T A T C T C A G C A C T A A C A
1705	Qy	 A G T G A G A T C A G T A A A C T C C A A T G T C G C A T A C T C T T C G T T G T A G T A G A A A G T T T G T T C T
1930	Db	 A C T G A G G T G A C T A A A C T C C A A A T C T C G T A G C C T C C G A T G C A G C A G A G G A G G T C A G G T T C T
1765	Qy	 G A C A A C T T T A G T C T A A - - A C C A C C C A A T G A A G T G C A T A A C T A A C A A A T A T G C T G C C T
1990	Db	 G G T T A C T T T A G C A T A A T A G A T A A T C C C A A G G A A T G C T T G A T G A T C A C C A T G T G C T T A C C G
1822	Qy	 A A A G T A T T C A C A C C T T T A G T T A G T C G G A T A T C G T G C A T A C A A A T T G C T G A A T T G C A C
2050	Db	 A T G G T T T T C T C A A C T T C A A T A A A T T T C A G T A C C G T G T G A A G T T A A T T C C T G A T A T A T G C
1882	Qy	 A T G C C C A C C A A A A G T T G C T G T A A A A T C A T T C G G T G T G A A G G T A C C C A A A G A A T A G G T
2110	Db	 A T G T C A T G T T C T A C C C G T T G G T C T G A T A C A A A G G G T G T G A G G T G C C A A G A G A A T T G A C
1942	Qy	 A A G T T G C G A C A T T A C A G G T T C T A G A G T A T G T A G A T A T C A G G G C G A C C A G T A G T A G A C A
2170	Db	 A A C C T A A A A G A G T T A C A G A T T C T A G A A G T C G T G A C A T C A A C A G A A C T A G T A G G A A G C G C
2002	Qy	 A T C A A A G A C T G G G C A G T T A A G C A A G C T A G G A A A T T A G G T G A T G A C A A A T T G C G T C G
2230	Db	 A T T G A A G A C T G G G G A G C T A A T T C A G T T A G A A A A T T A A G C G T G A C A A A A A A G G C C C
2062	Qy	 A C A A G A A A A A T G A A G A T A C T T T T G T C A G C C A A T T G A G A A G C T C T C T C C C T C C A A T A T
2290	Db	 A C A A A T A A A A G A T A C A G A T A T T T T G T C A G C G A T T G A A A G C T C T C T C T C T G C A A T C T
2122	Qy	 C T C T A T G T G A A T G C T G C A G A A T C T C A G A T G G T G G A A C A C T T G A G T G C C T A G A T T C T A T T
	Qy	 C A C T T A C C A T C T C A T C T T T A A C C A A T G C T T C T T A C C T A A G T A T T T T C C C T G A A G A T T T T

Db	2350	CTCGGTGTGATGCTGAGGGATTCTCAGATACATGGGAACACTTGGAGTGGCTCAATTGCGATT	2400
Qy	2182	TCCTCTCCTCCTCCCTACTCTGAGGACACACTCGTGTGTATGGAAGTCTTGAAGAGATGCGCT	2241
Db	2410	GCAATGCTCTCTCCATTTCTTGAAGACACTCAAGTTGAATGGATCTCTTGCAGATACACCA	2469
Qy	2242	AACGTGANTTGAAGAGCTACTCACTGAGAGAGATCTACTTATTGAGGAGCAACTAAAG	2301
Db	2470	AACGTGTTTGGGAACCTTAAGCAGCTGGTGAAGATGTGCTTATCCAGATGTGTGCTTACAA	2529
Qy	2302	GAAGGTAAACACATGCTGATACACTTGGGGCAATTGCCCAACCTCATGTCTTGGATCTTTAT	2361
Db	2530	GATGGTAAAACTATGAGAGTACTTGGGGCACTGCCCAACCTTATGGTTCCTTCGCTCTTAT	2589
Qy	2362	CGGAAAGCTTACCTCTGGGGAGAGCTAGTATTCAAAACAGGAGCATTTCCCAAATCTTAGA	2421
Db	2590	CGCAACGCATATCTGACGAGAAATGGCATTCAAGAGGGGAACATTTCCCAATCTCAGG	2649
Qy	2422	ACACTTTCGATTTTACGATTTGGATTCAGCTAAGAGAGATTAGATTGAGGACGGCAGCTCG	2481
Db	2650	TGTCCTTGATATTACTTGTCTGAAGCAACTTAGAGAGATAAGATTTCGAGGAGGSCACCTCG	2709
Qy	2482	CCCCAGTTCGAAAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGGATTATTGGTATT	2541
Db	2710	CCAAACAATGAAAGTATAGAAATTTATGGTTGCAGGTTGGAATCAGGGATTATTGGTATC	2769
Qy	2542	ATCCACCTTCCAAAGGCTCAAGAGAGATTTCACCTTGGATACGAAAGTAAAGTGGCTGGGCTT	2601
Db	2770	AAGCACCTTCCAGACTTAAGATTATTTCGCTTGAATATGATGTTAAAGTCGCGAAGCTT	2829
Qy	2602	GCTCAGCTGAGGGAGAGTGCSCACACACCCAAATCACCCTGCTGTCGGAAGAGGGAG	2661
Db	2830	GATGTGCTCAGAGAGAGTGAATACACACCCCAATCATACTGAACTGCAAAATGGCAGAG	2889
Qy	2662	GACCGAAGTGATCACGACCTTGCTTGT	2688
Db	2890	GATCGAAGTCATCATGACCTAGGAGGT	2916
RESULT 11			
ADM72238			
ID	ADM72238 standard; cDNA; 2982 BP.		
XX			
XX	ADM72238;		
DT	03-JUN-2004 (first entry)		
XX			
DE	O. minuta NBS1 polypeptide encoding cDNA.		
XX			
KW	P12; NBS1; plant protectant; gene therapy; rice; disease resistance;		
KW	gene; ss.		
XX			
OS	Oryza minuta.		
XX			
FH	Key		
FT	CDS		
FT	1. .2982		
FT	/*tag= a		
FT	/*product= "NBS1"		
XX			
PN	WO2004022715-A2.		
XX			
PD	18-MAR-2004.		
XX			
PF	08-SEP-2003; 2003WO-US027913.		
XX			
PR	09-SEP-2002; 2002US-0409216P.		
PR	18-MAR-2003; 2003US-0455713P.		
PR	05-SEP-2003; 2003US-00656394.		
XX			
PA	(OHIS) UNIV OHIO STATE.		
XX			
PI	Wang G;		
XX			

QY 997 AACCAAGCCTGGAGCTTTGGAGGAATGGTACCCCTAGGTTACAAACCCTACCATCC 1056
 DB 1204 AATCCAAATCGGTGAACCAATGAAGAGGTGGTAACCCCTAGTATCAATTAATCTGCCATCT 1263
 QY 1057 CATCTGAACCAATGCTTTTGTGATCTTAAGTATCTTCTGAGGATTTTGAATCAAAAGG 1116
 DB 1264 CATCTTAAGCCTTGTCTGATCTTTGCACTTCTCTGAGGATTTTGAATCAAAAGG 1323
 QY 1117 AATCGTCTAGTGGTATGATAGCAGAGGGTTTGTAGACCAAGGTTGGGATGACG 1176
 DB 1324 AAGCCCTAGTACATAGATGATGATGAGGGGTTTATAGAGCTAGGGTGGAGTGGGA 1383
 QY 1177 ACTAAGGATCGGAGAAAGTTACTTTAATGAGCTAATCAACCGAAGTATGATCAACGA 1236
 DB 1384 ATTGGGATGTGGCAAAAGATTTTGTGATGATTTGATGAGTTGATCAACCGAAGTATGATCAACGA 1443
 QY 1237 TCAAGAGTGGGATAGCAGGAAATTAAGACTTGTGCAATTCATGATATCATCGTGAT 1296
 DB 1444 TCTAGAGTGGATATAGAGGAAATTAATGAGCTGCCGAGTCCATGATATCATCGTGAT 1503
 QY 1297 ATCAAGTTTCAATCTCGAGACAGGAAATTTTGTATTGTTACCAATGGGAGATGGCTCT 1356
 DB 1504 GTCATGATATCAATATCTAGGAGAAATTTTGTATCTTGTATGATGGGTGATGATGAACT 1563
 QY 1357 GATTAGTTTCAAGGAAACACTCGCCACATAGCATTCATG---GGAGTATGCTCGTGA 1413
 DB 1564 AGTGTAGTGGAGGAAATTTTCCCATTTAGTGCACCATGATAGTCAAGTGTTCMAAT 1623
 QY 1414 ACAGATTTGGATTTGGAGCATTTATCGATCATTAAGTATTTTGG---TGACAGACCCCAAG 1470
 DB 1624 ATAGCTGGATTTGGAGCCATGTCGGTCAATTAACCTTTGTTGGCAATGAGAGACCCAAA 1683
 QY 1471 AGTCTAGCACATGCAAGTTTGTCCAGATCAATTTGAGGATGTTACGGGTCTTGGATCTTGA 1530
 DB 1684 GGGCTATCTCTTCAATTTGTTTCCCAATTTGAGATGCTAAGAGTCTGATCTTCAA 1743
 QY 1531 GATGTGACATTTCTTAATCACTCAAAAGATTTGACCGTATTTGCAATTTGTTGCACTTG 1590
 DB 1744 GATGTCAATTTGGGATGACACAAAGATATCGGAAATATAGGTTTGTGCGTCACTTG 1803
 QY 1591 AAATACTTGGATTTGGATTTGTCATCCATATTTCACTTCCAGATCCATTTGGTAA 1650
 DB 1804 AAAATGTGAATATTTGGAGGGCAATCAAGTATTTATGCACTTCTTAGGTATAGGAAA 1863
 QY 1651 CTACAGGCGCTACAACTTTGAACATGCCGAGCACATACATTTGAGCAGCACTACCAAGTGAG 1710
 DB 1864 TTAAGAGACTTGTGCACCTTTGGACATACTGACAGTTACATTAAGAACTACCAACTGAG 1923
 QY 1711 ATCAGTAACTCCAAATGCTGCATCTCTTGGTTAGTAGAAGTTTGTCTTGACAA 1770
 DB 1924 ATTAGTAAATTTGCAGAGTCTATGATTTCTCGTTGTAGAGGAAGACCAAACTCGGGGAT 1983
 QY 1771 TTTAGTCTAAACCCCAATGAAGTGCATACATACTAACACAAATAGCTGCTTAAAGTATTC 1830
 DB 1984 TTTAATCTAAATGATCTTAAGGATTTGCTAATGCTTCTCATGTTTGCCT---CTGCTT 2040
 QY 1831 ACACCTTTAGTTAGTGGGATGATCGTGCATACAAATTTGCTGAATTCACATGGCCACC 1890
 DB 2041 ATGGCTGCAACCGATTTGTATGAGGATTAATTAATATTTGCTGAGCTACAGTGGGTGT 2100
 QY 1891 AAAAGTTCTGCTATPAA-----ATCATTCTGGTGTGAAGGTACCCAAAGGAATAGGT 1941
 DB 2101 TCAAGTCAATGCTCTCTCTAATGGTGTACATATGGTGTGAGGTACCTAGAGGAATCAAG 2160
 QY 1942 AAGTTGCGAGACTTACAGGTTCTAGAGTATGATAGATATCAGCGGACCGAGTAGTAGCA 2001
 DB 2161 AATTTGAAAGGCTGTCAGGTGCTAGAGACAGTGGATATCAATCGAACCAGCAGTAGTCA 2220
 QY 2002 ATCAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTTAGTGTGATGACAAATGGCTCG 2061
 DB 2221 GTTGAAGAGTTGGGAGAGCTTATCCAGCTAAGAAACTAAGTGTAGTAACAAAGGGTCC 2280

QY 2062 ACAAGGAAATCTAGATACCTTTGTGCAGCCATTTGAGAGCTCTCTTCCTCCAAATAT 2121
 DB 2281 ACCAAGGAAATGCAAAATATCTGTACAGCCATTTGAGAAGCTAACTTCCTCCTCAAACT 2340
 QY 2122 CTCTATGTGAATGTGCGAGGAATCTCAGATGGTGGAAACACACTTTGAGTGCCTAGATCTTAT 2181
 DB 2341 CTCTATCTGAATGTCTATGACCCCTTGGATACTGGACACTTGAATGGCTACATCTTAT 2400
 QY 2182 TCCTCTCTCTCCCTCTATGAGGACACTCTGTTGTTGTTATGGAAGTCTTTGAAGAGATGCT 2241
 DB 2401 TCCCATCTTCTCTCC---CTGAGGATCATCAGATTTGATCGGATACATGAAGAGATGCC 2457
 QY 2242 AACTGGATTGAGCAGCTCACTCAGCTGAGAGATCTACTTATTGAGGAGCAAACTAAG 2301
 DB 2458 AACTGGTTTGGGAGCTCAGACAGCTGGTGAAGATTCATTTGCAAGATAGCAACTAGAG 2517
 QY 2302 GAAGTAAACCATCTGATCTTGGGGCATTTGCCAACCTCATGGTCTTGTATCTTTAT 2361
 DB 2518 GAGGATAAACATGGAGATACTCGGAGNACTGCTTAATCTCATGCTCTTCTTCTTAGT 2577
 QY 2362 CGGAAGCTTACCTTTGGGAGAAAGCTAGTATTCAAAACAGGAGCAATCCCAATCTTAGA 2421
 DB 2578 TGGCGAGC-----G 2586
 QY 2422 ACATTTGATTTAGATTTGGATCAGCTAAGAGAGATTAGATTTGAGACGGGAGCTCG 2481
 DB 2587 GTGCTAATCATTTCCNAATCAGAAGCAACTGAAGAGGTTGAGATTTGAAGAGGGAACCTCA 2646
 QY 2482 CCCAGTTTGGAAAGATAGAAATCAGATTTCTGAGTTTGAATCAGGATTTATCGTATT 2541
 DB 2647 CCTGGATGGAAAGATTTGATATCAGAGATTCAGATTCAGGATTCGCTGCTGATC 2706
 QY 2542 ATCCACCTTCAAGGCTCAAGGAGATTTCACTTTGGATACGAAAGTAAAGTGGCTGGCTT 2601
 DB 2707 AACACCTTCCGAGCTTAAAGGAGATTTCACTTTGAATACAGTGTCTTAAAGTGGTGGGCTA 2766
 QY 2602 GCTCAGCTGGAGGAGAGTGGCAGACACACCCCAATTCACCCGCTGCTCGAAAGAGGAG 2661
 DB 2767 GGTGAGCTAGAGGTTGAAATGGGACACACCCCAATCGACCCATGTTGCGCTGTTGGG 2826
 QY 2662 GACGAAAGTATCAGACCTTG 2683
 DB 2827 GAGCAAGCCGTATGACCTGG 2848

RESULT 13
 ADM72242
 ID ADM72242 standard; cDNA; 4147 BP.
 XX
 AC ADM72242;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE O. minuta NBS3 polypeptide encoding cDNA.
 XX
 KW P12; NBS3; plant protectant; gene therapy; rice; disease resistance;
 KW gene; sb.
 XX
 OS Oryza minuta.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1983
 FT /*tag= a
 FT /product= "NBS3"
 XX
 PN WO2004022715-A2.
 XX
 PD 18-MAR-2004.
 XX
 PF 08-SEP-2003; 2003WO-US027913.
 XX
 PR 09-SEP-2002; 2002US-0409216P.
 PR 18-MAR-2003; 2003US-0455713P.

PR 05-SEP-2003; 2003US-00656394.
XX (OHIS) UNIV OHIO STATE.
PA Wang G;
XX WPI; 2004-257576/24.
DR P-PSDB; ADM72243.
XX
XX New rice Pi2-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX Example 4; SEQ ID NO 5; 120pp; English.
XX
XX The invention relates to novel broad-spectrum resistance gene Pi2 and the
CC NBS (1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a cDNA
CC encoding a rice NBS3 polypeptide.
XX
XX Sequence 4147 BP; 1201 A; 831 C; 1029 G; 1086 T; 0 U; 0 Other;
Query Match 29.9%; Score 896.6; DB 12; Length 4147;
Best Local Similarity 60.6%; Pred. No. 3.8e-249;
Matches 2137; Conservative 0; Mismatches 629; Indels 763; Gaps 10;
QY 206 ATTCTATGACAGACATTCGCAATCAATCAGCTCGAATGTCGATGAAGCTGAGCTTG 265
DB 428 ATTTATTTATGGAAGACATTCGCAATCAATCAGCTAACCAATCGAGGAAGCTGATCTTG 487
QY 266 TTGGGTTTCTGACTCCAAAGAAAAGGCTGTTGAAATGATCGATACCAATGCTTAATGATG 325
DB 488 TGGGTTTTCTGGACCCAAAGAGAGTTCCTTGATCTTATAGATGTCATGCCAAGACG 547
QY 326 GTCCGGCCAAAGGTAATCTGTGTGTGGGATGGGTGTTAGGCAAGACAGCTCTTTGGA 385
DB 548 GACCTACAAAGGTTGATGTGTGTCGTAAGGTTGGTGGTGGTAAAGACTACTATTGCAA 607
QY 386 GGAAGATCTTTGAAGCGAAGACATTAAGAGAACTCCCTTGCATGCTTGGATTA 445
DB 608 GGAATAATTTAAGAAACAAAGAGGACATTCGAAAGAAATTTTCTGTGCTGTGGATTA 667
QY 446 CAGTGTCACAATCAATTTACAGGATTTGAGTACTTAAAGATATGATACGCCAACTCTTGTG 505
DB 668 CTGTTTCAAGCTCTTTGTTAGGTGGACACTCAAGGATTTGATGTGGAACCTTTTGG 727
QY 506 GCCCCAGTTCTCTGGATCAACTCTTTGCAAGAAATTCGAAGGAAGGTGGTGGTCAAGTAC 565
DB 728 GAGAGGAAGTACTGAAGAAGCGCGGAGAGAACTCGAAGGGA--GGTCCCAAGTAG 784
QY 566 ATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAAAGGTACTTTGTTGTTCTAG 625
DB 785 ATGACCTTGGCAGCTACCTCAGGACAGAGTTACATGAAAGAGGTACTTTGTTGCTTGG 844
QY 626 ATGATCTATGATTTTATCATGATTTGGAATTCGATTAATGAAATTCCTTAAGACA 685
DB 845 ATGACGTGTGAGTACAGATTCATGGAATGGAATTAATGATTTGCTTCCCTTGAATA 904
QY 686 ATAGAAGGGGAGTCAAAATAGTAATAACCACTTTGGAATGTTGATCTTTCGCGAGAAGTGTG 745
DB 905 ACNAAAAGGGAGCGGGGTAGTAAACAAGAGATGTTGGCTTAGCTAAGAAGTGA 964
QY 746 CCAGAGCTCTAGTGTACCACTTGTATTTCTGAGATGAACGATGCCATACATGTC 805
DB 965 CTTCTGAATTCCTTATCTACCAAGCTTAACCCCTAGAAATAAATATATGCAAAAGAGTTGC 1024
QY 806 TACTGAGAAAACAAATAAATAATCATGAAGACATGGAATCAATAAATAATATGCAAAAGA 865
DB 1025 TTCTACGGAAGCAATGAGCAATAGAGATATGGAAGTATGGAAGTATGGAAGTATGAGTGACA 1084
QY 866 TGGTTGAACGAATTTGTAATAAATGTTGGTTCGCTCTACCAATAGCAATCTTACAATAGGAG 925

DB 1085 TTATAACTAAATAAGTAAAGAAGTGTGGGTATTTACCGCTGGCTATATCTCACAATAGGAG 1144
QY 926 CTGTGCTTTGCAACTAAACAGGTGTGAGAAATCTTATGAAACACCTCTCTCTCAG 985
DB 1145 GCGTGTCTTCCACCAAGAGATAGAGAGTGGGAACTTTTATAGTCAGATACCTTCAG 1204
QY 986 AACTAGAAATAAACCCCAAGCCTGGAAGCTTTGAGGAGAATGGTGACCCCTAGGTACAAAC 1045
DB 1205 AGCTTGAGAGCAACCCCAACCTTGAAGCAATGAGAGGATAGTACCCTAAGTTACAACT 1264
QY 1046 ACCTACCATCCATCTGAAACCATGCTTTTGTATCTTAAGTATCTTTCTCAGAGATTTTG 1105
DB 1265 ACTTACCGTCTCATCTTTAAGCAATGCTTTTGTATCTAAGCATATTTCTCAGGATTTTG 1324
QY 1106 AAATCAAAAGCAATCGCTAGTAGATAGTAGAGAGGTTTGTATAGACCAAGG 1165
DB 1325 AAATTAATAGAACCGCTGCTGTAATAGATGATGATGAGAGGGGTTTATTAAGCTAGGA 1384
QY 1166 TTGGGATGACGACTAAGGATGTCGAGAGAAAGTTACTTTAATGAGCTAATCAACCGAAGTA 1225
DB 1385 CTATATATGACTATTGAAGATGTTGGGAAAGTTACTTTAAGAACTTATCAACCGTAGCA 1444
QY 1226 TGATTCAAAGATCAAGAGTGGGCATAGCAGGAAATTAAGACTTGTGCAATTCATGATA 1285
DB 1445 TGATTCAGTCAATCAAGAGCGGTTATACGAGGAGATTTTAAAGAGCTGTCGAGTCCATGACA 1504
QY 1286 TCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAATTTTGTATTTGTATTGTTACCAATGG 1345
DB 1505 TCATCCGTGATATTAACAATTTTCGATTTCTAGGAAGAAATTTTCAACTCTTACCCGATG 1564
QY 1346 GAGATGGCTCTGATTTTAGTTTCAAGGAAACACTCCGCCACATAGCAATTCATCGGAGTATGT 1405
DB 1565 GCATGACTATGATGTAGTACATGGAACACTCCGCCACATAGCAATTCACGGGAGTAGGT 1624
QY 1406 CTGTC---AAAAAGGATTTGGATTGGAGCAATTTTCATCATTAAGTATTTTGGTGACA 1462
DB 1625 ATTGCTCTGAAACAAGCTTGGACTGGAGCAATTAACGGTCAATTAAGTATTTGGTGAGA 1684
QY 1463 GACCAAGAGTCTAGCATCATGCTTTCAGATCAATTCAGGATGTTACGGGCTTTGG 1522
DB 1585 GGTCCGTAGAACTAGAGCATTCAGTTTGTTCATCTCAGTTGAGGATGTTACGGGCTTTGG 1744
QY 1523 ATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATTCATTTGTTGT 1582
DB 1745 ATCTAATAGATGCACAATTTCTATCACAAAATGATGTCGACAAATAGTCTCTTGT 1804
QY 1583 GCCACTTGAATACTTGAGTATTTGGAATA-----TTGCTCATCCATATATTTCAC 1630
DB 1805 GCCACTTGAATACTACGCAATTCGAAGATACAGATACCGTTTCCACATATATTTATTTCAC 1864
QY 1631 TTCCAGATCCATTTGTTAAACTACAGGCGCTACAAACTTTGAACTGCCGAGCATACA 1690
DB 1865 TTCCACAATCCATAGCTAGACTGCTGTCAGACATTTGAGCTTGGGTGAGAGGTACA 1924
QY 1691 TTGCAGCATACCAAGTGAGATCAGTAAATCTCCAAATGTCTGCATATCTCTCGTTGTAGTA 1750
DB 1925 TTTCAACACTGCCAACTCAGATTACT-AACTTCGGAGTCTCCGTAGCCTTCGATGATGA 1983
QY 1751 GAAAGTTTGTTCGACAACTTTAGTCTAAACCAACCAATGAAGTGCATATCAACACAA 1810
DB 1984 AAGAATAATTTTCTTCTTTT-----AAGAACATATTTAACTAACAT 2028
QY 1811 TATGCCCTGCTTAAAGTATTCACCTTTTAGTTAGTTCGAGATGTCGCAATACAAATTTG 1870
DB 2029 TATGCCCTGCCCATGATATTCACCTTTTCGTTAGTACTCGGATCGTTCTGAAACAATTTG 2088
QY 1871 CTGAATTTGCATATGGCCCAACAAAAGTTGCTGGTATAAATCAATTCGGTGTGAAGGTACCCA 1930
DB 2089 CTAAATTTGCACATGGCCCAACCAAGGCTTCCGTTCCAAATCAAAATGAGTGTCAAGGTACCAA 2148
QY 1931 AAGGAATAGGTAAAGTTCGGAGACTTACAG----- 1960
DB 2149 AAGGAATATGTAAAGTTGAGAGACTTACAAGAGGATTTGCTACGGTCCAGCAGGTTGTATCCG 2208

QY 1961 ----- 1960
Db 2209 GCGGTACTGTACCGCGCGGTACCAAAACCACTCTAACCCGTTGAATCCGGATGGGTAG 2268
QY 1961 ----- 1960
Db 2269 GATCGGAGAGAAAGATGACCAAGGTGGATGAGGAGTACCTGTTTCGAGTCGTGTT 2328
QY 1961 ----- 1960
Db 2329 CCCGCGCGCGCGGTGGAGTACTCTGTTTCGAGTCGTGTCGTGTTCCCGGTGGCGGCA 2388
QY 1961 ----- 1960
Db 2389 GAGCAACAAGGAGCGCCGCGCGCGGAGAGGATAAAGTCCGCGCGAGCGCGAGAGAG 2448
QY 1961 ----- 1960
Db 2449 AAAAAAGGAACGGGACCGTTCGGGAGAGGAACNAGGGAAGGAGCGCGCGCGGAAGA 2508
QY 1961 ----- 1960
Db 2509 GGAACAAGTCGACCGCGAGGAGGAAACACGCGCGCGGGAATAATCATCCAGGTAGC 2568
QY 1961 ----- 1960
Db 2569 TAGGGTTGAGCGCGCGGATCCAAACCATCTATTGCAAGGAAAGTTACTCTTTTACCC 2628
QY 1961 ----- 1960
Db 2629 TCCAACTCTCTTCCATGCGGTATCACCTAAGGACATATTTTGGTACCGTGGGTACCA 2688
QY 1961 ----- 1960
Db 2689 CGCAACATCAGCGTGGATCAGGCCAGATCCAAAGCGGCAGCAATTTGGTACCGTGGTA 2748
QY 1961 -----TTCTAGATATGTAGATATCAGCGGAC 1989
Db 2749 CGTTGGCAGTAAAAAACTCGACTTACAAATATGGAGGTAGTGGATATTAGAAGGACT 2808
QY 1990 AGTAGTAGCAATCAAGAGCTGGCGAGTTAAGCAGCTGAGGAATAGGTGTGATG 2049
Db 2809 AGCAGTAGCAATCAAGAGTTGGGCGAGTTAAGCAGCTTAAAGCAATTAATGTGGTA 2868
QY 2050 ACAATGGCTCGCAAAAGGAAAAATGTAAAGATCTTTGTGAGCCATTTGAGAAGCTCTCT 2109
Db 2869 ACNAGGGATCCACNAGGAAAAATGTAGATCTCTATACAGCTATCCAGAAGCTCTGT 2928
QY 2110 TCCCTCCAATATCTATGTGAATGCTGAGGAATCTCAGATGGTGGAAACACTTTGAGTGC 2169
Db 2929 TTCTCAATCTCTCCATGTGAATGCTGTGGATTTTCAGGTATTGGAACACTTTCAGTGT 2988
QY 2170 CTAGATCTATTTCTCTCTCCCTCCCTACTAGGACACTCGTGTGTATGGAAGTCTT 2229
Db 2989 ATAGATTTATTTTCTCTCTCCCTCCCTACTAGGACACTCAGGTGAATGGAAGTCTT 3048
QY 2230 GAAGAGATGCTTAATGATGAGCAGCTCACTCACCTGAAGAAGATCTACTTATGAGG 2289
Db 3049 GAGGAGATGCTTAATGATGAGCAGCTCAGCACCTGATGAAGTTCNACTTATGAGG 3108
QY 2290 AGCAAACTAAAGGAGGTAAACCATGCTGATCTTTGGGGCAATTCGCCAACCTCATGGTC 2349
Db 3109 AGCAAACTAAAGGAGGTAAACCATGTTGTGTAATTTGGCGGTGGCCCAACTCATGGTC 3168
QY 2350 CTTCATCTTTATCGGAAGCTTACTTTGGGAGAGCTAGTATTCAAAAACAGGAGCATTC 2409
Db 3169 CTTTATCTTCAATCCAAATGCTTACCATGGGAGAGCTAGTATTCAAAAATGGGAGCATTC 3228
QY 2410 CCAATCTTAGAACACTTTTCGATTTACGATTTGGATCAGCTTAAGAGAGATTAGATTTGAG 2469
Db 3229 CCAATCTTAGAACATTTTCGATTTACNATTTGGAGCAGCTTAAGAGAGATTAGATTTGAG 3288

QY 2470 GACGCGAGCTCGCCCGCTGGAAAGATAGAAATCAGATTTCTGCAGGTTGGAATCAGGG 2529
Db 3289 GACGCGAGCTCAATCTTGTGTTGAAAGATAGAAAT-----ATTGAGGGGTTGGAATCAGGG 3344
QY 2530 ATTATTGGTATTTATCCACCTTTCCAAAGCTCAAGGAGATTTTCACTTTGGATACGAAAGTAA 2589
Db 3345 ATTCTTGGTATCATTTCACTTTCCAAAGCTCAAGGAGATTTTCACTTTGGATACGAAAGTAA 3404
QY 2590 GTGCTGGCTTGTCTAGCTTGGAGGAGAAATGCGGACACACCCAAATCACCCTGTGCTG 2649
Db 3405 GTGCTAGGCTTGTCTAGCTTGGAGGAGAAATGCGGACACACCCAAATCACCCTGTGCTG 3464
QY 2650 CGAAGGAGGAGGAGCAAGGATGATCAGACCTTCTGTGAGCGCGGAGGATCCCTCTGT 2709
Db 3465 CGAATGAGGAGGAGGAGCAAGGATGATCAGACCTTCTGTGAGCGCGGAGGATCCCTCTGT 3524
QY 2710 GNACTGGAAGCAACCGGATCCCTCCAGAGCAGGAGGAGAG----- 2751
Db 3525 GAGTGGAGCAACAGATCCTGTGAGAGCTCGCAGTTGCAGTGTACGTTGACAAACA 3584
QY 2752 ----- 2751
Db 3585 ACAGAGGTCACTCACTCCCTACACGCGCATCTTAATGAACCTGTTTATCTCTTGTGAG 3644
QY 2752 -----AGCTCGCAGCGAGAGA 2768
Db 3645 ATCGATGATTTAACTCACCCCTTTCATCTCTCTCGTTCCTTAACCTAACAGCGAAGAGA 3704
QY 2769 TAAGCACAGCTCAAGCTGGTTTTATCAAGTATGATCTCTCTCCCTCAATTTGGCATCTCCGG 2828
Db 3705 TAAGCACACTTAAGCTGGTTTTATCAAGTATGATCTCTCTCCCTCAATTTGGCATCTCCGG 3764
QY 2829 TCGTCCCTGCTTTCGCGCTGCGCACACCTCGCTGTTTCCGAGGAGGGGTGCTGATCTAAG 2888
Db 3765 TCGTCCCTGCTTTCGCGCTGCG-----CACCTCGCTGCTCTGAGGAGGGGTGCTGATCTAAG 3822
QY 2889 GAGGCTTCCACTTTCTCAATTTGCTGCTCAGGCTCTCGATTTCTCCCTCTCGGATGAA 2948
Db 3823 GAGGCTTCCACTTTCTCAATTTGCTGCTCAGGCTCTCGATTTCTCCCTCTCGGATGAA 3882
QY 2949 TTGTTTCAATCTGACCTTTTCTCGTGATATGCTACTACTGGTTCAGCATGA 2997
Db 3883 TTG-TTCANCTGATATTTTCTCGGATCTGCTACTGTTCCAGCATGA 3930
RESULT 14
ID ADI57180 standard; DNA; 2351 BP.
XX AC ADI57180;
XX AC ADI57180;
DT 22-APR-2004 (first entry)
XX Oryza minuta P19 locus-related DNA sequence #2.
DE nucleotide binding site; NBS; P19; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; de.
XX Oryza minuta.
XX US2004006788-A1.
PD 08-JAN-2004.
XX 27-JAN-2003; 2003US-00352179.
XX 25-JAN-2002; 2002US-0352106P.
PR 01-FEB-2002; 2002US-0353304P.
XX (WANG/) WANG G.
PA (LIUG/) LIU G.
XX Wang G, Liu G;
PI

XX WPI; 2004-121064/12.
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
XX
XX Disclosure; SEQ ID NO 97; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present Oryza minuta DNA sequence was used in the
CC exemplification of the invention.
XX
SQ Sequence 2351 BP; 703 A; 420 C; 559 G; 651 T; 0 U; 18 Other;
Query Match 28.2%; Score 844.2; DB 12; Length 2351;
Best Local Similarity 68.1%; Pred. No. 4.8e-234;
Matches 1256; Conservative 0; Mismatches 568; Indels 21; Gaps 5;
854 ATATGCAAAAGATGGTTGAACGAATTGTAATAAATGTTGTCGTCTACCATTTAGCAATAC 913
Db 5 AAATCAAAAGAAATATTTCAAAAGATACATAAAGAAATGTGGAGGTCTACCGCTAGCTATAA 64
914 TTCAATAGGAGCTGCTGCTGCACTAAACAGGTGTGAGATGGAGAAATTTCTATGAAC 973
Db 65 TCACAAATAGGTGCAAGTCTTGAAGGGAAGATATAAAGAGTGGGAAATTTTGTATGCTC 124
974 ACCTTCTCTCAGAACTAGAAATAAACCAAGCCCTGGAAAGCTTTGAGGAGAAATGTTGACCC 1033
Db 125 AACTTCCATCAGAACTTGAAGCAATCCATCGCTGAACCAATGAAGAGTGTGAACCC 184
1034 TAGGTTCAACCACTACCATCCCATCTGAACCAATGCTTTTGTATCTAAGTATCTTTC 1093
Db 185 TTAGTTCAAAATTAAGTCTGCACTCATCTTAAGCCCTTGCTTTCTGATACCTTTGCACTTTC 244
1094 CTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGATGATGATGATGATGATGATG 1153
Db 245 CTGAGGATTTTGAATCAAAAGGAAGCGCCCTAGTACATAGATGATGATGATGATGATGATG 304
1154 TTAGACCAAAAGTTGGGATGACGATAGGATGTGGAGAAAGTTACTTTAATGAGCTAA 1213
Db 305 TTAGAGCTAGGGTGGAGTGGGAATTTGGATGTGGCAACAAAGTATTTTGTATGATGA 364
1214 TCAACCGAAGTATGATTTCAACGATCAAGAGTGGGATGAGGATGAGGAAATTAAGACTTTGTC 1273
Db 365 TCAACCGAAGTATGATTTCAAGCATCTAGAGTGGATATAGAGGAAATATTAAGAGCTGCC 424
1274 GAATTCATGATATCATCCGTCATATCAAGTTTCAATCTCCAGACAGGAAATTTTGTAT 1333
Db 425 GAGTCCATGATATCATCGGTGATGTGATGATCAATATCTAGGGAAGAAATTTTGTAT 484
1334 TGTTACCAA TGGGAGATGGCTCTGATTTAGTTTACGAAACCACTCGCCACATAGCATTTCC 1393
Db 485 ACTTGA TGGGTGATGATGAACTAGTGTAGTGGAGGAAATATTCGCCATTTAGTGACC 544
1394 ATGGAGTAT --- GTCTGCAAAA CAGGATTTGATTTGGATTTGGAGCATTTATGATCATATGCTA 1450
Db 545 ATGATACTAGCAAGTGTTCAAATATAGGCATGATTTGGAGCATGTACGGTCAATTAACCT 604
1451 TTTTGG --- TGACAGACCCAGAGTCTAGCACATGCAATTTGTCCAGATCAATTTGAGGA 1507
Db 605 TGTTTGGCAATGAGAGACCCAAAGGGCTATCTCTTCAATTTTGTTCCTCCCAATTTGAAGA 664
1508 TGTTACGGCTCTTGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACC 1567
Db 665 TGCTAAGAGTCTGGAUCTTCAAGATGTCAAAATTTGGATGACACAAAGATATCGAA 724
1568 GTATTGCA TTGTTGGCCACTTGAATACTTTAGTATTTGGATATTTGGTATCTCCATATATT 1627
Db 725 AAATAGGCTTGTGCGTCACTTTGAATATGTGAATATTTGGAGGGCAATTTCAAGTATTTATG 784

QY 1628 CACTTCCAGATCCATTGGTAAACTACAGGSCCTACAAACTTTTGAAATGCCGAGCAT 1687
Db 785 CACTTCCTAGGTGTATAGGAAAATTAAGAGACTTGTGCACCTTTGGACATAACTGACAGTT 844
QY 1688 ACATTGACGACATACCAAGTGAGATCAGTAAATCCCAATGTCTGCACTACTCTTGGTTGTA 1747
Db 845 ACATTACAGAACTACCAACTGAGATTAGTAATATGCAAGAGTCTATGTATTCTCCGTTGTA 904
QY 1748 GTAGAAAGTTTGTCTGACAACTTTAGTCTAAACCCCAATGAAGTGCATATACTACA 1807
Db 905 GAGGAAGACCAAACTCGGGGATTTTAATCTAAATGATCTTAAGGATTTGCTTAATTTGCT 964
QY 1808 CAATATGCCCTGCCCTAAAGATTTACACCTTTAGTTAGTCGCGATGATCGTCCAATACAAA 1867
Db 965 TCTCATGTTTGGCT --- CTGCTTATGGCTGCAACCGATTTCTGATGAACGTAATAAATAA 1021
QY 1868 TTGCTGAATTCACATCGCCACCAAAAGTTGCTGCT --- ATAAATCATTTGGGTG 1918
Db 1022 TTGCTGAGCTACACGTTGGTGTCAAGTCAATGGTCTCTTAATGGTGGTACATATGGTG 1081
QY 1919 TGAAGTACCCCAAGGATAGGTTAAGTTGCGAGACTTTACAGGTTCTAGAGTATCTAGATA 1978
Db 1082 TGAGGGTACCTTAGAGGAAATCAAGAAATTTGAAAAGGCTGCGAGTGTAGAGACAGTGGATA 1141
QY 1979 TCAGGCGGACCAAGTAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAAT 2038
Db 1142 TCAATCGAACCGACAGTAAGTCAAGTTGAGAGTTGGGAGAGCTTATCCAGCTNAGAAAC 1201
QY 2039 TAGGTGTGATGACAAATGGCTCGACAAAGGAAATGTAAGATATCTTTGTGACGCCATTG 2098
Db 1202 TAAAGTGTAGTAACAACAGGGTCCACCAAGGAAATGCAAAATACTCTGTACAGCCATT 1261
QY 2099 AGAGCTCTCTTCCCTCCAATATCTCTATGTGAATGCTGACAGGATCTCAGATGGTGAA 2158
Db 1262 AGAGCTTAACCTCCCTCAAACTCTCTATCTGAATGCTCA TGGACCTTTGGATACTGAA 1321
QY 2159 CACTTGAAGTCTAGATTTCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2218
Db 1322 CACTTGAATGGCTACATCTTATTTCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1378
QY 2219 ATGGAAGTCTTGAAGAGATGCTTAACTGGATGTAGCAGCTCACCTCACTGAAGAGATCT 2278
Db 1379 TCGGATACATGAAAGAGATGCCCACTGGTTAGGAGCTCAGACAGCTGGTGAAGATTC 1438
QY 2279 ACTTATTGAGGACCAACTAAAGAGTAAACCAATGCTGATACTCTGGGSCATTTGCCCA 2338
Db 1439 ACTTGCAGAAATAGCAACTAGAGGAGGATAAACAATGGAGATACTCGGAGACTGCTTA 1498
QY 2339 ACCTCATGGTCTTGTATCTTTATCGGAAAGCTTACCTTTGGGGGAGAGCTAGTATTTCAAAA 2398
Db 1499 ATCTCATGCTCTTTTCTTTAGTTGGCGAGCGTATGCTGGGGGAGAGCTGGTGTTCAGGG 1558
QY 2399 CAGGAGCATTTCCCAATCTTTAGAACACTTTTCGATTTACGATTTGGATTCAGCTAAGAGAGA 2458
Db 1559 AGGGAACTTTCTAAAATCTCAGGGTGTAACTCATTCGCAATCAGAAAGCAACTGAAAGAGG 1618
QY 2459 TTAGATTTGAGGACGGCAGCTCGCCCGAGTTGGAAAAGATAGAAATCAGATTTCTGCGAGT 2518
Db 1619 TGAGATTTGAAGAGGGAACCTCACCTCGGATGGAAAAGATTTGATATCAGAGAAATGTCAGAT 1678
QY 2519 TGGAAATCAGGGAATTTTGGTATTTATCCACCTTTCAAGCTCAAGGAGATTTTCACTTTGGAT 2578
Db 1679 TGACATCAGGGAATTTGCTGTTATCAAAACCTTCGAGGCTTAAGAGATTTTCACTTTGAAT 1738
QY 2579 ACGAAAGTAAAGTGGCTGGGCTTGCTCAGCTGGAGGAGAGAGTGGCGACACACCCCAATC 2638
Db 1739 ACAGTGTAAAAGTGGTCAGGCTAGGTGAGGTAGAGTTGAAATGGGCGACACACCCCAATC 1798
QY 2639 ACCCGTGTCCGAAAAGAGGAGGACCGAAGTGTATCAGACCTTG 2683
Db 1799 GACCATCTTGTGCGCTCTGTTTGGGAGGAGGACCGCTCATGACCTGG 1843

RESULT 15
ADIS7179
ID ADI57179 standard; DNA; 2265 BP.
XX AC ADI57179;
XX DT 22-APR-2004 (first entry)
XX XX Oryza minuta Pi9 locus-related DNA sequence #1.
DE DE nucleotide binding site; NBS; Pi9; bacterial blight; rice blast;
XX KW plant breeding; transgenic plant; plant; ds.
XX OS Oryza minuta.
XX US2004006788-A1.
XX PN 08-JAN-2004.
XX PD 27-JAN-2003; 2003US-00352179.
XX PF 25-JAN-2002; 2002US-0352106P.
PR PR 01-FEB-2002; 2002US-0353304P.
XX XX (WANG/) WANG G.
PA PA (LIUG/) LIU G.
XX Wang G, Liu G;
Pt PI WPI; 2004-121064/12.
DR DR Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX PS Disclosure; SEQ ID NO 96; 136pp; English.
XX CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present Oryza minuta DNA sequence was used in the
CC exemplification of the invention.
XX SQ Sequence 2265 BP; 638 A; 471 C; 558 G; 598 T; 0 U; 0 Other;
Query Match 25.1%; Score 751.8; DB 12; Length 2265;
Best Local Similarity 91.2%; Pred. No. 3.6e-207;
Matches 809; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
Qy 1863 ACAAAATGCTGAATTGCACATGGCACCAAAAAGTTGCTGTATAAATCATTCGGTGTAA 1922
Dd 91 ACAAAATGCTGAATTGCACATGGCCAACAAAAGTTGCTGTCTGAATCANTTCGGTGTAA 150
Qy 1923 GGTAACCCAAAGGAATAGTAAGTTGCCAGACTTACAGGTTCTAGAGTAGTAGATATACAG 1982
Dd 151 GGTAACCCAAAGGAATAGTAAGTTGCCAGACTTCCAGGTTCTAGAGTAGTAGATATACAG 210
Qy 1983 CGCGACCAGTAGTAGACAATCAAAGAAGCTGGGSCAGTTAAGCAAGCTGAGGAAATTAGG 2042
Dd 211 CGCGACCAGTAGTAGACAATCAAAGAAGCTGGGSCACTTAAGCAAGTTGAGGAAATTAGG 270
Qy 2043 TGATGATGACAAATGGCTCGCAAGGAAAAAATGTAAGTACTTTTGTCAGCCATTGAGAA 2102
Dd 271 TGTGATTAACAAAAGGCTCGCAAGGAAAAAATGTAAATATCTTTATGCAGCCATTGAGAA 330
Qy 2103 GCTCTCTTCCTCCAATATCTCTATGTGAATGCTGCAGGAATCTCAGATGGTGAACACT 2162
Dd 331 GCTCTCTTCCTCCAATCTCTATGTGAATGCTGCAGGTTATTATCAGATATTGAACACT 390
Qy 2163 TGAGTGCTAGATTCTATTTCTCTCTCTCTCTCCCTACTCAGGACACTCTCGTTGTTATGG 2222

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
C	1	1878	62.7	3159	9	CL964074	CL964074 OsIFCC010
	2	1290.2	43.0	2925	9	CL964072	CL964072 OsIFCC010
	3	946.6	31.6	3024	9	CL963354	CL963354 OsIFCC009
	4	522	17.4	662	9	AG210016	AG210016 Oryza sat
	5	501.8	16.7	698	9	AG208890	AG208890 Oryza sat
C	6	393	13.1	703	9	CL832740	CL832740 OR_CBa005
	7	364.8	12.2	709	6	CA147958	CA147958 SCEZR2101
	8	354.2	11.8	663	8	AQ578469	AQ578469 nbx0093A
	9	354.2	11.8	875	9	CL518670	CL518670 Op_Ba002
	10	342.8	11.4	737	9	CL958532	CL958532 OR_CBa008
C	11	342.6	11.4	740	9	CL861885	CL861885 OR_CBa009
	12	341.2	11.4	603	9	CL197270	CL197270 104_424_1
	13	331.6	11.1	709	9	CL801486	CL801486 OR_CBa001
	14	320.8	10.7	673	8	BZ338669	BZ338669 ia97a07_b
	15	320.2	10.7	808	9	CL582275	CL582275 OB_Ba004
C	16	317.4	10.6	551	9	CL197271	CL197271 104_424_1
	17	313.2	10.5	527	8	AQ510644	AQ510644 nbx0095D
	18	312.2	10.4	738	9	AB155403	AB155403 Oryza sat
	19	302.2	10.1	650	8	AQ579138	AQ579138 nbx00961
	20	289	9.6	716	9	CW527324	CW527324 Op_Ba005
C	21	273	9.1	846	9	CW503682	CW503682 Op_Ba001
	22	272.4	9.1	696	6	CD862821	CD862821 AZOI.104L
	23	262	8.7	613	9	AG023674	AG023674 Oryza sat
	24	260.8	8.7	618	9	CL577632	CL577632 OB_Ba003

Qy 2476 AGCTCGCCCCAGTTGGAAAAGATAGAAATCAGATTCTCCAGGTTGGAAATCAGGATTATT 2535
 Db 2884 AGCTCGCCCCATTTGGAAAAGATAGGAATCCGATACCTGCAGGTTGGAATAGGGATTATT 2943
 Qy 2536 GGTATTATCCACCTTTCCAAGGCTCAAGGAGATTTTCACTTGGATACGAAAGTAAAGTGGCT 2595
 Db 2944 GGTATCTTAACCTTATGAGGCTAAGGAAATATACCTTGGATACAGAGTTAAAGTTGGT 3003
 Qy 2596 GGGTTGCTAGCTGGAGGAGAGTGGCGACACACCCAAATCACCCCGTGTCTCGAAAG 2655
 Db 3004 TATCTTGGTCAGTTGGAAAAGAGAGTTGGCACACACCCCAATCGCCCGTGTACGATG 3063
 Qy 2656 AGGAGAGCCGAAGTGATCAGACCTTGCTTGTGAGCCGGAAGATCCCTTGTGTAAGTG 2715
 Db 3064 GAGGAGGACCGAAGCTGTGACGACCTGAGAAAGGATGGCAAGGATCAGCTGTAGAAATG 3123
 Qy 2716 GAAGCAACGGATCCCTCCAGAGCAGGAGGGAGAG 2751
 Db 3124 GACGCAACGGAGCCCTCCCTGAGCCCGAGAGCTAG 3159

RESULT 2

CL964072

LOCUS

DEFINITION OBIFCC010259 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION

CL964072

VERSION

CL964072.1

KEYWORDS

GSS.

SOURCE

Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 2925)

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,

Jiao, X., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,

Wong, G. K. S., Deng, X. W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and

its comparison to Arabidopsis

Unpublished (2004)

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Rice genomic sequence.

Class: exon-trapped.

FEATURES

source

1..2925

/organism="Oryza sativa (indica cultivar-group)"

/mol_type="genomic DNA"

/db_xref="taxon:39946"

/clone_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match

Best Local Similarity

Matches 1753; Conservative

0; Mismatches 728; Indels 6; Gaps 2;

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 Qy 385 AGGAAGATCTTTGAAAGCGAAGAGACATTAGGAAGAACTTTCCCTTGCAATGCTTGGATT 444
 Db 616 AGGAAGGCATATGAACAACAGGAACACAT--GAAGAACTTCTCGTGTGCTTGGATC 672
 Qy 445 ACAGTGTACAAATCATTTTACAGGATTCAGCTACTTAAAGATATGATACGCAACTTCTT 504
 Db 673 ACTGTGCTCAGTCATTTGACAGGAAAGAAATTTCTGAACAATAATGATCAGGCAACTTCT 732
 Qy 505 GGCCCCAGTTCTCTGGATCAACTCTTCAAGAAATTTCAAGGGAAGGTTGGTGCACAGTA 564
 Db 733 GGTGCTGATTCATTAGACAACTCTTGAAGAAATTTAGTGAGAAATGCTCGTGCAGATC 792
 Qy 565 CATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTACTTTGTTGTTCTA 624
 Db 793 CAGCATCTCGCTGATCACTTGTGAAGGCTAAGGAGAAAGGTACTTTGTTGTTCTT 852
 Qy 625 GATGATCTATGGATTTTACATGATTTGGAATTTGGAATAAATGAATTTGCTTAAGAAC 684
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 Qy 685 AATAAGAGGCGAGCTCAATAGTAATACCACTTTGGAAATTTGATCTTTCGCGAAGAGT 744
 Db 913 AACACAGAGGTAGTCCGCAATAAATAACAAACGCGAGATGCTGGCTTAGCTGGAGGTGT 972
 Qy 745 GCCACAGCCTCACTGGTGTACCACTTGTATTTCTTTCGAGATGAACGATGCTGCCTAGCT 804
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 Db 1033 CTACTGAGAAAAACAAATAAAGACTTTGAAGACATGAGAAATATGATGAGGACTTTGGSC 1092
 Qy 865 ATGGTTGAACGATTTGTAAATTAATGTTGCTTACCATTAGCAATGCAATTTTACAAATAG 924
 Db 1093 ATAGTTTCAAAATTTGGTAAAGAGGTGGTGTATTTACCGCTGGCTATCTACCAATAG 1152
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 Db 1153 GGCATTTCTGCTACTAGAGATTAATGAGTGGGGAATAATTTTACAGAGAACTTTCTTCA 1212
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 Db 1333 GAAATTCAAAGAGGGCCCTGGTAGATAGATGATGATGATGATGATGATGATGATGATG 1392
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FEATURES
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             immediately upstream of this sequence."

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Best Local Similarity 85.7%; Pred. No. 7e-129;
Matches 557; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 2070 A A A T G T A A G A T A C T T T G T G C A G C C A T T G A A G C T C T C T C C C T C C A A T A T C T C T A T G T 2129
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Qy 2130 G A A T G C T G C A G A A T C T C A G A T G T G G A A C A C T T T G A G T G C C T A G A T T C T A T T T C T C T C C 2189
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Qy 2190 T C C T C C C C T A C T A G G A C A C T C G T G T T G T A T G G A A G T C T T G A A G A G A T G C C T A A C T G G A T 2249
Db 121 T C C T C C C C T A T T G A G G A C A C T C A G T T G A A T G G A A G T C T T G A A G A G T T G C C T A C T G G A T 180

Qy 2250 T G A C C A C T C A C T C A C C T G A A G A G A T C T A C T T A T T G A G G A G C A A C T A A A G N A G T A A 2309
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Qy 2310 A A C C A T G C T A T A C T T G G G G C A T T G C C A A C C T C A T G T C C T T C T C T A T C T T T A T G G A A G C 2369
Db 241 A A C C A T G C T A T A C T T G G G G C A T T G C C A A C C T C A T G C T T C T C A T T T T T G T C A A T G C 300

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Qy 2430 G A T T A C G A T T G A T C A G C T A A G A G A T A G A T T T T G A G A C G G C A G C T G C C C C A G T T 2489
Db 361 G A C T T T C A A T T T G G A T C A G C A A A G A G A T A T T A G A T T T T G A G A C G G C A G C T C A C C C C A A T T 420

Qy 2490 G G A A A G A T A G A A T C A G A T T C T C A G T T G G A A T C A G S G A T T A T T G S T A T T A T C C A C C T 2549
Db 421 G G A A A G A T A G A A T A G C A G T G C A G A T T G G A A T C A G S G A T T A T T G S T A T T A T C A C C T 480

Qy 2550 T C C A A G G C T C A A G G A G A T T T C A C T T G G A T A C G A A A G T A A A G T G G C T T G C T C A G C T 2609
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Qy 2610 G G A G G A G A G T G G C G C A C A C C C A A A T C A C C C G T G C T G G A A A G A G G A G A C C G A A G 2669
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RESULT 6
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LOCUS
DEFINITION OR_CBa0055J06.r OR_CBa Oryza rufipogon genomic clone OR_CBa0055J06
3', genomic survey sequence.
ACCESSION CL832740
VERSION CL832740.1 GI:51078350
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 703)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
ONAP project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0055 row: J column: 06
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

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             /lab_host="DH10B T1 phage resistant"
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Query Match      13.1%; Score 393; DB 9; Length 703;
Best Local Similarity 72.7%; Pred. No. 2.5e-98;
Matches 507; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 1898 G C T G G T A T A A T C A T T C G G T G T G A A G G T A C C C A A A G A A T A G G T A A G T T G C G A C A C T T A C 1957
Db 698 G T T G G T C T G A T A C A A G G G T G A G G T G T C A A G A G A A T T G A C A C T A A A A G A G T T A C 639

Qy 1958 A G G T T C T A G A T A T A G A T A T C A G C G C A C C A G T A G T A G A C A A T C A A A G A G C T G G G C 2017
Db 638 A G A T T C T A G A A G T C G T G G A C A T C A A C A G A A C T A G T A G A A G G C G A T T G A A G A G C T G G G G 579

Qy 2018 A G T T A G C A A G C T A G A A A T T A G G T G T G A T G A C A A A T G G C T C A C A A A G A A A A T G T A 2077
Db 578 A G C T A A T T C A G T T A A G A A A A T T A A G C G T G A C A A A A A A G G C C C A C A A A T A A G A A G T A T C 519

Qy 2078 A G A T A C T T T G T G C A G C C A T T G A G A A G C T C T T C C C T C C A A T A T C T A T G T G A A T G C T G 2137
Db 518 A G A T A T T T T G C A G C A A T T G A A A G C T C T C T C T C T G C A A T C T C T C G T G T G A T G C T G 459

Qy 2138 C A G G A A T C T C A G A T G T G G A A C A C T T T G A G T G C C T A G A T T C T A T T T C C T C C T C C T C C C 2197
Db 458 A G G A T T C T C A G A T A C T G G A A C A C T T T G A G T G G C T C A A T T C G A T T G C A T G C T C C T C C A T 399

Qy 2198 T A C T G A G G A C A C T C G T G T T G T A T G G A A G C T T T G A A G A G A T G C C T A A C T A A G A T T A G A G A C 2257
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Qy 2258 T C A C T C A C C T G A A G A G A T C T A C T A T T T G A G G A G A C A A C T A A A G G A A G G T A A A A C C A T G C 2317
Db 338 T T A A G C A G C T G G T A G A G A T G T C T A T T C C A G A T G T G G C T A A A A G A T G G T A A A A C T A T G G 279

Qy 2318 T G A T A C T T G G G G C A T T G C C C A A C C T C A T G T C C T T G A T C T T T A T C G A A A A G C T T A C C T T G 2377
Db 278 A G A T A C T T G G G G C A C T G C C C A A C C T T A T G G T T C T T C G T C T T A T C G C A A C G C A T A T G C T G 219

Qy 2378 G G G A A G A G C T A G T A T T C A A A A C A G G A G C A T T C C C A A A T C T T A G A A C A C T T T C G A T T A C G 2437

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Class: BAC ends
High quality sequence stop: 224.
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/notes="vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

Query Match 11.8%; Score 354.2; DB 8; Length 663;
Best Local Similarity 72.8%; Pred. No. 1.9e-87;
Matches 469; Conservative 0; Mismatches 174; Indels 1; Gaps 1;

QY 768 CTTTGATTTCTTGAGATGAACGATGCCATAACATTCCTACTGAGAAAAACAATAAAAA 827
DB 650 CTTTAAACCTTGAATTAAGCTATGCAAAAGAGTTCCTCTAAGGAAGCAATTAAC 591
QY 828 TCATGAGACATGAATCAATTAATTAATATGCAAGATGGTTGCAACGAATTCATATA 887
DB 590 CACAGAAATATAGGAAGGATTAAGAGATGATGACATTTACTTAANATAGTAAAGAA 531
QY 888 ATGTGGTCTGCTACCATTAGCAATACCTACAATAGGAGCTGTGCTTGCACATTAACAGGT 947
DB 530 GTGTGGTTATTACCGCTGGCTATCTACAAATAGGGGGGTGCTTGCCACCAAGGAT 471
QY 948 GTCAGAAATGGAGAAATTTCTATGAACACCTTCCTTCAGAACTAGAAATTAACCAAGCCT 1007
DB 470 AAAAGAGTGGAAACCTTTTATAGTCAGATACCTTCAGAGCTTGAAGCAACCAACCT 411
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QY 1127 TAGGTAGATGGATAGCAGAGGGTTTGTAGACCAAAAGGTGGGATGACGACTAAGGATG 1186
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ORIGIN
Query Match 11.8%; Score 354.2; DB 8; Length 663;
Best Local Similarity 72.8%; Pred. No. 1.9e-87;
Matches 469; Conservative 0; Mismatches 174; Indels 1; Gaps 1;

QY 768 CTTTGATTTCTTGAGATGAACGATGCCATAACATTCCTACTGAGAAAAACAATAAAAA 827
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QY 828 TCATGAGACATGAATCAATTAATTAATATGCAAGATGGTTGCAACGAATTCATATA 887
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QY 888 ATGTGGTCTGCTACCATTAGCAATACCTACAATAGGAGCTGTGCTTGCACATTAACAGGT 947
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QY 948 GTCAGAAATGGAGAAATTTCTATGAACACCTTCCTTCAGAACTAGAAATTAACCAAGCCT 1007
DB 470 AAAAGAGTGGAAACCTTTTATAGTCAGATACCTTCAGAGCTTGAAGCAACCAACCT 411
QY 1008 GGAAGCTTTCAGGAGATGTGACCTTAGTTCAACACCTAGCATCCATCCATCGAACC 1067
DB 410 TGAAGCAATGAGAAGGATAGTACCCCTAAGTTTCACTTCTGCTATCTCTTAAGCA 351
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DB 290 TAAATAGATGGATGGCAGAGGGTTTATTAAAGCTAGGGCTAATATGACTATTGAAGATG 231
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QY 1247 GCATAGCAGAGAAATTAAGACTTGTGCAATTCATGATATCATCCGATATATCACAGTTT 1306
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QY 1307 CAATCTCGACACAGGAAATTTTGTATTGTACCATGGAGATGGCTCTGATTTAGTTC 1366
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DEFINITION 3', genomic survey sequence.
ACCESSION CW518670
VERSION CW518670.1 GI:53992892
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
REFERENCE 1 (bases 1 to 875)
AUTHORS SanMiguel P., Westerman, R., Kim, H., Yu, Y., Wisotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
TITLE OMAP Project - Purdue University
JOURNAL Unpublished (2004)
COMMENT Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Basescalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with Lucy version 1.198.
Bases 119-993 of the raw sequence (length 1389) were retained after clipping.
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Error: 0.00
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Location/Qualifiers
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ORIGIN
Query Match 11.8%; Score 354.2; DB 9; Length 875;
Best Local Similarity 65.4%; Pred. No. 2.1e-87;
Matches 567; Conservative 0; Mismatches 293; Indels 7; Gaps 3;

QY 266 TTGGGTTTCTGACTCAAGAAAGGCTGCTGAAATGATCGATACCAATGCTCAATGATG 325
DB 1 TAGGCTTTGACACCTCCAAAAGCGGTACTTCACAAGATAAATGATGCAATGATG 60
QY 326 GTCGCGCC---AAGGTAATCTGTGTGTGGGATGGGTGTAGGCAAGACAGCTCTTT 382
DB 61 ATGAGCACTGTCTGAGTGTCTTGGTGGTGGATGGAGGTGGGTAAGACTACTCTGG 120
QY 383 CGAGGAGATCTTTGAAGCGAAGAGACATTTAGGAGAACTTCCCTTGCATGCTTGA 442
DB 121 TAAGGAAGATCTTTTGAAGTAAGGAAGACATTCGAAATAATTTTACACATCGTCTTGA 180

Db 704 ATAGTTACAAAATTGGTAAAGGGTGTGGT 733

RESULT 11
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DEFINITION 5', genomic survey sequence.
ACCESSION CL861885
VERSION CL861885.1 GI:51276691
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 740)
AUTHORS Kim, H., Yu, Y., Wisotski, M., Yost, D., Stum, D., Rao, K., Luo, M.,
Jett, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
Wing, R.
TITLE OMAP project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0093 row: P column: 17
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

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ORIGIN
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Best Local Similarity 69.4%; Pred. No. 3.5e-84;
Matches 481; Conservative 0; Mismatches 209; Indels 3; Gaps 1;
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Db 47 GATTCCTACCTAGAAAGTGTCTCGCAATCGATCAGGTAGCAACACTGACGAGTCAGAAGCTT 106
Qy 265 GTTGGGTTTTCTGACTCCCAAGAAAGGCTGCTTGAATGATCGATACCAATGCTTAATGAT 324
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VERSION CL197270.1 GI:40709793
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clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 603)
AUTHORS Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,
Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.,
Trani, L., Isak, A., Zimmermann, C., Lakey, N. and Bedell, J.A.
Genethresher methylation filtered genomic sequences from Sorghum
bicolor
Unpublished (2004)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 424 row: C column: 19
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and electroporated into E. coli cells. This is a
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ACCESSION CL801486
VERSION CL801486.1 GI:51027447
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 709)
AUTHORS Kim H., Yu Y., Wisseki M., Yost D., Stum D., Rao K., Luo M.,
Jettly R., Kudrna D., Muller C., Hatfield J., Soderlund C. and
Wing R.
TITLE OMAP project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
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Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: <http://genome.arizona.edu>
PCR Primers
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BACKWARD: CAC TCA TTA GGC ACC CCA
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Qy 1102 TTTGAAATCAAAAGGAATCGTCTAGTAGTAGTAGGATAGCAGAGGCTTTGTTAGACCA 1161
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Qy 1222 AGTATGATTCACAGATCAAGATGGGCTAGCAGCAAAAATTAAGACTTGTGCAATTCAT 1281
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Qy 1282 GATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGAGAAATTTTGTATTGTTACCA 1341
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Qy 1402 ATGTCCTGCAAAACAGAGTTGGATTTGGATTTGAGCATTTATCGATCATTTAGCTATTTTGGTG-- 1459
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 1202784 seqs, 818138359 residues

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29 45.2 1.5 5134 3 US-09-301-085-157 Sequence 157, Appl
30 45.2 1.5 5134 5 PCT-US95-04589-157 Sequence 157, Appl
31 45 1.5 1662 3 US-09-004-838-6 Sequence 6, Appl
32 45 1.5 4163 3 US-09-004-838-70 Sequence 70, Appl
33 45 1.5 4208 3 US-09-004-838-1 Sequence 1, Appl
34 44.6 1.5 2353 3 US-09-004-838-2 Sequence 2, Appl
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ALIGNMENTS

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; APPLICANT: Yano, Masahiro
; APPLICANT: Iwamoto, Masao
; APPLICANT: Katayose, Yuichi
; APPLICANT: Sasaki, Takuji
; APPLICANT: Wang, Zi-Xuan
; APPLICANT: Yamanouchi, Utako
; APPLICANT: Ishimaru, Lisa
; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,330
; FILING DATE: 11-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 10-181455
; FILING DATE: 12-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/032001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 2:
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; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 82...3696
US-09-330-330-2


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; Sequence 3, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336.946B
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
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; TYPE: DNA
; ORGANISM: Oryza sativa
; US-09-336-946B-3

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Db 3184 GCTGTGATATACTCAGAGCACATATTAAAGATTGATCCACTGGGTGATGATGCTCAA 3243
Qy 803 TGCTACTGAGAAAACAAATAAATAATCATGAGNACATGGAATCAATATAAATAATATGAAA 862
Db 3244 GTCATTTGTTTTTTCAGTGGAGTTGTTGGCCAAAGGAATGAATTTCTCGGACATCTTACTG 3303
Qy 863 AGATGGTTGAACGAAATTTGATAATAATGCTGCTGTACCATTAGCAATACTTTACAATAG 922
Db 3304 AGTTTCTCATGATGATATAAATAATGCTGCTGCTGCCACTAGCAATACTATACAG 3363
Qy 923 GAGCTGTGCTTGCACACTTAAACAGGTGTGAGAAATGGAAGAAATTCATATGAACACCT 977
Db 3364 CCAGACATTTTAAAGCCAGCTGTTAGATGGAATGCAAGCAATGGAATCACATACAAAAT 3423
Qy 978 -----TCCTTCGAACTAGAAATAAACCCAGCCCTGGAAAGCTTTGAGGAGAATGGTGA 1030
Db 3424 CATGACTACTTCCAATTTTGAAGAAAATCCTACTTTTGCAGGGGATGAGGCAAGTACTCA 3483
Qy 1031 CCTTAGGTACCAACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTTAAGTATCT 1090
Db 3484 ACCTTATTACATTAATCTTCTCATTTGTTTGAAGCATGCTGTTATACCTTAGCATCT 3543
Qy 1091 TTCTCGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAAGGT 1150
Db 3544 ACAAGAGGACTACATAATTTAGGAAGGCCAACTTTGTTGAGGCAATGATGCTGAAGTT 3603
Qy 1151 TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGCGGAGAAAGTTACTTTTATGAGC 1210
Db 3604 TCATCAATTCATAGAAAATAAAGTCTATGGAAGAAGTTGCAGGGAACATATTTTGTATGAAC 3663
Qy 1211 TAATCAACCGAAGTATGATTCAGCATCAAGAGTGGGCATAGCAGGAAAATTTAAGACTT 1270
Db 3664 TTGTTGTTAGGGGCTTGGTCCAAACCATGATGTTAACTGCAAAAATGAGGTATTGTCAT 3723
Qy 1271 GTCGAATTCATGATATCATCCGTGATATCAGTTTCAATCTCGAGACAGGAAAATTT 1328
Db 3724 GTGTAGTGCACCATGTTTAAATTTTCATCAGGTGTAAGTCAATAGAGGAGAATTT 3781
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RESULT 4
US-09-336-946B-68
; Sequence 68, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336.946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 68
; LENGTH: 5222
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; ORGANISM: *Oryza sativa*

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Db	755	TAAAGAGAGAGGCT	TAAATTTCTGCT	TGGATGATATCTGGAGTTG	TGAAGTGTGGGATG	814				
Qy	656	GGATAAATGAAAT	TGCAATTTCC	TAAAGACAATAG	AGGGCAGCTCAAA	TAGTAATACCA	715			
Db	815	CGGTGA--	-GACGATGCTT	CCAACTGA	GACAAATG	CAGGAGTC	GAAATCTGTTGACTA	871		
Qy	716	CTTGGAAATGTTGA	TCTTCCG	GGAAGTGTGCC	CAGCCTCACTGGTGT	TACCACTTGAAT	775			
Db	872	CCCGTAATGATGA	AGTAGCTGTT	TATGCTGGTGT	TAGAGATTTTCTCTT	TCGGGATGAGCT	931			
Qy	776	TCTTGCAGATGA	ACGATGCCATAC	ATTGCTACTG	AGAAAAACAATATA	AAAAATCATGAAG	835			
Db	932	TCATGSGATCA	AGATGAGAGTTGG	AGTCTTTTCAA	AGTGCAGCATTTTCA	AGTGA-----	986			
Qy	836	ACATGGAAATCA	AAATATA	GCAAAAGATGGTTGA	ACCAATTTGTAAT	ATAAATGTTG	895			
Db	987	-----AGCA	TTTACCATGATG	TTCGAGACTGTT	TGGAAGCAAA	TGCGAGATG	GAATGTCACG	1042		
Qy	896	GTCTACCAAT	TAGCAATACT	CAATAAGGAGCTGT	GCTTGC	CAACTAAACAGG	TGTCAGAA	955		
Db	1043	GGTTACCAC	TAACTATT	TGTCGGTGT	CGGGCTTCTCA	AATCTAAAGGACA	ATAAGAG	1102		
Qy	956	GGGAGAAAT	CTTATGA	ACACCTTCC	CTCAGAACTAG	AAATAAACCC	AGCCTGGAAGCTT	1015		
Db	1103	ATTGGAAAA	CTGTTGCT	TAAAGATGCTCA	AGTCATTCGT	CAAAAATGAT	CTCTGATGAACGAT	1162		
Qy	1016	TGAGGAGAA	TGGTGAC	CCCTAGTGGTT	TACAAACAC	CTTACCATCC	CACTCTGAAACCA	TGCTTTT	1075	
Db	1163	GTTCA	CGTGTGCTTGG	GTGAGTTAC	GATC	CACTTGC	ACAGCGATCT	AAAAACA	TGCTTC	1222
Qy	1076	TGTATCTA	AGTATCTTTT	CCCTGAGGATTTT	GAAATCAAA	AGGAAATCGT	CTCTAGTAGG	TAGAT	1135	
Db	1223	TGCATTT	CGGAAATTTT	TTCC	AGAGACAGT	GTATTC	CAGTGA	AGAAATTT	GATGAGAT	1282
Qy	1136	GGATAG	CAGAGG	GGTTTGTTA	1156					
Db	1283	GGATGG	CTGAGGG	GTCTCTGA	1303					

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RESULT 11
US-09-360-186-2
; Sequence 2, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
US-09-360-186-2

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	Query Match	2.0k	Score 61	DB 3	Length 3099	
	Best Local Similarity	47.1k	0	Mis. No. 9e-08		
	Matches 264	Conservative		Predicates 285	Indels 12	Gaps 2
QY	596	TCAAGGAGAAGAGGTACTTTGTTCTTACAGATCTATCGATTTTACATGATTTGGAATT	655			
Db	847	TAAAGAGAAGAGGTACTTAAATTTGCTTGGATGATATCTGGAGTTGTGAAGTCTGGGATG	906			
QY	656	GGATAAATGAAATTGCACTTTTCTTAAGAACCAATAGAAGGGCCAGTCAAAATAGTAAATCAACA	715			

DB	907	CGGTGA---GACGATGCTTTTCCAACTGAAGACAATGCAGGAGTGCGAATACTGTTGACTA	963
QY	716	CTTGGAAATGTTGATCTTTGCGGAGAAGTGTGCCACAGCCTCACTGGTGTACCACTTGAAT	775
DB	964	CCCGTAATGATGAAGTAGCTGTTTATGCTGGTGTAGAGAAATTTTCTTTGGGATGAGCT	1023
QY	776	TCATTGCAGATGAACGATGCCATACATGCTACTGAGAAAAACAATAAAAAATCATGAAG	835
DB	1024	TCATGGATCAAGATGAGATGTGGAGTCTTTTCAAAAGTCAGCATTTTCCAAGTGA-----	1078
QY	836	ACATGGAAATCAATAAAAAATATGCCAAAGATGTTGAACGAATTTGTAATAAATAATGGTGC	895
DB	1079	-----AGCATTTACCATATGATTCGAGACTGTTGGAAGCAAAATCGCAGATGAATGTCACG	1134
QY	896	GTCATCACCATTAGCAATACTTACAATAGGAGCTGTGCTTGCAACTAAACAGGTCACGAAT	955
DB	1135	GGTTACCACCTAACTATTGTGCTGGTTCGAGGGCTTCTCAAACTCTAAAGAGCAATAGAG	1194
QY	956	GGGAGAAATCTTATGAACAACCTTCCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTT	1015
DB	1195	ATTGGAAAACTGTTGCTTAAAGATGTCAAGTCAITTCGTACAAAATGATCCTGTAGTGAACGAT	1254
QY	1016	TGAGGAGAAATGGTGACCCATAGGTTTACAAACACCTACCATCCATCTCTGAAACCATGCTTTT	1075
DB	1255	GTTCCAGCTGCTTGGGTGAGTTACGATCACTTGACAAGCGATCTTAAACACATGCTCTTC	1314
QY	1076	TGTAATCTAAGTATCTTTTCTTGAGGATTTTGAAATCAAAGGAAATCGTCTAGTAGGTAGAT	1135
DB	1315	TGCATTTCCGGAATTTTTCAGAGAGACAGTGAATATCCAGTGAAGAAATTTGATGAGATCAT	1374
QY	1136	GGATAGCAGAAGGGTTTGTTA	1156
DB	1375	GGATGGCTGAGGGGTTCTGA	1395

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RESULT 12
US-09-864-680A-2
; Sequence 2, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian J
; APPLICANT: Danilbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B22 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
; OTHER INFORMATION:
; US-09-864-680A-2

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Query March	2.08;	Score 61;	DB 4;	Length 3099;
Best Local Similarity	47.1%;	Pred. No. 9e-08;		
Matches 264;	Conservative	0;	Mismatches 285;	Indels 12; Gaps 2;
QY	596	TCAAGGAGAA	CAGGACTCTTTGTTCTTC	TAGATGATCTATCGGATTTTACATGATGGAAATT
Db	847	TAAAGAAAGA	GAGGTACTTAAATTTGTC	TTGGATGATATCTGGAGTGTGGAAGTCGGGATG
QY	656	GGATAAATGA	AAATTGCAATTTTCTTAAGAACAAATTAAGAGGGCCAGCTCAAAATAGTAAATAAACCA	715

Db 907 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGCGAGGAGTCGAATACTGTTGACTA 963
Qy 716 CTTGGAATGTTGATCTTTCGCGAGAAGTGTGCCACAGCCTCACTGGTGTACCACTTGAT 775
Db 964 CCGTAATGATGAAGTAGCTTGTATGCTGGTGTAGAGAAATTTTCTTTGGGATGAGCT 1023
Qy 776 TCTTGAGATGAACGATGCCATAACATTTGCTACTGAGAAAAACAATAAAAAATCATGAAG 835
Db 1024 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGCATTTTCAAGTGA----- 1078
Qy 836 ACATGGAAATCAAATAAAAAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGGTC 895
Db 1079 ----AGCATTTACCATATGATGTTGAGACTGTTGGAAGCAAAATCGCAGATGAATGTCAAG 1134
Qy 896 GTCTACCATTAGCAATCTTCAATAGGACTGTGCTTGCACCACTAAACAGGTGTCAAGAT 955
Db 1135 GGTACCACTAATCTTGTCTGGTGTGAGGGCTTCTCAATCTTAAAGGCAATAGAG 1194
Qy 956 GGGAGAAATTTCTATGAACACCTTCTTCCAGAACTAGAAATAAACCCAGCCTGGAAGCTT 1015
Db 1195 ATTGGAATACTGTTGCTAAAGATGTCAAGTCAATTCGTCACAAAATGATCCTGATGAACGAT 1254
Qy 1016 TGAGGAGAAATGGTGAACCTTAGTTTACCAACCACTTACCACTTCCATCTGAAACCATGCTTTT 1075
Db 1255 GTTCACGTGTCTTGGGTTGAGTTACGATCACTTGACAAGCGATCTAAAAACATGTCTTC 1314
Qy 1076 TGTATCTAAGTATCTTCTCTGAGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1135
Db 1315 TGCATTTTCGGAATTTTTCAGAAAGACGTGATATTCAGTAGAAGAAATTTGATGATCAT 1374
Qy 1136 GGATAGCAGAAGGTTTCTTGA 1156
Db 1375 GGATGGCTGAGGGGTTCTCTGA 1395

RESULT 13

US-09-360-186-1
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-360-186-1

Query Match 2.0%; Score 61; DB 3; Length 31491;

Best Local Similarity 47.1%; Pred. No. 6.1e-07;
Matches 264; Conservative 0; Mismatches 285; Indels 12; Gaps 2;

Qy 596 TCAAGGAGAAGAGGTACTTGTGTTCTAGATGATCTATGGATTTTACATGATTGGAATT 655
Db 2234 TAAAGAGAAAGAGGTACTTAATTTCTTGGATGATATCTGGAGTTGTGAAGTGTGGATG 2293
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Db 2411 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGCATTTTCAAGTGA----- 2465
Qy 836 ACATGGAAATCAAATAAAAAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGGTC 895
Db 2466 ----AGCATTTACCATATGATGTTGAGACTGTTGGAAGCAAAATCGCAGATGAATGTCAAG 2521
Qy 896 GTCTACCATTAGCAATCTTCAATAGGACTGTGCTTGCACCACTAAACAGGTGTCAAGAT 955
Db 2522 GGTTCACCACTAATCTTGTCTGGTGTGAGGGCTTCTCAATCTTAAAGGCAATAGAG 2581
Qy 956 GGGAGAAATTTCTATGAACACCTTCTTCCAGAACTAGAAATAAACCCAGCCTGGAAGCTT 1015
Db 2582 ATTGGAATACTGTTGCTAAAGATGTCAAGTCAATTCGTCACAAAATGATCCTGATGAACGAT 2641
Qy 1016 TGAGGAGAAATGGTGAACCTTAGTTTACCAACCACTTACCACTTCCATCTGAAACCATGCTTTT 1075
Db 2642 GTTCACGTGTCTTGGGTTGAGTTACGATCACTTGACAGGATCTTAAACATGTCTTC 2701
Qy 1076 TGTATCTAAGTATCTTCTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGAT 1135
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Qy 1136 GGATAGCAGAAGGTTTCTTGA 1156
Db 2762 GGATGGCTGAGGGGTTCTCTGA 2782

RESULT 14

US-09-864-680A-1
; Sequence 1, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tal, Thomas H
; TITLE OF INVENTION: B2 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-864-680A-1

Query Match 2.0%; Score 61; DB 4; Length 31491;

Best Local Similarity 47.1%; Pred. No. 6.1e-07;
Matches 264; Conservative 0; Mismatches 285; Indels 12; Gaps 2;

Qy 596 TCAAGGAGAAGAGGTACTTGTGTTCTTAGATGATCTATGGATTTTACATGATTGGAATT 655
Db 2234 TAAAGAGAAAGAGGTACTTAATTTCTTGGATGATATCTGGAGTTGTGAAGTGTGGATG 2293
Qy 656 GGATAAATGAATTTGCAATTTCTTAAAGAACAAATAAGAGGGCAGTCAATAGTAATAACCA 715
Db 2294 GCGTGA---GACGATGCTTTTCCAACTGAAGACAATGCGAGGAGTCGAATACTGTTGACTA 2350
Qy 716 CTTGGAATGTTGATCTTTCGCGAGAGAGTGTGCCACAGCCTCACTGGTGTACCACTTGAT 775
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Qy 836 ACATGGAAATCAAATAAAAAATATGCAAAAGATGGTTGAAACGAATTTGTAATAAATGTTGGTC 895

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2522	GTTTACCACATACTATTGTCTGCTGGTTCGAGGCTTCTCAAAATCTTAAAGGACCAATAGAAG	2581	
956	GGGAGAAATTCATGAACACCTTCCTTCAGAACTAGAAATAAACCAGGCTCGGAAGCTT	1015	
2582	ATTGGAAAACTGTTGCTTAAAGATGTCAAAGTCATTCGTGCACAAAATGATCTCGATGAACGAT	2641	
1016	TGAGGAGAAATGGTGACCTAGGTTTACAAACACCTACCATCCCATCTCGAAACCATGCTTTT	1075	
2642	GTTCACTGTGCTTGGGTTGAGTTTACGATCACCTTGACAAGCGATCTAAAAACATGCTTTC	2701	
1076	TGTATCTAAAGTATCTTTTCTCGAGGATTTTGAAATCAAAAGGAATCGTCTAGTAGGTAGAT	1135	
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RESULT 15

US-08-947-823-2
 / Sequence 2, Application US/08947823
 / Patent No. 6114605
 / GENERAL INFORMATION:
 / APPLICANT: Williamson, Valerie M.
 / APPLICANT: Kaloshian, Igouhi
 / APPLICANT: Yaghoobi, Jafar
 / APPLICANT: Bodeau, John
 / APPLICANT: Milligan, Stephen
 / TITLE OF INVENTION: Procedures and Materials for Conferring
 / TITLE OF INVENTION: Pest Resistance in Plants
 / NUMBER OF SEQUENCES: 5
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Townsend and Townsend and Crew LLP
 / STREET: Two Embarcadero Center, Eighth Floor
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94111-3834
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/947,823
 / FILING DATE: 09-OCT-1997
 / CLASSIFICATION: 800
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: PCT/US97/18802
 / FILING DATE: 09-OCT-1997
 / PRIOR APPLICATION DATA: US 60/028,191
 / APPLICATION NUMBER: US 60/028,191
 / FILING DATE: 10-OCT-1996
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Bastian, Kevin L.
 / REGISTRATION NUMBER: 34,774
 / REFERENCE/DOCKET NUMBER: 023070-070210US
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 576-0200
 / TELEFAX: (415) 576-0300
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 3997 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA

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GenCore version 5.1.6
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(without alignments)
16729.796 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2401.4	80.1	3095	17	US-10-352-179-88
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5	2395.2	79.9	99090	18	US-10-656-394A-13
6	2393.6	79.9	3099	18	US-10-656-394A-7
7	2377.6	79.3	3276	17	US-10-352-179-92
8	2359.8	78.7	3099	18	US-10-656-394A-3
9	2359.8	78.7	3674	18	US-10-656-394A-16
10	1696.2	56.6	2982	18	US-10-437-963-2483
11	1411	47.1	3220	17	US-10-352-179-90
					Sequence 11, Appl
					Sequence 37316, A
					Sequence 88, Appl
					Sequence 83, Appl
					Sequence 13, Appl
					Sequence 7, Appl
					Sequence 92, Appl
					Sequence 3, Appl
					Sequence 16, Appl
					Sequence 2483, Ap
					Sequence 90, Appl

12	1354.2	45.2	2422	18	US-10-656-394A-15	Sequence 15, Appl
13	1293.4	43.2	2940	17	US-10-352-179-84	Sequence 84, Appl
14	1290.2	43.0	2925	18	US-10-437-963-41016	Sequence 41016, A
15	1286.8	42.9	2982	18	US-10-656-394A-1	Sequence 1, Appl
16	987.6	33.0	3492	18	US-10-437-963-49433	Sequence 49433, A
17	946.5	31.6	3024	18	US-10-437-963-7778	Sequence 7778, Ap
18	921.2	30.7	2982	17	US-10-352-179-86	Sequence 86, Appl
19	896.6	29.9	4147	18	US-10-656-394A-5	Sequence 5, Appl
20	884.6	29.5	2711	18	US-10-437-963-38603	Sequence 38603, A
21	844.2	28.2	2351	17	US-10-352-179-97	Sequence 97, Appl
22	751.8	25.1	2265	17	US-10-352-179-96	Sequence 96, Appl
23	408.2	13.6	2439	18	US-10-437-963-74853	Sequence 74853, A
24	393.4	12.8	1389	18	US-10-656-394A-9	Sequence 9, Appl
25	333.8	11.1	1355	17	US-10-352-179-94	Sequence 94, Appl
26	320.8	10.7	2781	18	US-10-437-963-69440	Sequence 69440, A
27	230.4	7.7	667	18	US-10-437-963-51863	Sequence 51863, A
28	213.4	7.1	569	18	US-10-767-701-21019	Sequence 21019, A
29	202.2	6.7	4026	18	US-10-437-963-32604	Sequence 32604, A
30	199	6.6	1214	18	US-10-656-394A-14	Sequence 14, Appl
31	183.4	6.1	2931	18	US-10-437-963-70256	Sequence 70256, A
32	179.2	6.0	2862	9	US-09-354-453-35	Sequence 35, Appl
33	179.2	6.0	2862	14	US-10-267-718-35	Sequence 35, Appl
34	177.2	5.9	4542	18	US-10-437-963-55316	Sequence 55316, A
35	172	5.7	2954	9	US-09-354-453-34	Sequence 34, Appl
36	172	5.7	2954	14	US-10-267-718-34	Sequence 34, Appl
37	172	5.7	6760	9	US-09-354-453-33	Sequence 33, Appl
38	172	5.7	6760	14	US-10-267-718-33	Sequence 33, Appl
39	169	5.6	2373	18	US-10-437-963-48577	Sequence 48577, A
40	167.8	5.6	3012	18	US-10-437-963-78921	Sequence 78921, A
41	166.2	5.5	2883	18	US-10-437-963-75977	Sequence 75977, A
42	164.2	5.5	3155	17	US-10-425-114-31426	Sequence 31426, A
43	164.2	5.5	3430	18	US-10-425-115-34053	Sequence 34053, A
44	161.8	5.4	2886	18	US-10-437-963-51200	Sequence 51200, A
45	160.4	5.4	2981	18	US-10-437-963-98981	Sequence 98981, A

ALIGNMENTS

RESULT 1

US-10-656-394A-11
; Sequence 11, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: broad-spectrum resistance gene P12
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2997)
US-10-656-394A-11

Query Match 100.0%; Score 2997; DB 18; Length 2997;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2997; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCGGAGACGCTGCTGACATGGCGAGTTCGCTGTGGGAGCGGCATCAGCAAGGCC	60
Db	1	ATGCGGAGACGCTGCTGACATGGCGAGTTCGCTGTGGGAGCGGCATCAGCAAGGCC	60
Qy	61	GCCTCGCGCTCCGACGAGACGAGCCCTCTGCTCGGCTCGAGAAAGACATCTGTAC	120
Db	61	GCCTCGCGCTCCGACGAGACGAGCCCTCTGCTCGGCTCGAGAAAGACATCTGTAC	120

121 TTGTTTAGACATGGTGTGGACGGTCGAATGGTGGGCTGTGTGATGATGATGGTGGCATCT 180
121 TTGTTTAGACATGGTGTGGACGGTCGAATGGTGGGCTGTGTGATGATGATGGTGGCATCT 180
181 GGCACACAGTCATGCTTTAGCAATAGATTCCTATGCCAGAGACATTCGCAATCAATCAGCT 240
181 GGCACACAGTCATGCTTTAGCAATAGATTCCTATGCCAGAGACATTCGCAATCAATCAGCT 240
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241 CGAAATGTGGATGAAGCTGAGCTTTGGGTTTTCTGACTCCAGAGAAAGGCTGCTTGAA 300
301 ATGATCGATACCAATGCTAATGATGGTCCGCGCCAGGTAATCTGTGTGTGGGATGGGT 360
301 ATGATCGATACCAATGCTAATGATGGTCCGCGCCAGGTAATCTGTGTGTGGGATGGGT 360
361 GGTTTAGGCAAGACAGCTCTTTTCGAGGAAGATCTTTTGAAAGCGAAGAACATTTAGGAAG 420
361 GGTTTAGGCAAGACAGCTCTTTTCGAGGAAGATCTTTTGAAAGCGAAGAACATTTAGGAAG 420
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421 AACTTCCCTTGCATGCTTGGATTTACAGTGTCAATCATTTTTCACAGGATTTGAGCTACTT 480
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481 AAAGATATGATACGCCAACTTTCTGGCCCCAGTTCTCTGGATCAACTCTTTGCAAGAAATTG 540
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541 CAAGGGAAGGTGGTGGTGAAGTACATCATCTTTCTGAGTACCTGTATAGAGAGCTCAAG 600
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661 AATGAAATTTGATTTCTTCCTAAGAAACAATAAGAGGGCAGTCAAAATAGTAATAACACATTGG 720
661 AATGAAATTTGATTTCTTCCTAAGAAACAATAAGAGGGCAGTCAAAATAGTAATAACACATTGG 720
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721 AATGTTGATCTTGGGAGAGTGTGGCAGACCTCTACCTGGTGTACCACTTGTGATTTCTTG 780
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781 CAGATGAACGATGCCATAACATTTCTACTGAGAAAAACAATAAAAAATCATGAAGACATG 840
841 GAATCAAAATAAATAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGGTCTGCTA 900
841 GAATCAAAATAAATAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGGTCTGCTA 900
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901 CCATTAGCAATATCTTAAGAGAGTGTGCTTGCATTAACAGAGTGTGCAAGATGGGAG 960
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961 AATTTCTATGAACACCTTCTTCAAGACTAGAAATAAACCAGCTTGGAGCTTTGAGG 1020
1021 AGAATGGTGACCTTAGGTTACAAACACCTACCTCCATCTGAAACCATGCTTTTGTAT 1080
1021 AGAATGGTGACCTTAGGTTACAAACACCTACCTCCATCTGAAACCATGCTTTTGTAT 1080
1081 CTAAGTATCTTTCTGAGGATTTTGAAATCAAAAGGAATCGTCTAGTAGGTAGATGGATA 1140
1081 CTAAGTATCTTTCTGAGGATTTTGAAATCAAAAGGAATCGTCTAGTAGGTAGATGGATA 1140
1141 GCAGAGGGTTGTAGACCAAGGTTGGGATGACGCTAAGGATGTCCGGAAGATTAC 1200
1141 GCAGAGGGTTGTAGACCAAGGTTGGGATGACGCTAAGGATGTCCGGAAGATTAC 1200
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1201 TTTAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAA 1260
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1261 ATTAAGAGCTTGTGCAATTCATGATATCATCCGTCATATCACAGTTTCAATCTCGAGACAG 1320
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1321 GAAAAATTTTGTATTTGTACCAATGGGAGATGGCTCTGATTTAGTTTTCAGAGAAAAACACTCGC 1380
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1561 TTGCAACCGTATTTGCAATTTGTCCTTGAATTTAGTATTTGGAATTTGGAATTTGCTCATCC 1620
1561 TTGCAACCGTATTTGCAATTTGTCCTTGAATTTAGTATTTGGAATTTGCTCATCC 1620
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1621 ATATATTTCACTTCCCAGATCCATTTGGTAAACTACAGGGCTTACAAACTTTTGAACATGCCG 1680
1681 AGCACATACATTCGAGCACTTACCAAGTGTAGATCAGTAAACTCCCAATCTCTGCACTACTCTT 1740
1681 AGCACATACATTCGAGCACTTACCAAGTGTAGATCAGTAAACTCCCAATCTCTGCACTACTCTT 1740
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1741 CGTTGATAGTAAAGTTTGTCTGCAAACTTTAGTCTAAACCAACCAATGAAAGTGCAATA 1800
1801 ACTTAACACATATGCTGCTTAAAGTATTCACACCTTTAGTCTGCGATGATTCGTCGCA 1860
1801 ACTTAACACATATGCTGCTTAAAGTATTCACACCTTTAGTCTGCGATGATTCGTCGCA 1860
1861 ATACAAATTCCTGAATTTGCACTGGGCCACCAAAAGTTTGTGCTGATTAATCAATTCGGTGTG 1920
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1921 AAGGTACCCAAAGGAATAGTAAAGTTGCGAGACTTACAGGTTCTTAGAGTATGTAGATATC 1980
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1981 AGGCGNACAGTATGAGCAATCAAGAGCTGGGCGAGTTAAGAGTACTTTGTGCGAGCAATTTGAG 2040
2041 GGTGTGATGACAAATGGCTCGACAAAGGAAAAATGTAAGATACTTTGTGCGAGCAATTTGAG 2100
2041 GGTGTGATGACAAATGGCTCGACAAAGGAAAAATGTAAGATACTTTGTGCGAGCAATTTGAG 2100
2101 AAGCTCTCTTCCCTCCAAATATCTATGTGAATGCTGCGAGAAATCTCAGATGTTGGGAAACA 2160
2101 AAGCTCTCTTCCCTCCAAATATCTATGTGAATGCTGCGAGAAATCTCAGATGTTGGGAAACA 2160
2161 CTTGAGTGGCTAGATTTCTATTTCTCTCTCCCTCCCTCTAGGAGCACTCGTCTTGTAT 2220
2161 CTTGAGTGGCTAGATTTCTATTTCTCTCTCTCCCTCTAGGAGCACTCGTCTTGTAT 2220
2221 GGAAGTCTTCAAGAGATGCTTAATCTGATTTAGCAGCTCACTCACTGAAAGAAATCTTAC 2280
2221 GGAAGTCTTCAAGAGATGCTTAATCTGATTTAGCAGCTCACTCACTGAAAGAAATCTTAC 2280
2281 TTTATGAGGAGCAAACTAAAGGAGGTAAACCAATGCTGATATCTTGGGGCATTCGCCAAC 2340
2281 TTTATGAGGAGCAAACTAAAGGAGGTAAACCAATGCTGATATCTTGGGGCATTCGCCAAC 2340

Db 2281 TTATTGAGGCAAACTAAAGGAAGTTAAACCATGCTGATATCTTGGGGCATTCGCCAAC 2340
Qy 2341 CTCATGTCCTTGATCTTTATCGAAAGCTTACCTTGGGGGAAGAGCTAGTATTCAAAACA 2400
Db 2341 CTCATGTCCTTGATCTTTATCGAAAGCTTACCTTGGGGGAAGAGCTAGTATTCAAAACA 2400
Qy 2401 GGAGCATCCCAATCTTAGACACTTTCGATTTACGATTTGGATCAGCTAAGAGATT 2460
Db 2401 GGAGCATTCCTCAATCTTAGAACACTTTCGATTTACGATTTGGATCAGCTAAGAGATT 2460
Qy 2461 AGATTGAGGACGCGAGCTCGCCCGAGTTGGAAAGATAGAAATCAGATTCTGAGGTTG 2520
Db 2461 AGATTGAGGACGCGAGCTCGCCCGAGTTGGAAAGATAGAAATCAGATTCTGAGGTTG 2520
Qy 2521 GAATCAGGGATTATTGGTATTATCCACTTCCAAAGGCTCAAGGAGATTTCATTTGGATAC 2580
Db 2521 GAATCAGGGATTATTGGTATTATCCACTTCCAAAGGCTCAAGGAGATTTCATTTGGATAC 2580
Qy 2581 GAAAGTAAAGTGGCTGGGCTTGCTCAGCTGGAGGAGAGTGGCCACACACCCCAATCAC 2640
Db 2581 GAAAGTAAAGTGGCTGGGCTTGCTCAGCTGGAGGAGAGTGGCCACACACCCCAATCAC 2640
Qy 2641 CCGTGCTGCGAAAGAGGAGGACCGAAGTGATCACGACCTTGCTTGAGCGCCGAAGGA 2700
Db 2641 CCGTGCTGCGAAAGAGGAGGACCGAAGTGATCACGACCTTGCTTGAGCGCCGAAGGA 2700
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Db 2701 TCCCTGCTGGAAGTGAAGCAACGATCCCTCCAGAGGAGGAGGAGAGCTCGAG 2760
Qy 2761 CGAAGATAAGCACAGCTCAAGCTGTTTATCAAGTGATGATCTCCTCCTCATTTGGC 2820
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Qy 2821 ATCTCCGCTGCTCCTGCTGCTGCGGCTGGCGCACCTCGCTGTTCCGAGGAGGGTCT 2880
Db 2821 ATCTCCGCTGCTCCTGCTGCTGCGGCTGGCGCACCTCGCTGTTCCGAGGAGGGTCT 2880
Qy 2881 GATCAAGGAGGCTTCCACTTTCTCAATTGCGTCTCACGCTCTCGATTCTTCCTCTCG 2940
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Qy 2941 GGTATGAATTGTTTCAATCTGACCTTTTCTGCGTATGCTACTGTTCCAGCATGA 2997
Db 2941 GGTATGAATTGTTTCAATCTGACCTTTTCTGCGTATGCTACTGTTCCAGCATGA 2997

RESULT 2

US-10-437-963-37316
; Sequence 37316, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)/B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 37316
; LENGTH: 4596
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1
US-10-437-963-37316

Query Match 80.4%; Score 2408.6; DB 18; Length 4596;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches 99; Indels 3; Gaps 1;
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Qy 229 AATCAATCAGCTCGAATGATGCGATGCAATGCTTAAGTGGTCCGCGCAAGTAATCTGTGT 288
Db 61 AATCAATCAGCTCGAATGATGCGATGCAATGCTTAAGTGGTCCGCGCAAGTAATCTGTGT 120
Qy 289 AGGCTGCTTGAATGATGCGATGCAATGCTTAAGTGGTCCGCGCAAGTAATCTGTGT 348
Db 121 AGGCTGCTTGAATGATGCGATGCAATGCTTAAGTGGTCCGCGCAAGTAATCTGTGT 180
Qy 349 GTTGGGATGGTGGTGGGCAAGACAGCTCTTTCGAGGAAGATCTTTTGAAGCGAAGNA 408
Db 181 GTTGGGATGGTGGTGGGCAAGACAGCTCTTTCGAGGAAGATCTTTTGAAGCGAAGNA 240
Qy 409 GACATTAGGAAGAACTTCCCTTGCATGCTTGGATTACAGTGTCAATCATTTTCAACAGG 468
Db 241 GACATTAGGAAGAACTTCCCTTGCATGCTTGGATTACAGTGTCAATCATTTTCAACAGG 300
Qy 469 ATTGAGCTACTTAAAGATATGATAAGCAACTTCTTGGCCCCAGTTCTTGGATCAACTC 528
Db 301 ATTGAGCTACTTAAAGATATGATAAGCAACTTCTTGGCCCCAGTTCTTGGATCAACTC 360
Qy 529 TTGCNAGAAATGCAAGGAAGTGGTGGTGCAGTACATCATCTTCTGAGTACTGATA 588
Db 361 TTGCNAGAAATGCAAGGAAGTGGTGGTGCAGTACATCATCTTCTGAGTACTGATA 420
Qy 589 GAAGAGCTCAAGGAGAAAGAGTACTTGTGTTCTAGATGATCTATGATTTTACATCAT 648
Db 421 GAAGAGCTCAAGGAGAAAGAGTACTTGTGTTCTAGATGATCTATGATTTTACATCAT 480
Qy 649 TGGAAATGGAATAAATGCAATTTCTTAAGAACAAATGAAGAGGAGGAGTCAAAATAGTA 708
Db 481 TGGAAATGGAATAAATGCAATTTCTTAAGAACAAATGAAGAGGAGGAGTCAAAATAGTA 540
Qy 709 ATAAACCACTTGGAAATGTTGATCTTGGGAGAAAGTGGTGCACAGGCTCAGCTGGTGTACC 768
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Qy 769 CTGATTTCTGAGATGAAAGTGGTGCATTAACATTTCTTCTAGAGAAAACAAATAAAAT 828
Db 601 CTGATTTCTGAGATGAAAGTGGTGCATTAACATTTCTTCTAGAGAAAACAAATAAAAT 660
Qy 829 CATGAAGACATGGAATCAAAATAAAATATGCAAAAGATGGTGAACGAAATTTGTAATAAA 888
Db 661 CATGAAGACATGGAATCAAAATAAAATATGCAAAAGATGGTGAACGAAATTTGTAATAAA 720
Qy 889 TGTGGTGTCTACCATTTAGCAATCTTACAAATAGGAGCTGTGCTTGAACATTAACAGGTG 948
Db 721 TGTGGTGTCTACCATTTAGCAATCTTACAAATAGGAGCTGTGCTTGAACATTAACAGGTG 780
Qy 949 TCAGAAATGGGAGAAATTTCTATGAACACTTCTTCAAGAACTAGAAATAAAACCCAGCTG 1008
Db 781 TCAGAAATGGGAGAAATTTCTATGAACACTTCTTCAAGAACTAGAAATAAAACCCAGCTG 840
Qy 1009 GAAGCTTTTGAAGGAGAAATGGTGAACCTTAGGTTTACAAACCACTTACCCTCCCATCTGAAACCA 1068
Db 841 GAAGCTTTTGAAGGAGAAATGGTGAACCTTAGGTTTACAAACCACTTACCCTCCCATCTGAAACCA 900
Qy 1069 TGTCTTTTGTATCTAAGTATCTTTCTGAGGATTTTGAAGATTTTGAAGATTCGTCTAGTA 1128
Db 901 TGTCTTTTGTATCTAAGTATCTTTCTGAGGATTTTGAAGATTTTGAAGATTCGTCTAGTA 960
Qy 1129 GGTAGATGGAATGACAGAGGGTTTGTAGAACCAAGGTTTGGGATGAGGACTTAAGGATGTC 1188
Db 961 GGTAGATGGAATGACAGAGGGTTTGTAGAACCAAGGTTTGGGATGAGGACTTAAGGATGTC 1020

Qy 1189 GGAGAAAGTTACTTTAATAGACTAATCAACGGAAGTATGATTCAAACGATCAAGAGTGGG 1248
Db 1021 GGAGAAAGTTACTTTAATAGACTAATCAACGGAAGTATGATTCAAACGATCAAGAGTGGG 1080
Qy 1249 ATAGCAGGAAATTAAGACTTGTGCGAATTCATGATATCATCGGTGATATCACAGTTTCA 1308
Db 1081 ATAGCAGGAAATTAAGACTTGTGCGAATTCATGATATCATCGGTGATATCACAGTTTCA 1140
Qy 1309 ATCTCGAGACAGGAAATTTTGTATTTGTTTGAATCGCAATGGAGATGCTCTGATTTAGTTTCAG 1368
Db 1141 ATCTCGAGACAGGAAATTTTGTATTTGTTTGAATCGCAATGGAGATGCTCTGATTTAGTTTCAG 1200
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Qy 1849 GATGATCGTGCAATACAAATTCGTAATTCGACATGCGCACCAAAAGTTGCTGTATAAA 1908
Db 1681 GATGATCGTGCAAAACAAATTCGTAATTCGACATGCGCACCAAAAGTTGCTGTCTGAA 1740
Qy 1909 TCATTCGGTGTGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAG 1968
Db 1741 TCATTCGGTGTGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAG 1800
Qy 1969 TATGTAGATATCAGCGCGACAGTAGTAGAGCAATCAAAGAGCTGGGGCGAGTTAAGCAAG 2028
Db 1801 TATGTAGATATCAGCGCGACAGTAGTAGAGCAATCAAAGAGCTGGGGCGAGTTAAGCAAG 1860
Qy 2029 CTGAGGAAATTAGTGATGACAAATGGCTCGCAAGAGGAATAATGTAAGATACTTTGT 2088
Db 1861 CTGAGGAAATTAGTGATGACAAATGGCTCGCAAGAGGAATAATGTAAGATACTTTAT 1920
Qy 2089 GCAGCCATTGAGAAAGCTCTCTTCCTCCCAATATCTCTATGTGAATGCTGCAGGAATCTCA 2148
Db 1921 GCAGCCATTGAGAAAGCTCTCTTCCTCCCAATCTCTCCATGTGGATGCTGTGTTATTCTCA 1980
Qy 2149 G---ATGGTGAAACATTGAGTGCTAGATTCTATTTCTCTCTCTCCCTCCCTACTGAGG 2205
Db 1981 GGTATTATGGAACACATTGAGTGCTAGATTCTATTTCTCTCTCTCCCTCCCTACTAAGG 2040
Qy 2206 ACATCTGTTGTATGGAAGCTTTGAAGAGATGCTCAACTGGATTGAGAGCTCACCTCAC 2265
Db 2041 ACATCAGGTTGAATGGAAGCTTTGAAGAGATGCTCAACTGGATTGAGAGCTCACCTCAC 2100
Qy 2266 CTGAAGAAGATCTACTTTATTGAGGAGCAAACTAAAGGAAGGTAAACCACTGCTGATACTT 2325

Db 2101 CTGAAGAAGTTTCAGCTTTACGGAGAGTAAACTAAGGAAGGTAAACCATGCTGATACTT 2160
Qy 2326 GGGGCATTGCCCAACCTCATGCTCTTGTATCGGAAAGCTTACCTTTGGGGAGAAG 2385
Db 2161 GGGGCATTGCCCAACCTCATGCTCTTGTATCGGAAAGCTTACCTTTGGGGAGAAG 2220
Qy 2386 CTAGTATTCAAAAACAGGAGCAATCCCAAATCTTAGAACACTTTTCGATTTACGATTTGGAT 2445
Db 2221 CTAGTATTCAAAAACGGGAGCAATCCCAAATCTTAGAACACTTTGTATTACGAATTTGAT 2280
Qy 2446 CAGCTAAGAGAGATTAGATTGAGGACGGCAGCTCGCCCCAGCTTTGAAAAAGATAGAAATC 2505
Db 2281 CAGCTAAGAGAGATTAGATTGAGGACGGCAGCTCAACCTTTGGGAAAAAGATAGAAATA 2340
Qy 2506 AGATTCTGCAAGTTTGGAAATCAGGAGTATTATGTTATTTATCCACTTCCAAAGCTCAAGGAG 2565
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Qy 2566 ATTTCACTTCGATACGAAAGTAAAGTGGCTGGGCTTCTCAGCTGAGAGGAGAAAGTCGCG 2625
Db 2401 ATTTCAATTTACATACGGAAGTAAAGTGGCTGGGCTTGGTCAAGCTGGAGGAGAAAGTGAAC 2460
Qy 2626 ACACACCCAAATCACCCCTGCTGCGAAAGAGGAGGAGCCGAAGTGATCAAGACTTTGCT 2685
Db 2461 ACACACCCAAATCGCCCGCTGCTGCTAAATGTACAGTGACCGAAGGTATCACGACCTGGGG 2520
Qy 2686 TGTGAGCGCCGAAGGATCCCTGTTGAAGTGGAAGCAACGATCCCTCCCGAGAGCAGGAG 2745
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Qy 2746 GGA 2748
Db 2581 GGA 2583

RESULT 3

US-10-352-179-88
; Sequence 88, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Plant
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3096)
; OTHER INFORMATION:
; US-10-352-179-88

Query Match 80.1%; Score 2401.4; DB 17; Length 3096;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 2456; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 202 ATAGATTCTATGAGAGACATTCGCAATCAATCAAGTCTGAAATGTGGATGAAGCTGAG 261
Db 427 ATGGAATCTTATGAGAGACATTCGCAATCAATCAAGTCTGAAATGTGGATGAAGCTGAG 486
Qy 262 CTTGTTGGGTTTCTGACTCCAGAAAGGCTGTTGAAATGATCGATACCAATGCTAAT 321
Db 487 CTTGTTGGGTTTCTGACTCCAGAAAGGCTGTTGAAATGATCGATACCAATGCTAAT 546

QY 322 GATGTCGGCCAGGTAATCTGTGTTGTTGGGATGGGTGCTTTAGGCAAGACAGCTCTT 381
Db 547 GATGTCGGCCAGGTAATCTGTGTTGTTGGGATGGGTGCTTTAGGCAAGACAGCTCTT 606
QY 382 TCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCATGCTTGG 441
Db 607 TCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCATGCTTGG 666
QY 442 ATTACAGTGTCAATCATTTTCAAGGATGAGCTTAAAGATATGATACGCCAACTT 501
Db 667 ATTACAGTGTCAATCATTTTCAAGGATGAGCTTAAAGATATGATACGCCAACTT 726
QY 502 CTTGGCCCCAGTCTCTGAGTCAACTCTTGCAGAAATTTGCAAGGGAAGGTGGTGGCAA 561
Db 727 CTTGGCCCCAGTCTCTGAGTCAACTCTTGCAGAAATTTGCAAGGGAAGGTGGTGGCAA 786
QY 562 GTACATCATCTTTCTGAGTACTGATAGAGAGCTCAAGGAGAGAGAGTACTTTTGTGTT 621
Db 787 GTACATCATCTTTCTGAGTACTGATAGAGAGCTCAAGGAGAGAGAGTACTTTTGTGTT 846
QY 622 CTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGAAATTTGCAATTTCCCTAAG 681
Db 847 CTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATGAAATTTGCAATTTCCCTAAG 906
QY 682 AACATAAGAGGGGAGTCAATAGTATATACCCTTGGAAATTTGATCTTGGCGAGAG 741
Db 907 AACATAAGAGGGGAGTCAATAGTATATACCCTTGGAAATTTGATCTTGGCGAGAG 966
QY 742 TGTGCCACAGCTCACTGCTGTACACCTTGATTTCTTGCAGATGAACGATGCCATAACA 801
Db 967 TGTGCCACAGCTCACTGCTGTACACCTTGATTTCTTGCAGATGAACGATGCCATAACA 1026
QY 802 TTGCTACTGAGAAAAAACHAATTAATAATCATGAAGACATGGAATCAATAAATAATGCAA 861
Db 1027 TTGCTACTGAGAAAAAACHAATTAATAATCATGAAGACATGGAATCAATAAATAATGCAA 1086
QY 862 AAGATGTTGAACGAATTTAAATTAATAGTGGTGTCTACCATTTAGCATACTTTACATA 921
Db 1087 AAGATGTTGAACGAATTTAAATTAATAGTGGTGTCTACCATTTAGCATACTTTACATA 1146
QY 922 GGAGCTGTCTGCAACTTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACACTTCTCT 981
Db 1147 GGAGCTGTCTGCAACTTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACACTTCTCT 1206
QY 982 TCAGAACTAGAAATTAACCCCAAGCTTGAAGCTTTGAGGAGAAATGGTGACCTTAGTTAC 1041
Db 1207 TCAGAACTAGAAATTAACCCCAAGCTTGAAGCTTTGAGGAGAAATGGTGACCTTAGTTAC 1266
QY 1042 AACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCTGAGGAT 1101
Db 1267 AACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCTCTGAGGAT 1326
QY 1102 TTTGAAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAGGGTTTGTAGACCA 1161
Db 1327 TTTGAAATCAAAAGGAATCGTCTAGTAGGTAGATGGATAGCAGAGGGTTTGTAGACCA 1386
QY 1162 AAGTGTGGGATGACGACTTAAGGATGTTCGAGAAAGTTACTTTTAATGAGCTAATCAACCGA 1221
Db 1387 AAGTGTGGGATGACGACTTAAGGATGTTCGAGAAAGTTACTTTTAATGAGCTAATCAACCGA 1446
QY 1222 AGTATGATTCACGATCAAGAGTGGGATAGCAGAGAAAAATTAAGATCTTGTGCAATTCAT 1281
Db 1447 AGTATGATTCACGATCAAGAGTGGGATAGCAGAGAAAAATTAAGATCTTGTGCAATTCAT 1506
QY 1282 GATATCATCCGTGATATACAGTTTCAATCTCGAGACAGGAAATTTTGTATTTCTTACCA 1341
Db 1507 GATATCATCCGTGATATACAGTTTCAATCTCGAGACAGGAAATTTTGTATTTTACCA 1566
QY 1342 ATGGGAGATGCTCTGATTTAGTTTACGAGAAACACTCGCCACATAGCAATTCATGGGAGT 1401
Db 1567 ATGGGAGATGCTCTGATTTAGTTTACGAGAAACACTCGCCACATAGCAATTCATGGGAGT 1626
QY 1402 ATGTCCTGCAAAAACAGGATTCGATTTGGAGCATTTATTCGATCATTTAGCTATTTTGGTGAC 1461

Db 1627 ATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTTGGTGAC 1686
QY 1462 AGACCCAAAGAGTCTAGCACATTCGAGTTTGTCCAGATCAATTTGAGGATGTTTACGGGCTTTG 1521
Db 1687 AGACCCAAAGAGTCTAGCACATTCGAGTTTGTCTAGATCAATTTGAGGATGTTTACGGGCTTTG 1746
QY 1522 GATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGGTATTTGCAATTTG 1581
Db 1747 GATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGGTATTTGCAATTTG 1806
QY 1582 TGCCACTTTGAAATTAATTTGAGTATTTGGATATTTGCTCATTCATATATTTACTTTCCAGATCC 1641
Db 1807 TGCCACTTTGAAATTAATTTGAGTATTTGGATATTTGCTCATTCATATATTTACTTTCCAGATCC 1866
QY 1642 ATTGSTAAACTPACAGGGCCTACAAACTTTGAAATGTCGAGACACATATCATTTGCGACACTA 1701
Db 1867 ATTGSTAAACTPACAGGGCCTACAAACTTTGAAATGTCGAGACACATATCATTTGCGACACTA 1926
QY 1702 CCAAGTGAGATCAGTAAACTCCCAATGTCGATATCTTTCGTTGTAGTAGAAAGTTTGT 1761
Db 1927 CCAAGTGAGATCAGTAAACTCCCAATGTCGATATCTTTCGTTGTAGTAGAAAGTTTGT 1986
QY 1762 TCTGACAACTTTAGTCTTAAACCCCAATGAGTGCATTAACACAAATATGCTGCT 1821
Db 1987 TATGACAACTTTAGTCTTAAACCCCAATGAGTGCATTAACACAAATATGCTGCT 2046
QY 1822 AAAGTATTTACACCTTTAGTTCGCGATGATCGTCAATPACAAATTTGCTGAAATTTGCAC 1881
Db 2047 AAAGTATTTACACCTTTAGTTCGCGATGATCGTCAAAACAAATTTGCTGAAATTTGCAC 2106
QY 1882 ATGSCCAACCAAAAGTCTGCTGATATAATTCATTTCCGTTGTAAGGTACCCCAAGAAATAGGT 1941
Db 2107 ATGSCCAACCAAAAGTCTGCTGATCTGAATTCATTTCCGTTGTAAGGTACCCCAAGAAATAGGT 2166
QY 1942 AAGTTGCGAGACTTACAGGTTCTAGAGTATGATATATCAGGCGGACAGTAGTAGACA 2001
Db 2167 AAGTTGCGAGACTTACAGGTTCTAGAGTATGATATATCAGGCGGACAGTAGTAGACA 2226
QY 2002 ATCAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAAATTTAGGTGTGATGACAAATGGCTCG 2061
Db 2227 ATCAAGAGCTGGGGCAGTTTAAAGCAAGTGTGAGGAAATTTAGGTGTGATGACAAAGGCTCG 2286
QY 2062 ACAAGGAAAAATTAAGATATCTTTGTGCAAGCTTACAGAGCTCTCTTCCCTCCAAAT 2121
Db 2287 ACAAGGAAAAATTAAGATATCTTTGTGCAAGCTTACAGAGCTCTCTTCCCTCCAAAT 2346
QY 2122 CTCTATGTGAATGCTGCGAGGATCTCAGATGGTGGAACTTTGAGTGGCTTAGATCTTAT 2181
Db 2347 CTCTATGTGAATGCTGCGGTTATTTATCAGATATTTGAAACACTTTGAGTGGCTTAGATCTTAT 2406
QY 2182 TCCTCTCTCTCTCTCTCTCTGAGGACACTCGTGTGTGATGGAAGTCTTTGAAGAGATGCT 2241
Db 2407 TCATCTCTCTCTCTCTCTCTGAGGACACTCGGTTGATGGAAGTCTTTGAAGAGATGCT 2466
QY 2242 AACTGGATTGAGCAGCTCAGTCACTCAGGAGAGATCTACTTTATTTGAGGAGCAAACTAAAG 2301
Db 2467 AACTGGATTGAGCAGCTCAGTCACTCAGGAGAGATCTACTTTATTTGAGGAGCAAACTAAAG 2526
QY 2302 GAAGGTAACCATGCTGATATCTTGGGGCATTTGGCCAACTCATGCTGCTTGTATCTTAT 2361
Db 2527 GAAGGTAACCATGCTGATATCTTGGGGCATTTGGCCAACTCATGCTGCTTGTATCTTAT 2586
QY 2362 CGGAAAGCTTACCTTTGGGGAGAGCTAGTATTTCAAAAACAGGAGCATTTCCCAAACTTTAGA 2421
Db 2587 TGGATGCTTACCTTTGGGGAGAGCTAGTATTTCAAAAACAGGAGCATTTCCCAAACTTTAGA 2646
QY 2422 ACACCTTTTCGATTTTACGATTTGGATCAGCTAAGAGAGATTTAGATTTGAGGACGGCAGCTCG 2481
Db 2647 ACACCTTCGATTTTACGATTTGGATCAGCTAAGAGAGATTTAGATTTGAGGATGCGCAGCTCA 2706
QY 2482 CCCAGTTGGAAAAAGATAGAAAAACAGATTTCTGCAAGTTGGAATCAGGGAATTTATTTGGTAT 2541

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Db 2707 CCCCTGTTGGAAAAGATAGAAATCTCTTGTCTGCAGGTTGGAAATCAGGGATTAATTGGGTATC 2766
Qy 2542 ATCCACCTTCCAAGGCTCAAGGAGATTTCACTTTGGATACGAAAGTAAAGTGGCTGGGCTT 2601
Db 2767 ATTCACCTTCCAAGGCTCAAGGAGATTTCACTTTGAATACAAAAGTAAAGTGGCTAGGCTT 2826
Qy 2602 GCTCAGCTGGAGGAGAAAGTCGCACACACCCAAATCAACCCCGTCTGCGGAAAGAGGAG 2661
Db 2827 GGTCACTGGAGGAGAAAGTGAACACACACCAAAATCGCCCGTCTCGGAATGGAACAGT 2886
Qy 2662 GACCGAAGTGAATCAGACCTTCTTGTGACCGCGAAGGATCCCTGTTGAAGTGGAGCA 2721
Db 2887 GACCGAAGGATACAGACTGGGGCTGAAGCCGAAGGATCTTATAGAAAGTGCAACA 2946
Qy 2722 ACCGATCCCTCCAGAGCAGAGGGA 2748
Db 2947 GCAGATCTGTCTCTGATGCCGAGGA 2973

RESULT 4
US-10-352-179-83
; Sequence 83, Application US/10352179
; Publication No. US2004006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 2727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 76272
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-83

Query Match 80.1%; Score 2401.4; DB 17; Length 76272;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 2456; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 202 ATAGATTCCTATGCAGAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAGCTGAG 261
Db 39513 ATGATTCCTATGCAGAGACATTCGCNATCAATCAGCTCGAATGTGGATGAAGCTGAG 39572

Qy 262 CTTGTTGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAATGATCGATACCAATGCTTAAT 321
Db 39573 CTTGTTGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAATGATCGATACCAATGCTTAAT 39632

Qy 322 GATGGTCGGCCAAAGTAACTCTGTGTTGGGATGGTGGTTTAGGCAAGACAGCTCTT 381
Db 39633 GATGGTCGGCCAAAGTAACTCTGTGTTGGGATGGTGGTTTAGGCAAGACAGCTCTT 39692

Qy 382 TCGAGGAAGATCTTTTGAAGGGAAGAGACATTAAGGAAGACTTCCCTTGCATGCTTGG 441
Db 39693 TCGAGGAAGATCTTTTGAAGGGAAGAGACATTAAGGAAGACTTCCCTTGCATGCTTGG 39752

Qy 442 ATTACAGTGTCACAATCAATTTACAGGATTCAGCTACTTAAAGATATGATACGCCAACTT 501
Db 39753 ATTACAGTGTCACAATCAATTTACAGGATTCAGCTACTTAAAGATATGATACGCCAACTT 39812

Qy 502 CTTGGCCCCAGTTCTCTGGATCAACTCTTGCAAGAAATTCGAGGGAAGGTTGGTGCAG 561
Db 39813 CTTGGCCCCAGTTCTCTGGATCAACTCTTGCAAGAAATTCGAGGGAAGGTTGGTGCAG 39872

Qy 562 GTACATCACTTTCTGAGTACTCTGATAGAGAGCTCAAGGGAAGAGAGTACTTTGTTGTT 621
Db 39873 GTACATCACTTTCTGAGTACTCTGATAGAGAGCTCAAGGGAAGAGAGTACTTTGTTTAT 39932

Qy 622 CTAGATGATCTATGGATTTTATCATGATTTGGAATTTGGATAAATGAAATTCCTTAAG 681
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Db 39933 CTAGATGATCTATGGATTTTACATGATTTGGAAATTTGGAAATTTGCAATTTCCCTTAAG 39992
Qy 682 AACAAATGAAGAGGCGAGCTCAAAATAGTAATAACCACTTTGGAAATTTGATCTTTGCCGAGAG 741
Db 39993 AACAAATGAAGAGGCGAGCTCGAATAGTAATAACCACTCGGAATTTGATCTTAGCGGAGAG 40052
Qy 742 TGTGCCACAGCCTCACCTGGTGTACCACTTTGATTTCTTGAGATGAACGATGCCATAACA 801
Db 40053 TGTGCCACAGCCTCACCTGGTGTACCACTTTGATTTCTTGAGATGAACGATGCCATAACA 40112
Qy 802 TTGCTACTGAGAAAAAACAATATAAATCATGAAGACATGGAATCAAAATAAATAATATGCAA 861
Db 40113 TTGCTACTGAGAAAAAACAATATAAATCATGAAGACATGGAATCAAAATAAATAATATGCAA 40172
Qy 862 AAGATGCTTGAACGAATTTGTAATAAATGTTGCTCTACCATTAGCAATACTTACAAATA 921
Db 40173 AAGATGCTTGAACGAATTTGTAATAAATGTTGCTCTACCATTAGCAATACTTACAAATA 40232
Qy 922 GGAGCTGTGCTTGCAACTAAACAGGCTGCAGAAATGGGAGAAATTTCTATGAACACTTCTCT 981
Db 40233 GGAGCTGTGCTTGCAACTAAACATGTGTGAGAAATGGGAGAAATTTCTATGAACACTTCTCT 40292
Qy 982 TCAGAACTAGAAATAAACCAGCCTGGAAGCTTTGAGGAGAAATGGTGACCCCTAGGTTAC 1041
Db 40293 TCAGAACTAGAAATAAACCAGCCTGGAAGCTTTGAGGAGAAATGGTGACCCCTAGGTTAC 40352
Qy 1042 AACCCACTACCATCCCATCTGAAACCATGCTTTTGTGATCTTAAGTATCTTTTCCCTGAGAT 1101
Db 40353 AACCCACTACCATCCCATCTGAAACCATGCTTTTGTGATCTTAAGTATCTTTTCCCTGAGAT 40412
Qy 1102 TTTGAAATCAAAAGGAATCGCTCTAGTAGGTAGATGGATAGCAGAGGGTTTGTGTAGACCA 1161
Db 40413 TTTGAAATCAAAAGGAATCGCTCTAGTAGGTAGATGGATAGCAGAGGGTTTGTGTAGACCA 40472
Qy 1162 AAGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGCTAATCAACCGA 1221
Db 40473 AAGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGCTAATCAACCGA 40532
Qy 1222 AGTATGATTCGAAGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTTGTTCGAATTCAT 1281
Db 40533 AGTATGATTCGAAGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTTGTTCGAATTCAT 40592
Qy 1282 GATATCATCCGCTGATATCAGAGTTTCAATCTCGAGACAGGAAAAATTTGTATTGTATACCA 1341
Db 40593 GATATCATCCGCTGATATCAGAGTTTCAATCTCGAGACAGGAAAAATTTGTATTATTACCA 40652
Qy 1342 ATGGGAGATGGCTCTGATTTTAGTTTCAAGAAAAAACHCTCGCCACATAGCAATTCCTAGGGAGT 1401
Db 40653 ATGGGAGATGGCTCTGATTTTAGTTTCAAGAAAAAACHCTCGCCACATAGCAATTCCTAGGGAGT 40712
Qy 1402 ATGTCCTGCAAAAACAGGATTTGGATTTGGAGCAATTAATTCGATCATTTTGTGGTGAC 1461
Db 40713 ATGTCCTGCAAAAACAGGATTTGGATTTGGAGCAATTAATTCGATCATTTTGTGGTGAC 40772
Qy 1462 AGACCCAAAGAGTCTAGCACATGCAAGTTTGTCCAGATCAATTTGAGGATGTTACGGGCTTGT 1521
Db 40773 AGACCCAAAGAGTCTAGCACATGCAAGTTTGTCCAGATCAATTTGAGGATGTTACGGGCTTGT 40832
Qy 1522 GATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTTCGATTTGTTG 1581
Db 40833 GATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTTCGATTTGTTG 40892
Qy 1582 TGGCACTTTGAAATACCTTGAATTTGGATATTCGTCATCCATATATTCACATTTCCAGATCC 1641
Db 40893 TGGCACTTTGAAATACCTTGAATTTGGATATTCGTCATCCATATATTCACATTTCCAGATCC 40952
Qy 1642 ATTGGTAAAATACAGGGCCCTACAACTTTGAAATGCGCGAGCACATACATTTGCAGCACTA 1701
Db 40953 ATTGGTAAAATACAGGGCCCTACAACTTTGAAATGCGCGAGCACATACATTTGCAGCACTA 41012
Qy 1702 CCAAGTGAGATCAGTAAATCTCCAAATGTCTGCACTACTCTTCGTTGTAGTAGAAGTTGTT 1761
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Db 41013 CCAAGTGAGATCAGTAAACTCAATGTCTGCATACCTCTTCTGTGTAGTAGAAAAGTTTGTT 41072
Qy 1762 TCTGACAACTTTAGTCTAAACCCACCCCAATGAAGTGCATAACTAACACAAATATGCTGCT 1821
Db 41073 TATGACAACTTTAGTCTAAACCCACCCCAATGAAGTGCATAACTAACACAAATATGCTGCT 41132
Qy 1822 AAAGTATTACACACTTTAGTGTAGTGCAGATGATCGTCAATACAAATTTGCTGAATTCGAC 1881
Db 41133 AAAGTATTACACACTTTAGTGTAGTGCAGATGATCGTCAAAACAAATTTGCTGAATTCGAC 41192
Qy 1882 ATGCCCAACAAAGTGTCTGTATATAATCAATTCGGTGTGAAGGTACCCAAAGGAATAGGT 1941
Db 41193 ATGCCCAACAAAGTGTCTGTCTGAATCATTCGGTGTGAAGGTACCCAAAGGAATAGGT 41252
Qy 1942 AAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGCGACAGTAGTAGACGA 2001
Db 41253 AAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGCGACAGTAGTAGACGA 41312
Qy 2002 ATCAAGAGCTGGGCGAGTTAAGCAAGCTGAAGAAATTTAGGTGTGATGACAAATGGCTCG 2061
Db 41313 ATCAAGAGCTGGGCGACTTAAGCAAGTTAGGAAATTTAGGTGTGATGACAAAGGCTCG 41372
Qy 2062 ACAAGGAAATGTAGATATCTTTGTGCGACCAATTTGAGAGCTCTCTTCCCTCCAATAT 2121
Db 41373 ACAAGGAAATGTAGATATCTTTATGACGCCATTTGAGAGCTCTCTTCCCTCCAATCT 41432
Qy 2122 CTCTATGTGAATGCTGCAGGAATCTCAGATGGTGGAACTTGTAGTGCCTAGATCTTATT 2181
Db 41433 CTCTATGTGAATGCTGGGCTTATTATCAGATATTGAACACTTTGAGTGCCTAGATCTTATT 41492
Qy 2182 TCCT 2241
Db 41493 TCATCT 41552
Qy 2242 AACTGGATTGAGCAGCTCACTCACTGAAGAGATCTACTTTATTGAGGAGCAAACTAAAG 2301
Db 41553 AACTGGATTGAGCAGCTCACTCACTGAAGAGATCTACTTTATTGAGGAGCAAACTAAAG 41612
Qy 2302 GAAGGTAACCACTGCTGATCTTTGGGCGATGCCCCAACCTCATGGTCTTTGATCTTTAT 2361
Db 41613 GAAGGTAACCACTGCTGATCTTTGGGCGATGCCCCAACCTCATGGTCTTTGATCTTTAT 41672
Qy 2362 CGGAAAGCTTACCTTGGGAGAGCTAGTATTCAAACAGGAGCATTTCCCAATCTTTAGA 2421
Db 41673 TGGAAATGCTTACCTTGGGAGAGCTAGTATTCAAACAGGAGCATTTCCCAATCTTTAGA 41732
Qy 2422 ACATTTTCGATTTACGATTTGGATCAGCTAAGAGAGATTTAGATTGAGGACGGCAGCTCG 2481
Db 41733 ACATTTTCGATTTACGATTTGGATCAGCTAAGAGAGATTTAGATTGAGGATGGGAGCTCA 41792
Qy 2482 CCCAGTTGGAAGAGATAGAAATCAGATTCTGCAAGTTGGAATCAGGGATTTATGGTATT 2541
Db 41793 CCCCTGTTGGAAGAGATAGAAATCTTGTCTGCAAGTTGGAATCAGGGATTTATGGTATC 41852
Qy 2542 ATCCACTTTCAGAGCTCAGGAGATTTCACTTGGATACGAAAGTAAAGTGGCTGGGCTT 2601
Db 41853 ATTCACTTTCAGAGCTCAGGAGATTTCACTTGAATACAAAAGTAAAGTGGCTAGGCTT 41912
Qy 2602 GCTCAGCTGGAGGAGAGTGGCAGACACACCAATCAACCCGCTGCTGCGAAGAGGGAG 2661
Db 41913 GGTCACTGGAGGAGAGTGGACACACACCAATCAACCCGCTGCTGCGAATGGACAGT 41972
Qy 2662 GACCGAAGTATCAGGACCTTGTCTGTGAAGCCGAGGATCCCTGTTGAAAGTGGAAAGCA 2721
Db 41973 GACCGAAGGATCAGGACCTGGGGGCTGAGCCGAGGATCTTCTATAGAGTGCACAA 42032
Qy 2722 ACGATCCCTTCCAGAGCAGGAGGA 2748
Db 42033 GCAGATCCTGTTCTGTGATGCGGAGGA 42059

RESULT 5

US-10-656-394A-13

; Sequence 13, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE OF INVENTION: broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 99090
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 23216
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-13

Query Match 79.9%; Score 2395.2; DB 18; Length 99090;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 197 TAGCAATAGATTCTATGCAAGAGACATTCGCAATCAATCAGCTCGAAATGTGATGAAG 256
Db 77939 TTGACATGGAATTCCTATGCAAGAGACATTCGTAATCAGTCAGCTCGCAATGTGATGAAG 77998
Qy 257 CTGAGCTTGTGTGGTCTTCTGACTCCAAAGAAAGGCTGTTGAAATCATCGATACCAATG 316
Db 77999 CTGAGCTTGTGTGGTCTTCTGACTCCAAAGAAAGGCTGTTGAAATCATCGATACCAATG 78058
Qy 317 CTAAATGATGTCCGGCCAAAGTAAATCTGTGTGTGGATCGGTGTTTAAAGCAAGACAG 376
Db 78059 CTAAATGATGTCCGGCCAAAGTAAATCTGTGTGTGGATCGGTGTTTAAAGCAAGACAG 78118
Qy 377 CTCTTTCAGGAAGATCTTTGAAAGCGAAGACATTTAGAGAAATTCCTCTTTCGAATG 436
Db 78119 CTCTTTCAGGAAGATCTTTGAAAGCGAAGACATTTAGAGAAATTCCTCTTTCGAATG 78178
Qy 437 CTGGATACAGTGTCAATCAATTTTCAAGGATGAGCTTAAAGATATGATACGCC 496
Db 78179 CTGGATACAGTGTCAATCAATTTTCAAGGATGAGCTTAAAGATATGATACGCC 78238
Qy 497 AACTTCTTGGCCCGAGTTCTCTGATCAACTCTTTCGAGATTAAGGATGAGTGGTGG 556
Db 78239 AACTTCTTGGCCCGAGTTCTCTGATCAACTCTTTCGAGATTAAGGATGAGTGGTGG 78298
Qy 557 TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTGCTTG 616
Db 78299 TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTGCTTG 78358
Qy 617 TTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGAATTAATGAAATTCATTC 676
Db 78359 TTGTTCTAGATGATCTATGGAATTTTACATGATTTGGAATTTGGAATTAATGAAATTCATTC 78418
Qy 677 CTAAAGCAATAAGAGGGCAGTCAATAGTAATACCACTTTGGAATTTGATCTTCGG 736
Db 78419 CTAAAGCAATAAGAGGGCAGTCAATAGTAATACCACTTTGGAATTTGATCTTCGG 78478
Qy 737 AGAAGTGTGCACAGCTCTCACTGCTGTACCACTTGTATTTCTTTCAGATGAACGATGCCA 796
Db 78479 AGAAGTGTGCACAGCTCTCACTGCTGTACCACTTGTATTTCTTTCAGATGAACGATGCCA 78538
Qy 797 TAACTTGTCTAGGAG 856
Db 78539 TAACTTGTCTAGGAG 78598
Qy 857 TGCAAGAGATGGTGAACGAATTTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 916
Db 78599 TGCAAGAGATGGTGAACGAATTTGAAATTAATTAATTAATTAATTAATTAATTAATTA 78658

Query Match				79.9%	Score 2393.6	DB 18	Length 3099
Best Local Similarity				96.1%	Pred. No. 0		
Matches 2453				Conservative 0	Mismatches 99	Indels 0	Gaps 0
QY	197	TAGCAATAGATTTCTATGCGAGAGACATTCGCAATCAATCAGCTCGGAATGTCGATGCAAG	256				
DB	422	TTGACATGGGATTTCTATGCGAGAGACATTCGTAATCAGTCAGCTCGCAATGTCGATGAGG	481				
QY	257	CTGAGCTTGTGGGTTTTCTGACTCCAGAAAGGCTGCTTGAATGATCGATACCAATG	316				
DB	482	CTGAGCTTGTGGGTTTTCTGACTCCAGAAAGGCTGCTTGAATGATCGATACCAATG	541				
QY	317	CTAATGATGTCGCGCCAAAGGTAACTCTGTGTTGTTGGGATGCGGTGTTTAGGCAAGACAG	376				
DB	542	CTAATGATGTCGCGCCAAAGGTAACTCTGTGTTGCGGATGCGGTGTTTAGGCAAGACAG	601				
QY	377	CTCTTTTCGAGGAGATCTTTGAAAGCGAAGACACATATAGGAGACATTCCTCCCTTGCATG	436				
DB	602	CTCTTTTCGAGGAGATCTTTGAAAGCGAAGACACATATAGGAGACATTCCTCCCTTGCATG	661				
QY	437	CTTGGATTACAGTGTCAAAATCAATTTCAAGGATTTGAGCTACTTTAAAGATATGATACGCC	496				
DB	662	CTTGGATTACAGTGTCAAAATCAATTTCAAGGATTTGAGCTACTTTAAAGATATGATACGCC	721				
QY	497	AACCTTCTGCGCCAGTCTCTCGATCAACTCTTTGCAAGAAATTCGAAGGAAAGGTGGTG	556				
DB	722	AACCTTCTGCGCCAGTCTCTCGATCAACTCTTTGCAAGAAATTCGAAGGAAAGGTGGTG	781				
QY	557	TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGAGTACTTTG	616				
DB	782	TGCAAGTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGAGTACTTTG	841				
QY	617	TTGTTCTAGATGATCTATGGATTTTACATCAATTTGGAATTCGATATAATGAAATTTGCAATTC	676				
DB	842	TTGTTCTAGATGATCTATGGATTTTACATCAATTTGGAATTCGATATAATGAAATTTGCAATTC	901				
QY	677	CTAAGAACAAATAGAAAGGGCAGTCAATAGTAAATACCACTTGGAAATGTTGATCTTTGCCG	736				
DB	902	CTAAGAACAAATAGAAAGGGCAGTCAATAGTAAATACCACTTGGAAATGTTGATCTTTGCCG	961				
QY	737	AGAAGTGTGCCACAGCCTCACTGGTGATCACCTTGAATTTCTTTCGAGATGAACGATGCCA	796				
DB	962	AGAAGTGTGCCACAGCCTCACTGGTGATCACCTTGAATTTCTTTCGAGATGAACGATGCCA	1021				
QY	797	TAAATTTGCTACTGAGAAAAACAAATAAAATTCATGAAGACATGGAATCAAAATAAAAAATA	856				
DB	1022	TAAATTTGCTACTGAGAAAAACAAATAAAATTCATGAAGACATGGAATCAAAATAAAAAATA	1081				
QY	857	TGCAAAAGATGGTTGAACGAAATTTGAATTAATTTGTCGTCCTACCAATTAGCAATACTTA	916				
DB	1082	TGCAAAAGATGGTTGAACGAAATTTGAATTAATTTGTCGTCCTACCAATTAGCAATACTTA	1141				
QY	917	CAATAGAGAGCTGTCTTGCAACTTAACAGAGTGTACAGATGGGAGAAATTCATAGAACACC	976				
DB	1142	CAATAGAGAGCTGTCTTGCAACTTAACAGAGTGTACAGATGGGAGAAATTCATAGAACACC	1201				
QY	977	TTCCCTTCAGAACTAGAAATAAACCCAGCCTCGAAGCTTTTGGAGAGATGGTCACCCCTAG	1036				
DB	1202	TTCCCTTCAGAACTAGAAATAAACCCAGCCTCGAAGCTTTTGGAGAGATGGTCACCCCTAG	1261				
QY	1037	GTTTACAACCACTACCACTCCATCTGAAACCATGCTTTTTTGTATCTAAGTATCTTTTCCCTG	1096				
DB	1262	GTTTACAACCACTACCACTCCATCTGAAACCATGCTTTTTTGTATCTAAGTATCTTTTCCCTG	1321				
QY	1097	AGGATTTTGAATCAAAAGGAATTCGTCTAGTAGTATGATAGAGAGAGGTTTGTGA	1156				
DB	1322	AGGATTTTGAATCAAAAGGAATTCGTCTAGTAGTATGATAGAGAGAGGTTTGTGA	1381				
QY	1157	GACCAAGGTTGGGATGACCACTTAAGATCTCGGAGAGAGTTACTTTTAATGAGCTAATCA	1216				
DB	1382	GACCAAGGTTGGGATGACCACTTAAGATCTCGGAGAGAGTTACTTTTAATGAGCTAATCA	1441				


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Db      2522  TAAAGGAAGGTAAACCACTGCTGATCTTGGGGCACTGCCCAACCTCATGTGCTCTTCATC 2531
Qy      2357  TTTATCGGAAGCTTACCTTGGGGAAGCTAGTATTCAAAACACAGGAGCATTCCTCAATC 2416
Db      2582  TTTATCGGAATGCTTACCTTGGGGAAGCTAGTATTCAAAACACAGGAGCATTCCTCAATC 2641
Qy      2417  TTAGAACAATTCGATTTTACGATTTGGATCAGCTTAAGAGAGATTAGATTTGAGGACGGCA 2476
Db      2642  TTAGAACAATTTGATTTTGAATTTGATCAGCTTAAGAGAGATTAGATTTGAGGACGGCA 2701
Qy      2477  GCTCGCCCAAGTTGGAAAAAGATAGAAATCAGATTTCTGAGGTTGGAATTCAGGGAATTATG 2536
Db      2702  GCTCACCCCTGTTGGAAAAAGATAGAAATAGCGAGTGCAGGTTGGAATCTGGGATTACTG 2761
Qy      2537  GTATTATCCACCTTCCAAAGCTCAAGGAGATTTCACCTTGGATAGAAAGTAAAGTGCTG 2596
Db      2762  GTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCCAATTTAGATACGGAAGTAAAGTGCTG 2821
Qy      2597  GGCTTTGCTCAGCTGGAGGGAAGTGGCGACACACCCAAATCACCCGCTGCTGCGAAAGA 2656
Db      2822  GGCTTTGCTCAGCTGGAGGGAAGTGAACGACACACCCAAATCGCCGCTGCTGCTAATGT 2881
Qy      2657  GGGAGGACCGAAGTGATCAGACCTTGCTTTGTGACGCGCAAGGATCCCTCTGTAAGTGG 2716
Db      2882  ACAGTGACCGAAGGTATCACGACCTGGGGGCTGAAGCGGAAGGATCTTCTATAGAAGTGC 2941
Qy      2717  AAGCAACGGATCCCTCCAGAGCAGGAGGA 2748
Db      2942  AAACAGCAGATCCTGTTCTCTGATCCGAAGGA 2973

RESULT 7
US-10-352-179-92
; Sequence 92, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Lib, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3276)
; OTHER INFORMATION:
US-10-352-179-92

Query Match      79.3%; Score 2377.6; DB 17; Length 3276;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 2443; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy      197  TAGCAATAGATTCTTATGCAAGACATTCGCAATCAATCAGCTCGAAATGTGGATGAAG 256
Db      599  TTGACATGGATTCTTATGCAAGACATTCGTAATCAGTCAGCTCGCAATGTGGATGAAG 658
Qy      257  CTGAGCTGTGTTGGTTTTCTGACTCCAGAAAAGGCTGCTTTGAAATGATCGATACCAATG 316
Db      659  CTGAGCTGTGTTGGTTTTCTGACTCCAGAAAAGGTTGCTTTGAAATGATCGATACCAATG 718
Qy      317  CTAATGATGTCGGCCAGGTAATCTGTGTTGTTGGATCGGTGGTTAGGCAAGACAG 376
Db      719  CTAATGATGTCGGCCAGGTAATCTGTGTTGTTGGATCGGTGGTTAGGCAAGACAG 778
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Qy      377  CTCTTTGCGAAGAGATCTTTGAAAGCGAAGACATTAGAAGAACTTCCTCTTGCATG 436
Db      779  CTCTTTGCGAAGAGATCTTTGAAAGCGAAGACATTAGAAGAACTTCCTCTTGCATG 838
Qy      437  CTTGGATTACAGTGTCAATCATTTTCAAGGATTGAGCTACTTAAAGATATGATACGCC 496
Db      839  CTTGGATTACAGTGTCAATCATTTTCAAGGATTGAGCTACTTAAAGATATGATACGCC 898
Qy      497  AACTTCTTGCCCGCAGTTCCTGGATCAAATCTTTCGCAAGAAATTCGAAGGAAGTGTGG 556
Db      899  AACTTCTTAGTCCCAATCTCTGAAACAATCTTTCGCAAGAAATTCGAAGGAAGTGTGG 958
Qy      557  TGCAAGTACATCATCTTTCTGAGTACCTGATAGAAAGCTCAAGGAAGAGGTACTTTG 616
Db      959  TGCAAGTACATCATCTTTCTGAGTACCTGATAGAAAGCTCAAGGAAGAGGTACTTTG 1018
Qy      617  TTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATTTGCAATTC 676
Db      1019  TTATTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGATTAATTTGCAATTC 1078
Qy      677  CTAAGAACAAATTAAGAGGCGAGTCAAATAGTAATTAACCACTTTGGAATTTGTCGGG 736
Db      1079  CTAAGAACAAATTAAGAGGCGAGTCAAATAGTAATTAACCACTTCGGAATTTGTCAGCG 1138
Qy      737  AGAAGTGTGCGACAGCCCTCACTGCTGTACCACTTGAATTTCTTTCAGATGAACGATGCCA 796
Db      1139  AGAAGTGTGCGACAGCCCTCACTGCTGTACCACTTGAATTTCTTTCAGATGAACGATGCCA 1198
Qy      797  TAACATTTGCTACTGAGAAAAAACAATAAATCATGAAACATGGAATCAATTAATAATA 856
Db      1199  TAACATTTGCTACTAAGAAAAAACAATAAATCATGAAACATGGAATCAATTAATAATA 1258
Qy      857  TGCAAAAAGATGGTTGAACGAATTTGTAATAAATGCTGTCTACCACTTAGCAATACTTA 916
Db      1259  TGCAAAAAGATGGTTGAACGAATTTGTAATAAATGCTGTCTACCACTTAGCAATACTTA 1318
Qy      917  CAATAGGAGCTGTGCTTTGCAAACTAAACACAGGTGTGAGAAATGGGAGAAATTTCTATGAACACC 976
Db      1319  CAATAGGAGCTGTGCTTTGCAAACTAAACACATGTGTGAGAAATGGGAGAAATTTCTATGAACACC 1378
Qy      977  TTCTTTGAGAACTAGAAATTAACCCCAAGCCCTGGAGCTTTGAGGAGAAATGGTGAACCTAG 1036
Db      1379  TTCTTTGAGAACTAGAAATTAACCCCAAGCCCTGGAGCTTTGAGGAGAAATGGTGAACCTAG 1438
Qy      1037  GTTACAAACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCTG 1096
Db      1439  GTTACAAACCACTTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGTATCTTTCTG 1498
Qy      1097  AGGATTTTGAATCAAAAGGAATCGTCTAGTGTAGATGATAGCAGAAAGGTTTGTTA 1156
Db      1499  AGGATTTTGAATCAAAAGGAATCGTCTGTGTAGGTAGATGATAGCAGAAAGGTTTGTTA 1558
Qy      1157  GACCAAAAGGTTGGATGACGACTAAGGATGTCGGAAGAAAGTTACTTTAATGAGCTAATCA 1216
Db      1559  GACCGCAGGTTGGGATGACGACTAAGGATGTCGGAAGAAAGTTACTTTAATGAGCTAATCA 1618
Qy      1217  ACCGAAGTATGATTTCAACGATCAAGAGTGGCGATAGCAGAAAGAAATTTAAGACTTTGTGAA 1276
Db      1619  GCCGAAGTATGATTTCAACGATCAAGAGTGGCGATATCAGGAAGAAATTTAAGACTTTGTGAA 1678
Qy      1277  TTCAATGATATCATCCGTTGATATCAAGTTCCTCGAGACAGGAAAAATTTTGTATTGT 1336
Db      1679  TTCAATGATATCATCCGTTGATATCAAGTTCCTCGAGACAGGAAAAATTTTGTATTGT 1738
Qy      1337  TACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAAACATCGCGCAATAGCATTCATG 1396
Db      1739  TACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAAACATCGCGCAATAGCATTCATG 1798
Qy      1397  GGAGTATGCTCTGCAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTTG 1456
Db      1799  GGAGTATGCTCTGCAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTTG 1858
Qy      1457  GTGACAGACCCAGAGTCTAGCACATGCAAGTTCCTCGAGATCAATTTGAGGATGTTACGGG 1516
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Db 1859 GTGACACCCAGAGCTAGCACATGCGATTTCTAGATCAATGAGGATTCGCG 1918
Qy 1517 TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTGACCGTATTGCAT 1576
Db 1919 TCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTGACCGTATTGCAT 1978
Qy 1577 TGTGTGCGCACTTGAANAATCTTGAAGTATGTGATATTCGTATCATATATTCATCTCCCA 1636
Db 1979 TGTGTGCGCACTTGAANAATCTTGAAGTATGTGATATTCGTATCATATATTCATCTCCCA 2038
Qy 1637 GATCCATTTGGTAAACTACAGGCGCTACAAACTTTTGAACATGCGCAGACACATACATTCGAG 1696
Db 2039 GATCCATTTGGTAAACTACAGGCGCTACAAACTTTTGAACATGCTGAGAACATACATTCGAG 2098
Qy 1697 CACTACCAAGTGAGATCAGTAAACTCCAAATGCTGCTATCTCTTCGTTGTAGTAGAAGT 1756
Db 2099 CACTACCAAGTGAGATCAGTAAACTCCAAATGCTGCTATCTCTTCGTTGTAGTAGAAGT 2158
Qy 1757 TTGTTTCTGCAAACTTTAGTCTAAACCAACCAATGAAGTGATTAACATAATATGCTCC 1816
Db 2159 TTGTTTATGCAAACTTTAGTCTAAACCAACCAATGAAGTGATTAACATAATATGCTCC 2218
Qy 1817 TGCCTAAAGTATTCACACCTTTAGTCTAGTGCAGATGATCGTCAATCAAAATTCCTGAAT 1876
Db 2219 TGCCTAAAGTATTCACACCTTTAGTCTAGTGCAGATGATCGTCAAAATCAAAATTCCTGAAT 2278
Qy 1877 TGCACATGGCCACCAAAAGTTGCTGGTATTAATCAATTCGGTGTGAAGTACCCCAAGAA 1936
Db 2279 TGCACATGGCCACCAAAAGTTGCTGGTGTGAATCAATTCGGTGTGAAGTACCCCAAGAA 2338
Qy 1937 TAGCTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGGACCACTAGTA 1996
Db 2339 TAGCTAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGCGGACCACTAGTA 2398
Qy 1997 GAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAGCAATTAAGTGTGATGACAAATG 2056
Db 2399 GAGCAATCAAGAGCTGGGCGACTTAAAGCAAGTTGAGCAATTAAGTGTGATGACAAATG 2458
Qy 2057 GCTCGACAAAGGAAAATGTAAGATCTTTGTGAGCCATTTGAGAAGCTCTCTTCCCTCC 2116
Db 2459 GCTCGACAAAGGAAAATGTAAGATCTTTGTATGAGCCATTTGAGAAGCTCTCTTCCCTCC 2518
Qy 2117 AATATCTCTATGTGAATGCTGACGAAATCTCAGATGGTGGAACTTTGAGTGCCTAGATT 2176
Db 2519 AATCTCTATGTGAATGCTGCGTTATCAGATATTTGAACACTTTGAGTGCCTAGATT 2578
Qy 2177 CTATTTCTCTCTCCCTCTCTGAGGACACTCGTGTGTATGGAAGTCTTGAAGAGA 2236
Db 2579 CTATTTCTCTCTCTCTCTGAGGACACTCGGTTTGAATGGAAGTCTTGAAGAGA 2638
Qy 2237 TGCCTAACTGGATTTGAGCAGCTCACTCACCTGAAGAAGATCTACTTATGAGGAGCAAAAC 2296
Db 2639 TGCCTAACTGGATTTGAGCAGCTCACTCACCTGAAGAAGATCTACTTATGAGGAGCAAAAC 2698
Qy 2297 TAAAGGAAGGTAAACCACTGCTGATCTTGGGGCAITTTGCCAACTCATGCTCTTGATC 2356
Db 2699 TAAAGGAAGGTAAACCACTGCTGATCTTGGGGCAITTTGCCAACTCATGCTCTTTATC 2758
Qy 2357 TTTATCGGAAAGCTTACCTTGGGAGAGCTAGTATTTCAAAAACAGGAGCATTTCCCAATC 2416
Db 2759 TTTATCGGAAAGCTTACCTTGGGAGAGCTAGTATTTCAAAAACAGGAGCATTTCCCAATC 2818
Qy 2417 TTAGAACACTTTTCGATTTTACGATTTGGATCAGCTTAAGAGATTTAGATTTGAGGACGCA 2476
Db 2819 TTAGAACACTTTTCGATTTTACGATTTGGATCAGCTTAAGAGATTTAGATTTGAGGATGGCA 2878
Qy 2477 GCTGCCCGGAGTTGGAAGATAGAAATCAGATTTCTGAGGTTGGAATCAGGGATTTTG 2536
Db 2879 GCTCACCCCTGTTGGAAGATAGAAATCTCTTCTGCGAGTTGGAATCAGGGATTTTG 2938
Qy 2537 GTATTATCCACCTTTCCAAAGGCTCAAGGAGATTTTCACTTTGGATACGAAAGTAAAGTGCTG 2596
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Db 2939 GTATCATTTACCTTCCAAAGGCTCAAGGAGATTTCACTTGAATACAAAAGTAAAGTGCTA 2998
Qy 2597 GGCTTGTCTAGCTGGAGGAGAGTGCACACACCAAAATCAACCCGCTGCTGCAAGA 2656
Db 2999 GGCTTGTCTAGCTGGAGGAGAGTGAACACACACCAAAATCGCCGCTGCTGCAATGG 3058
Qy 2657 GGGAGGACCAAGTGTACAGACCTTGTCTGTGAGCGGAGGATCCCTGTTCAAGTGG 2716
Db 3059 ACAGTGAACCAAGGATCAAGACCTGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTGC 3118
Qy 2717 AAGCAACGATCCCTCCACAGAGCAGGAGGA 2748
Db 3119 AAACAGCAGATCTCTGTCTGATGCCGAAGA 3150
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RESULT 8
US-10-656-394A-3
; Sequence 3, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3099)
US-10-656-394A-3

Query Match 78.7%; Score 2359.8; DB 18; Length 3099;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

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Qy 202 ATAGATTCCTATGCAAGAGACATTCGCAATCAATCACTCGAATGTGGATGAAGCTGAG 261
Db 427 ATGGAATTCCTATGCAAGAGACATTCGCAATCAATCACTCGAATGTGGATGAAGCTGAG 486
Qy 262 CTGTGCGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATATGATGATACCAATGCTAAT 321
Db 487 CTGTGCGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATATGATGATACCAATGCTAAT 546
Qy 322 GATGCTCCGCCCAAGGTAATCTGTGTTTGGGATGGTGGTTTGAAGACAGCTCTT 381
Db 547 GATGCTCCGCCCAAGGTAATCTGTGTTTGGGATGGTGGTTTGAAGACAGCTCTT 606
Qy 382 TCAGGAGATCTTTGAAGCGAAGACATTTAGGAAGAACTTCCCTTGCATGCTTGG 441
Db 607 TCAGGAGATCTTTGAAGCGAAGACATTTAGGAAGAACTTCCCTTGCATGCTTGG 666
Qy 442 ATTACAGTGTCAAACTCATTTTCAAGGATGAGCTACTTAAAGATATGATACGCCAACTT 501
Db 667 ATTACAGTGTCAAACTCATTTTCAAGGATGAGCTACTTAAAGATATGATACGCCAACTT 726
Qy 502 CTTGGGCCCAAGTTCCTGAGTCAACTCTTCGATCAACTCTTCGATGAATTTGCAAGGAAAGTGGTGGTCA 561
Db 727 CTTGGTCCCAAGTTCCTGAGTCAACTCTTCGATGAATTTGCAAGGAAAGTGGTGGTCA 786
Qy 562 GTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGTACTTTGTTGTT 621
Db 787 GTACATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGTACTTTGTTGTT 846
Qy 622 CTAGATGATCTATGGAATTTTACATGATTTGGATTAATGAAATGCAATTTCCCTAAG 681
Db 847 CTAGATGATCTATGGAATTTTACATGATTTGGATTAATGAAATGCAATTTCCCTAAG 906
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APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE OF INVENTION: Broad-spectrum resistance gene P12
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 3674
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-656-394a-16

Query Match 78.7%; Score 2359.8; DB 18; Length 3674;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy	202	ATAGATTCCTATGCGAAGACATTCGCAATCAATCAGCTCGAATGTGGATGAGCTGAG	261
Db	435	ATGATTCCTATGCGAAGACATTCGCAATCAATCAGCTCGAATGTGGATGAGCTGAG	494
Qy	262	CTTGTGGGTTTCTGACTCCAGAAAAGGCTGCTGAAATGATCGATACCAATGCTAAT	321
Db	495	CTTGTGGGTTTCTGACTCCAGAAAAGGCTGCTGAAATGATCGATACCAATGCTAAT	554
Qy	322	GATGTCGGCCAAAGGTAATCTGTGTTGTTGGATGGTGGTTTGGCAAGACAGCTCTT	381
Db	555	GATGTCGGCCAAAGGTAATCTGTGTTGTTGGATGGTGGTTTGGCAAGACAGCTCTT	614
Qy	382	TCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCATGCTTG	441
Db	615	TCGAGGAAGATCTTTGAAAGCGAAGACATTTAGGAAGAACTTCCCTTGCATGCTTG	674
Qy	442	ATTACAGTGTACAAATCAATTTACAGGATTTGAGCTACTTAAAGATATGATACGCCA	501
Db	675	ATTACAGTGTACAAATCAATTTACAGGATTTGAGCTACTTAAAGATATGATACGCCA	734
Qy	502	CTTGGCCCCAGTCTCTGGATCAACTCTTGCAAGAAATTCGAAGGAAAGTGGTGGTCA	561
Db	735	CTTGGCCCCAGTCTCTGGATCAACTCTTGCAAGAAATTCGAAGGAAAGTGGTGGTCA	794
Qy	562	GTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAAAGAGGTACTTTGTTGTT	621
Db	795	GTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAAAGAGGTACTTTGTTGTT	854
Qy	622	CTAGATCATCTGATGATTTACATGATTTGGAATTTGGATTAATGAAATGCAATTCCT	681
Db	855	CTAGATCATCTGATGATTTACATGATTTGGAATTTGGATTAATGAAATGCAATTCCT	914
Qy	682	AACAATGAAGGGCAGCTCAATAGTAATACCACTTTGGAATTTGATCTTTGGGAGAG	741
Db	915	AACAATGAAGGGCAGCTCGAATAGTAATACCACTCGGAATTTGATCTAGCGGAGAG	974
Qy	742	TGTGCCACAGCTCACTGGTGTACCACTTGAATTTCTTGAGATGAACGATGCCATAACA	801
Db	975	TGTGCCACAGCTCACTGGTGTACCACTTGAATTTCTTGAGATGAACGATGCCATAACA	1034
Qy	802	TTGCTACTGAGAAAACAAATAAATCATGAACATGGAATCAAAATAAATAATATGCAA	861
Db	1035	TTGCTACTGAGAAAACAAATAAATCATGAACATGGAATCAAAATAAATAATATGCAA	1094
Qy	862	AAGATGGTGAACGAAATTTGAAATAAATTTGGTCTGCTACCATTTAGCAATATACATA	921
Db	1095	AAGATGGTGAACGAAATTTGAAATAAATTTGGTCTGCTACCATTTAGCAATATACATA	1154
Qy	922	GGAGCTGTGCTGCAACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACACCTTCT	981
Db	1155	GGAGCTGTGCTGCAACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGAACACCTTCT	1214
Qy	982	TCAGAACTAGAAATAAACCCAGGCTTGGAGGAAATTTGGAGGAAATTTGGTGAACCT	1041
Db	1215	TCAGAACTAGAAATAAACCCAGGCTTGGAGGAAATTTGGAGGAAATTTGGTGAACCT	1274

Qy	1042	AACCACCTACATCCCATCTGAAACCAATGCTTTTGTATCTAAGTATCTTTCCTGAGAT	1101
Db	1275	AACCACCTACATCCCATCTGAAACCAATGCTTTTGTATCTAAGTATCTTTCCTGAGAT	1334
Qy	1102	TTTGAATCAAAAGGAATCGCTAGTAGGTAGATGGAATAGCAGAGGTTTGTGTAGACCA	1161
Db	1335	TTTGAATCAAAAGGAATCGCTAGTAGGTAGATGGAATAGCAGAGGTTTGTGTAGACCA	1394
Qy	1162	AAGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTAATGAGCTAATCAACCGA	1221
Db	1395	AAGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTAATGAGCTAATCAACCGA	1454
Qy	1222	AGTATGATTCACGATCAAGATGGGATAGCAGGAAAAAATTAAGACTTGTGCAATTCAT	1281
Db	1455	AGTATGATTCACGATCAAGATGGGATAGCAGGAAAAAATTAAGACTTGTGCAATTCAT	1514
Qy	1282	GATATCATCTCGTATATCAGATTTCAATCTCGAGACAGGAAAAATTTTGTATTTACCA	1341
Db	1515	GATATCATCTCGTATATCAGATTTCAATCTCGAGACAGGAAAAATTTTGTATTTACCA	1574
Qy	1342	ATGGGAGATGGCTCTGATTTAGTTTCAAGAAAAACACTCGCCACATAGCATTCATGGGAGT	1401
Db	1575	ATGGGAGATGGCTCTGATTTAGTTTCAAGAAAAACACTCGCCACATAGCATTCATGGGAGT	1634
Qy	1402	ATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTTTGGTGAC	1461
Db	1635	ATGTCCTGCAAAAACAGGATTTGGATTTGGAGCATTTATTCGATCATTTAGCTATTTTTGGTGAC	1694
Qy	1462	AGACCCAAAGAGTCTAGCACATGCAATTTGTCAGATCAATTTGAGGATTTTACGGGCTTTG	1521
Db	1695	AGACCCAAAGAGTCTAGCACATGCAATTTGTCAGATCAATTTGAGGATTTTACGGGCTTTG	1754
Qy	1522	GATCTTGAAGATGTACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCAATTTGTG	1581
Db	1755	GATCTTGAAGATGTACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTGCAATTTGTG	1814
Qy	1582	TGCCACTTGAAATATCTTGAGTATTTGGATATTTGGATATTTGGTATTTTCCATATATTT	1641
Db	1815	TGCCACTTGAAATATCTTGAGTATTTGGATATTTGGTATTTTCCATATATTTCCATATTT	1874
Qy	1642	ATTGGTAACTACAGGCTTACAACTTTGAAACATGCGGACACATACATTTGAGCACTA	1701
Db	1875	ATTGGTAACTACAGGCTTACAACTTTGAAACATGCGGACACATACATTTGAGCACTA	1934
Qy	1702	CCAAGTGAGATCAGTAACTCCAACTGTCGATCTCTTGGTGTAGTAGAAAGTTTGT	1761
Db	1935	CCAAGTGAGATCAGTAACTCCAACTGTCGATCTCTTGGTGTAGTAGAAAGTTTGT	1994
Qy	1762	TCTGACAACTTTAGTCTAAACCAACCAATGAGTGCATACTAAACAAATATGCTGCT	1821
Db	1995	TCTGACAACTTTAGTCTAAACCAACCAATGAGTGCATACTAAACAAATATGCTGCT	2054
Qy	1822	AAAGTATTCACACTTTAGTTAGTTCGGATGATCGTCAATACAAATTTGCTGAATTCAC	1881
Db	2055	AAAGTATTCACACTTTAGTTAGTTCGGATGATCGTCAATACAAATTTGCTGAATTCAC	2114
Qy	1882	ATGSCCAACAAAAGTTGCTGCTAATAATCAATTCGGTGTGAAGGTACCCAAAGGAATAGGT	1941
Db	2115	ATGSCCAACAAAAGTTGCTGCTAATAATCAATTCGGTGTGAAGGTACCCAAAGGAATAGGT	2174
Qy	1942	AAGTTCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGTAGAGCA	2001
Db	2175	AAGTTCGAGACTTACAGGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGTAGAGCA	2234
Qy	2002	ATCAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTTAGGTGTGATGACAAATGGCTCG	2061
Db	2235	ATCAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTTAGGTGTGATGACAAATGGCTCG	2294
Qy	2062	ACAAAGGAAAAATGTAAGATACATTTTGGCAGGCACTTTGAGAGGCTCTCTCCCTCCAATAT	2121
Db	2295	ACAAAGGAAAAATGTAAGATACATTTTGGCAGGCACTTTTGAAGGCTCTCTCTCCCTCCAATAT	2354

D _b	1198	CAGCTTCCTTCAGAACCTTGAAAGCAACCCCAAGCCTTCAAGCTTTGAGGAGAAATGGTGACC	1251
Q _y	1033	CTAGGTTACAACCACTACCATCCCATCTGAAACCATGCTTTTGTATCTAAAGTATCTTT	1092
D _b	1258	CTTGGCTACAACCACTGCCATCTCATCTGAAATCATGCTTTTGTACCTTAAGTATCTTC	1317
Q _y	1093	CCTGAGGATTTTGAAATCAAAAGGAATCGTCTAGTACGTTAGATGGATAGCAGAAAGGGTTT	1152
D _b	1318	CCTGAGGATTTTGAGATCAAAAGGAGTCCGCTTGGTGTAGACAGATGGAATTCGAGAGGGGTTT	1377
Q _y	1153	GTTTAGCCAAAGGTTGGGATGACCATCAAGGATGTCGAGGAAAGTTACTTTTAATGAGCTA	1212
D _b	1378	GTTTAGGCCAAGGTTGGGATGACGACCAAGGATGTTGGGGACAGTTACTTTTAATGAGCTA	1437
Q _y	1213	ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAATTTAAAGACTTGT	1272
D _b	1438	ATCAACCGAGTATGATTTCAAGATCAAGAGTGGGCATAGAGGAAAAATTTAAGAGTTGC	1497
Q _y	1273	CGAATTCAATGATATCATCCGTGATATCACAGTTCATCTCGAGACAGGAAAAATTTTGTGA	1332
D _b	1498	CGAGTCCATGATATCATCGGTGATATCACAGTTCATCTCTAGAGAGGAGAACTTTTGTGA	1557
Q _y	1333	TTGTTACCAATGGGAGATGGCTCTGATTTAGTTCAGGAAAAACACTCCGCACATAGCAATTC	1392
D _b	1558	TTCTTACCGATGCATGATGGCTCCAAATCTTAGCACAGGAAAACTCCGCCACATAGCAATG	1617
Q _y	1393	CATGGGAGTATGTCCTCGAAAAACAGGATTGGATGGAGCAATATTCGATCATTTAGCTATT	1452
D _b	1618	CATGGGAGCATGTCCTCGAAAAACAGGATTGGATTTGGAGCAATATTCGATCCTTAGCTATT	1677
Q _y	1453	TTTGGTGACAGACCCAAAGAGTCTAGCACATGTCAGTTCCTCCAGATCAATTTGAGGATGTTA	1512
D _b	1678	TTTGGTGACAGACCCCAATATCTTAGCACACACATATTTGTTCAAATAAATTCAGGATGTTA	1737
Q _y	1513	CGGCTCTTGATCTTTGAAGATGTGACATCTTAATCATCTCAAAAGATTTTCGACCGTATT	1572
D _b	1738	CGGCTGTGGATCTTTGAAGATGTGAAGTTTTTAATCAACAAAAAGATTTCAACAAATATA	1797
Q _y	1573	GCATTTGTTGSCCACTTTGAAATACCTTCAGTATTCG-----ATATTCGTCATCCATATAT	1626
D _b	1798	GCATTTGTTGCTCACTTTGAAGTACTTGAGCTTTGGAGAAATATTCCTCATATGCAATATAT	1857
Q _y	1627	TCATCTCCCAGATCCATTTGGTAAACTACAGGCGCTACAAACTTTTGAACTGCCGAGCACA	1686
D _b	1858	ACTCTTCCCAGATCTATTGTTGAATATACATGGCTTACAGACCTTGAATATGTCAAGTACA	1917
Q _y	1687	TACATTCGAGCATACCAAGTGAGATCAGTAAACTCCAATGTCTGCAATCTCTTCGTTGT	1746
D _b	1918	TACATTTGCAACACTACCAACTGAGATCAGTAAACTCCAATGTCTGCGCACTCTTCGTTGT	1977
Q _y	1747	AGTAGAAAGTTTGTTCCTGACAACTTTAGTCTAAACCAACCAATGAAGTGCATAACTAAC	1806
D _b	1978	ACAAGGATCTCAATAATACAAATTTAGTATAAATCACCCGGTGAAGTGCCTTAACATAAC	2037
Q _y	1807	ACAAATATGCTCCCTAAAGTATTCACACCTTTTACTTGTAGTCGCGATGATCGTGCAATACAA	1866
D _b	2038	ACAATGTCTGCTCTAATATATTCACACCTTCAGTTAGTAGGAGACAATCGTGCCAAACAA	2097
Q _y	1867	ATTGCTGAATTGACATGGGCCACCAAAGTTGCTGGTATAAATCAATTCGGTGTGAAGGTA	1926
D _b	2098	ATTGCTGAATTTGCATATGGGCCACCAAAGTTGTTGGTCTGAATCATACAGTGTGAAGGTA	2157
Q _y	1927	CCCAAGGAATAGTGAAGTTGCGAGACTTACAGGTTCTAGAGTATGTAGATATCATGCGCG	1986
D _b	2158	CCCAAGGATATAGGCAAGTTGGGAGAAATACAGATCTAGAGCATGTGGATATCAGAGG	2217
Q _y	1987	ACCAAGTATAGGCAATCAAAAGAGCTCGGGCAGTTTAAGCAAGCTTGAGGAAATAGGTGTG	2046
D _b	2218	ACTAGTACTAGTGCAATCCAAGATTTGGCGAACTTAGCAAGCTGACTAAATTAAGTGTG	2277
Q _y	2047	ATGACAAATGGCTCGACAAAGGAAAAATGTGAAGATCTTTGTGCGACCATGTGAGAAGCTC	2106
D _b	2278	ACAAACAAAGGATCCACAGAGGAAAAATGTGAAGTACTCTATAGAGCATCTCAAAGGCTC	2337

QY	2107	TCCTCCCTCCAAATATCTCTAATGAAATGCTGCAGGAATCTCAGATGGTGAACACCTTGAG	2166
DB	2338	TGTTCCCTGCAATCTCTCCGTGTGGATGTCTGAGGGGTCTCTCAGGAAATGGAACACTTAA	2397
QY	2167	TGCTCTAGATCTTATTTCTCTCTCTCTCCCTACTCTAGGACACTCGTGTGTGATGGAAGT	2226
DB	2398	TGCTCTAGATCTTATTTCTTATCTCTCTCTGTTTAAAGACACTCAAGTTGTATGGAGAT	2457
QY	2227	CTTGAAGAGATGCTTAACTGGATTGAGCAGCTCACTCACTGTAAGAGATCTTACTTTATTG	2286
DB	2458	CTTGAAGAGATGCCAACTGGAATTGAGCAGCTCTCGCACCTCATGAAGTTCTACTTTATTA	2517
QY	2287	AGGAGCAAACTAAAGGAAAGTAAACCAATGCTGATCTTGGGCGATTGCCCAACCTCATG	2346
DB	2518	GGGAGTAAACTAAAGGAAAGAAACCAATGCTGATCTTGGGCGATTGCCCAACCTCATG	2577
QY	2347	GTCCCTTGATCTTTATCGAAAGCTTACCTTGGGGAGAAAGCTAGTATTTCAAAACAGAGCA	2406
DB	2578	CTGCTTTGCTTTTCACTTTGATGCTTAACTCGGGAGAAATCTAGTATTCAGNACAGAGCA	2637
QY	2407	TTCCCAAACTTTTGAACACATTTTCGATTTTACGATTTTGGATCAGCTAAGAGAGATTAGATTT	2466
DB	2638	TTCCAAAGCTCAGGACACTTTGGTTTGAACAAGCTGGATCAGCTAAGAGAGATTAGTGT	2697
QY	2467	GAGGAGCGCAGCTCGCCCCAGTTTGGAAAGATAGAATCAGATTTCTGCAGTTTGGAAATCA	2526
DB	2698	GAGAACGACAGCTCGCCCCCTATTTGGAAAGATAGGAATCCGATCTGCAGTTTGGAAATA	2757
QY	2527	GGGATTTTGGTATTTATTCACCTTCCAAAGGCTCAAGGAGATTTTCACTTGGATACGAAAGT	2586
DB	2758	GGGATTTTGGTATCTCTAAACCTTATGAGGCTTAAGGAAATTTACATTTGGATACAGATT	2817
QY	2587	AAAGTGTCTGGGCTTGTCTAGCTTGGAGGGAGAAAGTGGCGACACACCCCAATCACCCCGTG	2646
DB	2818	AAAGTTGGTTATCTTGTGTCAAGTTTGGAAAGAGAAAGTTGGCACACACCCCAATCCCCCGTG	2877
QY	2647	CTCGGAAGAGGGAGGAGCGGAAGTGATCAGACCTTGTCTGTCAGCCGGAAGGATCCCT	2706
DB	2878	CTACGTTATGAGAGAGGACCGAAGCTGTCCGACTCTGAGAAAGGATGGCAAAAGGATCAGCT	2937
QY	2707	GTTGAAGTGAAGCAACGGATCCCTCTCCAGAGCAGGAGGGAGAG	2751
DB	2938	GTAGAAATGGAAGCAACGGAGCCCTCTCTCTGAGCCCGGAGAGCTTAG	2982

RESULT 11

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US-10-352-179-90
; Sequence 90, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materi
; FILE REFERENCE: 27277/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 3220
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-90

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Query Match	47.1%;	Score 1411;	DB 17;	Length 3220;
Best Local Similarity	74.1%;	Pred. No. 0;		
Matches 1893; Conservative	0;	Mismatches 620;	Indels 40;	

Qy 206 ATTCTATGCAGAGACATTGCGAATCAATCAGCTCGGAATGTGGATGAAGCTGAGCTTG 265

Db 431 ATTTATTTATGGAAGACATTTCCCAACCAATTAAGCTAAACAACATTTGAGGAAGCTGATCTTG 490
Qy 266 TTGGGTTTTCTGACTCCAAGAAAAGGCTGCTTGAATGATCGATACCAATGCTTAATGATG 325
Db 491 TGGGTTTTTCTGGACCCAAAGAGAGAGTTGCTTGATCTTATAGATGTCCATGCCAATGACG 550
Qy 326 GTCCGGCCAAAGGTAAATCTGTGTTGTTGGGATGGGTGTTAGGCAAGACAGACTCTTTCCGA 385
Db 551 GACCTACAAAAGTTGATGTGTCTCGTATGGGTGGTTGGGTAAAGACTACTATTGCA 610
Qy 386 GGAAGATCTTTGAAAGCGAAGAAACATTTAGGAAGAACTTCCCTTGGCAATGCTTTGGATTA 445
Db 611 GGAATAATTTATGAAAGCAAGAGACATTTGCAAGAAATTTTTCTGTGCTTTGGATTA 670
Qy 446 CAGTGTCACAATCATTTTCAAGGATTCAGCTACTTTAAGATATCATCGCCAACTTCTTG 505
Db 671 CTGTTTTACAGTCTCTTTGTAGGGTGAACCTACTCAAGGATTTGATGGTGAACCTTTTTG 730
Qy 506 GCCCCAGTTCTCTGGATCAACTCTTTGCAAGAAATTCGAAGGAAGGTGGTGGTCAAGTAC 565
Db 731 GAGAGGAAGTACTGAAGAGCGGCTGAGAGAACTCGAAGGGAA--GTTTTCCACAAGTAG 787
Qy 566 ATCATCTTTCTGAGTACTGTATGAGAGCTCAAGAGAGAGAGTACTTTGTTGTTCTAG 625
Db 788 ACGACTCGCCAGCTACTCTCAGGACAGAGTTTAAATGAAAGGAGGTACTTTGTTGTGCTTG 847
Qy 626 ATGATCTATGATTTTACATGATTTGGAATTCGATTAATGAAATGCAATTTCTTAAGACA 685
Db 848 ATAACGTGTGGAGTACAGATTCATGGAAATGGAATTAATGATGATTTGCTTCCCTTGAANA 907
Qy 686 ATAGAAAGGGCAGTCAAAATAGTAATAACCACTTGGAAATTTGATCTTTGCGGAGAGTGTG 745
Db 908 ACAATAAAGGAGCGGGTATGATTAACAAGAGATTTGGCTTAACCTAAGGAGTGA 967
Qy 746 CCACAGCCTCTACCTGGTGTACCACTTGATTTCTTGAGATGAAGAGTGCCTTAACATGTC 805
Db 968 CTTCTGAATTTGCTTATCTACAGCTTAAACCCCTAGAAATAAACCTATGCAAAAGAGTTGC 1027
Qy 806 TACTGAGAAACAAATAAATAANTCATGAGACATGGAATCAATAAATAATGCAAAAGA 865
Db 1028 TTCTACGGAAGCAATAAAGCAATAGAGATATGGAAGTGAATAAAGATAGTGACA 1087
Qy 866 TGGTTGAACGAATTTGATAAATAATGCTGCTTACCATTAGCAATACTTACAAATAGGAG 925
Db 1088 TTATAACTAAATAAATAAGAGTGTGGCTATTACCGCTGCTTACTCACATAGGAG 1147
Qy 926 CTGTGCTTGCAACTAAACAGGTGTAGAAATGGGAGAAATTTCTATGAACACCTTCCCTCAG 985
Db 1148 GCGTGTCTTTCCACCAAGAGATAAGAGATGGGAAACTTTTTTATAGTCAGATACCTTTCAG 1207
Qy 986 AACTAGAAATAAACCAGCTCGAAGCTTTGAGGAGATGGTGACCTTAGGTTTACAAACC 1045
Db 1208 AGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAAGGATAGTACCCTAAGTTTACAAC 1267
Qy 1046 ACCTPACCATCCATCTGAAACCAATGCTTTTGTATCTAAGTATCTTTCTGAGGATTTTG 1105
Db 1268 ACTTACCGTCTCATCTTAAAGCAATGCTTTTGTATCTAAGCATATTTCTTGAGGATTTG 1327
Qy 1106 AAATCAAAAGAAATCGTCTAGTAGGTAGATGATAGAGAGAGGTTGTTAGACCAAGG 1165
Db 1328 AAATTAATAGAACCGTCTGGTAAATAGA TGGATGGCAGAGGGGTTTTATTAAGACTAGGA 1387
Qy 1166 TTGGGATGACGACTAAAGATGTCGGAGAAAGTTACTTTTATGAGCTAATCAACCGAAGTA 1225
Db 1388 CTAATATGACTATTGGAAGATGTTGGGAAAGTTTACTTTAAGAACTTATCAACCGTAGCA 1447
Qy 1226 TGATTTCAACGATCAAGAGTGGGCAATAGCAGGAAAAATTTAAGACTTTGTCGAATTCATGATA 1285
Db 1448 TGATTCAGCCATCAAGAGCGGGTATACGAGGAGATTTTAAAGAGCTGTGAGTCCACGACA 1507
Qy 1286 TCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTTGTACCAATGG 1345
Db 1508 TCATGCGTGATATTACAAATTTCCGATTTCTAGAGAAAGAAATTTTCACTCTTACCCGATG 1567

Qy 1346 GAGATGGCTCTGATTTAGTTTTCAGGAAAAACACTCGCCACATAGCAATTCATGGGAGTATGT 1405
Db 1568 GCATGACTATGATGATAGTACATGGGAACACTCGGCACATAGAAATTTTACGGGAGTAAGT 1627
Qy 1406 CTTGTC---AATAACAGGATTTGGAGCAATTTATTCGATCAATTAGCTATTTTGGTGACA 1462
Db 1628 ATTGCTCTGAAAACAAGCTTGGACTGGAGCAATTAACGGTCATTAACCTATGTTTGGTGAGA 1687
Qy 1463 GACCAAGAGTCTAGACATGCAATGTTTGTCCAGATCAATTTGAGGATGTTTACGGGCTTTGG 1522
Db 1688 GGTCCGTAGAACTAGAGCAATTCAGTTTGTTCATCTCAGTTGAGGATGTTTACGGGCTTTGG 1747
Qy 1523 ATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTATTTGCAATGTTGT 1582
Db 1748 ATCTAACAGATGCAAAATTTTCTATCACAAATGATGTCGACAAATAGTGTCTTTGT 1807
Qy 1583 GCCACTTTGAAATACTTCTGAGTATT-----GGATATTCTGTCATCCATATATTCACATT 1632
Db 1808 GCCACTTTGAAATACCTATGCAATTAAGATACAGATACCGTTTACCATATATTTATTCACATT 1867
Qy 1633 CCCAGATCCATTTGGTAAACTACAGGGCTTACAACTTTTGAACATGCCGAGCACATACATT 1692
Db 1868 CCACAATCCATAGCTAGACTGCAATGGTCTGAGACATTTGGACTTTGGGTTCAGACGTACATT 1927
Qy 1693 GCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCATCTCTTTCTGTTGTAGTAGA 1752
Db 1928 TCAACACTGCACTCAGATTACT-AACTTGGGAGTCTCCGTAGCTTTCGATGATGAAA 1986
Qy 1753 AAGTTTGTCTGCAAACTTTAGTCTAAACACCCAAATGAAGTGCAATAACACAAATA 1812
Db 1987 GAATATTTTCTTCTTCTTT-----AACAAATATTTAACTTAACACATTA 2031
Qy 1813 TGCTGCTTAAAGTATTTCACACCTTTTAGTTCGCGATGATCGTGCAATACAAATTCCT 1872
Db 2032 TGCTGCTCCATGATATTTCACACCTTTCTGTTAGTACCTCGGATCGTTCTGAACAAATTCCT 2091
Qy 1873 GAATTTGACATGGCCACCAAAAGTTTGTGCTGATATAAATCAATTCGGTGTGGAAGGTACCCAAA 1932
Db 2092 AATTTGACATGGCCACCAAAAGCTTCCGTTCAAAATCAATGTTGTCNAGGTACCAAAA 2151
Qy 1933 GGAATAGGT---AAGTTGCGAGACTTACAGGTTCTAGAGTATGATAGATACAGCGGAC 1988
Db 2152 GGAATATGTAATAAAAAAACTCGACTTACAAATATTCGAGGTAGTGGATATAGAAAGAC 2211
Qy 1989 CAGTAGTAGACATCAAGAGCTGGGGCAGTTTAAGCAAGCTGAGGAAATTTAGGTGTGAT 2048
Db 2212 TAGCAGTAGAGCAATCAAGAGTTTGGGGCAGTTTAAGCAAGCTGAGGAAATTTATGTGGT 2271
Qy 2049 GACAAATGGCTCGACAAAGGAAATAATGTAAGATACTTTGTGACGCCATTTGAAGAAGTCTC 2108
Db 2272 AACAAAGGATCCAAAGGAAATAATGTGAGATACTCTATACAGCTATCCAGAAGCTCTG 2331
Qy 2109 TTCCCTCCAATATCTCTATGTGAATGTCGAGGAATCTCAGATGGTGGAAACATTTGAGTG 2168
Db 2332 TTTCTCAATCTCTCATGTGAATGCTGTGGGATTTTCAGGTATTTGGAACACATTCAGTG 2391
Qy 2169 CTTAGATTTCTATTTCCTCTCTCTCCCTACTGAGGACACTCGTGTGTTGATGGAAGTCT 2228
Db 2392 TATAGATTCTATTTCATCTCTCTCCCTACTGAGGACACTCAGGTTTGAATGGAAGTCT 2451
Qy 2229 TGAAGAGATCGCTAACTGGGATTTGAGCAGCTCAGCTCAGTGAAGAAGATCTACTTTATTGAG 2288
Db 2452 TGAGGAGATGCTTAATCTGGATTTGAGCAGCTCACGCCCTGATGAAGTTTCACTTTATGGAG 2511
Qy 2289 GAGCAAACTAAAGAGGTAAAAACCATGCTGTAATTTGGGGCATTTGCCAACCTCATGGT 2348
Db 2512 GAGCAAACTAAAGAGGTAAAAACCATGTTGGTACTTTGCGCGTTCGCCAACCTCATGGT 2571
Qy 2349 CTTTGTCTTTTATCGGAAAGCTTACCTTGGGAGAAAGCTAGTATTTCAAAACAGGAGCAATT 2408
Db 2572 CTTTATCTTTTATTTCCAAATGCTTACCATGGGGAGAAAGCTAGTATTTCAAAATGGGAGCAATT 2631

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QY 2409 CCCAAATCTTAGAACACATCTTCGATTTACGATTTGGATCAGCTAACGAGAGATTAGATTTGA 2468
DB 2632 CCCAAATCTTAGAACATTTTCGATTTACATTTGGAGCAGCTAACGAGAGATTAGATTTGA 2691
QY 2469 GGACGGCAGCTCGCCCAAGTTGGAAAAGATAGAAATCAGATTTCTGCAGGTTTGGAAATCAGG 2528
DB 2692 GGACGGCAGCTCAATCTTTGTTGGAAAAGATAGAAAT----ATTACGGGTTTGGAAATCAGG 2747
QY 2529 GATTATTGGTATTATTCAGACCTTCCAAAGCTCAGAGAGATTTTCACTTTGGATACGAAAGTAA 2588
DB 2748 GATTGTTGGTATCAATTCACCTTCCAAAGCTCAGAGAGATTTTCACTTTGGATACGAAAGTAA 2807
QY 2589 AGTGGCTGGGCTTGTCTCAGCTGGAGGAGAGAGTGGCACACACCCAAATCACCCCGTGCT 2648
DB 2808 AGTGGCTAGGCTTGTCTCAGCTGGAGGAGAGAGTGGCACACACCCAAATCACCCCGTGCT 2867
QY 2649 GCGAAGAGGGAGGAGCGAAGTGATCACGACCTTGTGTGACGCGCGAAGGATCCCTGT 2708
DB 2868 GCGAATGAGGAGGAGCGAAGTGATCACGACCTTGTGTGACGCGCGAAGGATCCCTGT 2927
QY 2709 TGAAGTGAAGCAACGGATCCCTCCCGAGAGA 2741
DB 2928 TGAAGTGAAGCAACAGATCTGTGAGAGCTCA 2960

RESULT 12
US-10-656-394A-15
; Sequence 15, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656.394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2422
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2014, 2043, 2099, 2114, 2154, 2172, 2178, 2199, 2205, 2236,
; LOCATION: 2268, 2299, 2333, 2337, 2339, 2356
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-15

Query Match 45.2%; Score 1354.2; DB 18; Length 2422;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1254 AGGAAAATTAGACTTGTGCAATTCATGATATCATCGGTGATATCAGTTTCAATCTC 1313
DB 1 AGGAAAATTAGAACTTGTGCAATTCATGATATCATCGGTGATATCAGTTTCAATCTC 60
QY 1314 GAGACAGAAATTTTGTATTGTTTACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAA 1373
DB 61 GAGACAGAAATTTTGTATTATTTACCATGGGAGATGGCTCTGATTTAGTTTCAGGAAA 120
QY 1374 CACTCGCCACATAGCATTTCCATGGGAGTATGCTCTGCAAAAACAGGATTTGGATGGAGCAT 1433
DB 121 CACTCGCCACATAGCATTTCCATGGGAGTATGCTCTGCAAAAACAGGATTTGGATGGAGCAT 180
QY 1434 TATTGATCATTTAGTATTTTGTGTGACAGACCCAAAGAGTCTAGCACATGAGTTTGTC 1493
DB 181 TATTGATCATTTAGTATTTTGTGTGACAGACCCAAAGAGTCTAGCACATGAGTTTGTC 240
QY 1494 AGATCAATTGAGGATTTACGGCTTGGATCTTGAAGATGTGACATTTCTTATCACTCA 1553
DB 241 AGATCAATTGAGGATTTACGGGCTTGGATCTTGAAGATGTGACATTTCTTATCACTCA 300
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QY 1554 AAAAGATTTGACCGTATTGCAATTTGTTGTGCCACTTGAATACTTGTAGTATTGGATATTC 1613
DB 301 AAAAGATTTGACCGTATTGCAATTTGTTGTGCCACTTGAATACTTGTAGTATTGGATATTC 360
QY 1614 GTCATCCATATATTCACTTCCAGATCCATTTGGTAAACTACAGGCGCTTACAACTTTGCA 1673
DB 361 GTCATCCATATATTCACTTCCAGATCCATTTGGTAAACTACAGGCGCTTACAACTTTGCA 420
QY 1674 CATCCGAGCACAATATTGCGACCTACCAAGTGAGATCAGTAAACTTCCAACTTGTCTGCA 1733
DB 421 CATCCGAGCACAATATTGCGACCTACCAAGTGAGATCAGTAAACTTCCAACTTGTCTGCA 480
QY 1734 TACTCTTCTGTTAGTAGAAGATTTGTTCTGACAACTTTAGTCTTAAACCAACCCATGAA 1793
DB 481 TACTCTTCTGTTAGTAGAAGATTTGTTCTGACAACTTTAGTCTTAAACCAACCCATGAA 540
QY 1794 GTGCATAACTAAACAATATGCCCTGCTTAAAGTATTCACACTTTAGTCTGCGATGA 1853
DB 541 GTGCATAACTAAACAATATGCCCTGCTTAAAGTATTCACACTTTAGTCTGCGATGA 600
QY 1854 TCGTCAATACAAATTTGCTGAATTTGCATGGCCACCAAAAGTTGCTGTTAATAATCAAT 1913
DB 601 TCGTCAATACAAATTTGCTGAATTTGCATGGCCACCAAAAGTTGCTGTTAATAATCAAT 660
QY 1914 CGGTGTGAAGGTACCCAAAGGAATAGTAAAGTTGCGAGACTTA CAGGTTCTAGAGTATGT 1973
DB 661 CGGTGTGAAGGTACCCAAAGGAATAGTAAAGTTGCGAGACTTGCAGGTTCTAGAGTATGT 720
QY 1974 AGATATCAGCGGACCACTAGTAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAG 2033
DB 721 AGATATCAGCGGACCACTAGTAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAG 780
QY 2034 GAAATTAAGTGTGATGACAAATGGCTGCAAAAGGAAAAATGTAAGTACTTTTGTGAGC 2093
DB 781 GAAATTAAGTGTGACAAACAAACGGCTGCAAAAGGAAAAATGTAAGTACTTTTGTGAGC 840
QY 2094 CATTGAGAAGCTCTTTCCCTCCAATATCTTATGTGAATGCTGACAGAAATCTCAGATGG 2153
DB 841 CATTGAGAAGCTCTTTCCCTCCAATATCTTATGTGAATGCTGACAGAAATCTCAGATGG 900
QY 2154 TGGACACTTGTAGTGCCTAGATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2213
DB 901 TGGACACTTGTAGTGCCTAGATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
QY 2214 GTTGTATGGAAGTCTTGAAGAGATGCTTAACCTGATTTGAGCAGCTCACTCACTCTGAAGAA 2273
DB 961 GTTGTATGGAAGTCTTGAAGAGATGCTTAACCTGATTTGAGCAGCTCACTCACTCTGAAGAA 1020
QY 2274 GATCTACTTATTGAGGAGCAAACTAAAGGAAGGTAAACCATGCTGATCTCTGTTGGGCAAT 2333
DB 1021 GATCTACTTATTGAGGAGCAAACTAAAGGAAGGTAAACCATGCTGATCTCTGTTGGGCAAT 1080
QY 2334 GCCCACTCATGGTCTTGTATCTTTATCGGAAAGCTTACCTTGGGGAGAGCTTAGTATT 2393
DB 1081 GCCCACTCATGGTCTTGTATCTTTATCGGAAAGCTTACCTTGGGGAGAGCTTAGTATT 1140
QY 2394 CAAAAAGAGGAGCTTCCCAATCTTGAACACTTTGATTTGATTTGATTTGATTTGATTTGAT 2453
DB 1141 CAAAAAGAGGAGCTTCCCAATCTTGAACACTTTGATTTGATTTGATTTGATTTGATTTGAT 1200
QY 2454 AGAGATTTAGATTTGAGGAGCGGAGCTCGCCCGAGTTGGAAGGATAGAAATCAGATTTCTG 2513
DB 1201 AGAGATTTAGATTTGAGGAGCGGAGCTCGCCCGAGTTGGAAGGATAGAAATCAGGAGTG 1260
QY 2514 CAGGTTGGAATTCAGGAGTATTGATTTATTCACCTTTCCAAAGCTCAAGGAGATTTCACT 2573
DB 1261 CAGGTTGGAATTCAGGAGTATTGATTTATTCACCTTTCCAAAGCTCAAGGAGATTTCACT 1320
QY 2574 TGGATACGGAAGTAAAGTGGCTGGCTTGTCTGAGCTGGAGGAGAGTGGCGACACACCC 2633
DB 1321 TAGATACGGAAGTAAAGTGGCTGGCTTGTCTGAGCTGGAGGAGAGTGGACACACACCC 1380
QY 2634 AAATCACCCCGTCTCGAAAGAGGGAGGACCGAAGTGATCACGACCTCTCTTGTGACGC 2693
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Db      1381  AAATCGCCCGTGTCTGTAATGTATACAGTGACCGAAGGTATCACGACCTGGGGCTGAAGC 1440
Qy      2694  CGAAGGATCCCTGTTTGAAGTGAAGCAACGGATCCCTCCAGAGCAGGAGGA 2748
Db      1441  CGAAGGATCTTATAGNAGTGCMAACAGCAGATCCTGTTCTGTATCCCGAAGGA 1495

RESULT 13
US-10-352-179-84
; Sequence 84, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Plants
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2940)
; OTHER INFORMATION:
US-10-352-179-84

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Query Match	43.2%; Score 1293.4; DB 17; Length 2940;
Best Local Similarity	70.6%; Pred. No. 0;
Matches 1755; Conservative	0; Mismatches 726; Indels 6; Gaps 2;
Qy	205 GATTCCTATGCAGAGACATTCGCAATCAATCAGCTCGAATGTGGATGAAGCTGACCTT 264
Db	
433	GATTCCTACCTAGAAGATGCTCGCAATCGATCAGGTAGCAACATGTACGAGTCAGAACTT 492
Qy	265 GTTGGGTTTTCTGACTCCAAAGAAAGCTGCTTGAAATGATCGATACCAATGCTAATGAT 324
Db	
493	GTGGGCTTTGCCAAGACTAAAGATGATGTGCTTAACTGATAGATGTCATTAATCAATGAC 552
Qy	325 GGTCCGGCCCAAGGTAATCTGTGTGTTGGGATGGTGGTTTAGGCAAGACAGCTCTTTTCG 384
Db	
553	GGTCCAGCTAAAGTGATATGTGTGGTTGGAAATGGGTGGATTTAGGCAGAGACTACCTTGCA 612
Qy	385 AGGAAGATCTTTTGAAGCGAAGAGACATTAGGAAGAACTTCCCTTGCAATGCTGGATT 444
Db	
613	AGGAAGGCATATGAACAACAGGAACACAT--GAAGAACTTCTCGTGTGCTTGGATC 669
Qy	445 ACAGTGTCAAACTCAATTTCCAGAGTTGAGCTACTTAAAGATATGATACGCCAACTTCTT 504
Db	
670	ACTGTGCTCAGTCAATTTGACAGGAAGAAATTTCTGAAAACAAATGATCAGGCAACTTCTG 729
Qy	505 GGCCCCAGTTCTCTGGATCAACTCTTGCAGAAATTTGCAAGGAGGTGGTGGTGCAGTA 564
Db	
730	GGTGCTGATTCATTAGACAACTCTTGAAGAAATTTTATGAGAGAGTTGCTCGTGCAGATC 789
Qy	565 CATCATCTTTCTGATGACTGATAGAGAGCTCAAGGAGAGAGGTACTTTGTGTGTTCTA 624
Db	
790	CAGCATCTCGCTGATCACTTGGTTGAAGGGCTTAAAGGAGAAAGGTACTTTGTGTCCTT 849
Qy	625 GATGATCTATGGATTTTACATGATTGGAAATTTGGAATAAATGCAATTTCTTCAAGAAC 684
Db	
850	GATGACCTATGGACCATAGATGCATGGAATTTGGATTCATGATCTGCTTTCCGAGATT 909
Qy	685 AATAAGAGGGCAGCTCAAAATAGTAAATACCACTTTGGAAATGTTGATCTTTCGGAGAGTGT 744
Db	
910	AACAACAGAGGTAGTCGCATAATAATAACAAACGCGAGATGCTGGCTTTAGCTGGAAGGTGT 969

Qy	745	GCACAGCCTC	ACTGGTGTAC	CAACCTTGA	TTCCTTGC	GAGTGA	ACGATG	CAACAT	TTCG	804
Db	970	ACCTCTGA	ATC	CTATTATTT	TACCACTTGA	ACCGTGT	TACAT	TAGATG	TGCTAT	1029
Qy	805	CTACTGAG	AAAAACA	CAATAA	AAAAAT	CAATGA	GACATG	GAATCA	ATAA	864
Db	1030	CTACTAG	CAAGACA	CAACAT	TAAGACT	TGAAG	ACATG	GAATA	ATGATG	1089
Qy	865	ATGTTTGA	ACGAAT	TGTAA	ATAAT	TGGT	CGTCT	ACCA	TATAG	924
Db	1090	ATAGTTAC	AAAAAT	TGGTAA	AAAGGT	TGGTGT	TATTT	TACCG	TGCTA	1149
Qy	925	GCTGTG	CTTGC	CAACTAA	CAAGGTG	TCAGAA	TGGGAG	AAATCT	TATGA	984
Db	1150	GGCAAT	CTTGT	CTACTA	GAAGATA	TAATG	GAAT	TGGGAAAA	TTTTAC	1209
Qy	985	GA	ACTAGA	ATAA	CAACCA	CGCTGG	AGCTTT	CAGGAG	ATG	1044
Db	1210	GAGCTT	GAGAG	CAATCC	AGCCTAG	AAAGCC	ATGAGG	AGATGG	TGAC	1269
Qy	1045	CACCTAC	CACTCC	CAATCT	GAAACCA	TGCTTTT	TGTAT	CTAAG	ATCTTT	1104
Db	1270	CATTCAC	CACTCAT	CTTAA	CAACAG	CTTCTTT	TACCTA	AGTATTT	CTCTC	1329
Qy	1105	GAAATCA	AAAGS	AATCGT	CTAGT	AGTATG	ATGAT	AGCAG	AAGGGT	1164
Db	1330	GAAATCA	AAAGG	GGCGC	CTGGT	AGATAG	TAGAT	AGCAG	AGGGT	1389
Qy	1165	GTTGGG	ATGAC	CTAAG	ATGCTCG	GAGAA	AGTTT	CTTTA	ATGAGCT	1224
Db	1390	GATGGG	GTGA	CAATG	AGGATGT	TGGAA	ATAGT	CAC	TTTAT	1449
Qy	1225	ATGATTC	CAACG	ATCA	GAGTGG	GCATAG	CAGGAAAA	AAATTA	AGACT	1284
Db	1450	CTGATTC	AGCCCTC	AAAAAGT	TAGTAC	ATGAGT	GTGTT	AAAGAT	GTG	1509
Qy	1285	ATCATCC	GATATC	ACAGT	TTTCA	ATCTCG	AGACAG	AAAAATTT	TGTTAT	1344
Db	1510	ATCATG	CGTGAT	ATCAT	TAGTTT	CAATTT	CTAGAG	AGGAAAA	TTTTG	1569
Qy	1345	GGAGAT	GGCTC	ATGATTT	AGTTT	CAGAAAA	CACTCG	CCACAT	ATAGCAT	1629
Db	1570	GAGAAG	ATCACT	GTGT	TAGCG	AGAGAG	CATCCG	CCATCT	AGCAT	1464
Qy	1405	TCCTGCA	AAACAG	ATTTGG	ATTCG	AGCATTA	TTTCG	ATCATTT	AGT	1464
Db	1630	TGCTCA	AAATAT	GTCT	TGGAGT	GGAA	CCATCT	CGGCT	CAGT	1689
Qy	1465	CCCAAG	AGTCT	ATG	CAATG	CAATTT	GTCC	AGATG	TTTAC	1524
Db	1690	CCTCGG	GGGGA	CACTG	CACTTT	GTTC	ACC	CAATTT	AGGAT	1749
Qy	1525	CTTGA	AGATGT	GA	CA	TTCTTA	ATC	CTCA	AAAA	1584
Db	1750	CTGGA	AGATG	CAAAA	ATTTCA	CAAAA	ATGAT	ATCAG	GAAT	1809
Qy	1585	CAC	TTGAAT	TACTTG	ATTTGG	ATTTG	CGTAT	TTCC	ATAT	1644
Db	1810	CA	ATGAA	ATTTTGA	ATTTTGA	AGAG	CCCTCA	ATATTT	ATAC	1859
Qy	1645	GGTAA	ACTAC	AGG	CCCTAC	AAAACTTT	GAA	CATG	CCG	1704
Db	1870	GGAA	ATTTG	CAGT	GTCTG	CAAAATTT	TGAA	CATG	AGG	1929
Qy	1705	AGT	GAG	ATC	AGTAA	CTCC	AAATGT	CTCT	TGTTAG	1764
Db	1930	ACT	GAG	TG	GACTAA	CTCC	AGAA	ATCT	CGT	1989
Qy	1765	GAC	AACTTT	TAGT	CTAA	---ACC	CCCA	ATG	AGT	1821
Db	1990	GGTT	ACTTTT	TAG	CAATA	TAG	ATAAT	TCC	CA	2049
Qy	1822	AA	AGTAT	TC	CAC	CTTT	TAGT	TAG	TCG	1881

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; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41016
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1
US-10-437-963-41016

2050 ATGTTTCTCAACTTCATAAAATTTAGTGACCGTGTGAAGTTAAATTCCTGAGATATGC 2109
1882 ATGGCCACCAAAAGTTGCTGTGATATAATTCATTCGGTGTGAAGGTACCCAAAGGAATAGGT 1941
2110 ATGTCATGTTCTACCCGTTGGTCTGATACAAAGGGGTGTAGGGTGTGCAAGAGGAATTCAC 2169
1942 AAGTTGCGAGACTTACAGGTTCTAGAGTATCTAGATATACAGCGGACGAGTAGTAGCA 2001
2170 AACCTAAAGAGTTTACAGATTTCTAGAGTCTGAGACATCAACAGAACTAGTAGAAGCG 2229
2002 ATCAAAGAGCTGGGGCAGCTTAAGCAAGCTGAGGAAATTTAGGTGTGATGACAAATGGCTCG 2061
2230 ATTGAGAGCTGGGGAGCTAATTCAGTTTAAAGAAATTTAAGGTGACAAACAAAGGGGCC 2289
2062 ACAAAGGAAATTTAGATATCTTTGTGACGCCATTTGAAAGCTCTCTTCCTCCCAATPAT 2121
2290 ACAAATGAAGATATCAGATATTTGTGACGCGATTTGAAAGCTCTCTCTCTGCAATCT 2349
2122 CTCTATGTGAATGCTGCAGGATCTCAGATGGTGGAAACACTTGATGCTAGATCTTATT 2181
2350 CTCGTGTGGATGCTGAGGGAATCTCAGATCTGGAACACTTGATGCTCAATTCGAT 2409
2182 TCCTCTCTCTCCCTACTGAGGACACTCGTGTGTATGAAAGTCTTTGAAGAGATGCT 2241
2410 GCATGCTCTCTCCATCTTGAAGACACTCAAGTTGAATGATCTTTGACAGATACCA 2469
2242 AACTGGATTGAGCAGCTCACTCAGCTGAAGAGATCTACTTATTGAGGAGCAAACTAAAG 2301
2470 AACTGGTTGGGAACCTTTAAGCAGCTGGTGAAGATGCTTTATCCAGATGTGCTACAA 2529
2302 GAAGGTAACCATGCTGATACCTTTGGGCACTTGGGCACTTGGCCAACTCATGCTTGTAT 2361
2530 GATGGTAAACTATGAGAGATCTTTGGGCACTTGGGCACTTGGCCAACTTATGGTCTTTAT 2589
2362 CGGAAAGCTTACCTTTGGGGAAGCTAGTATTTCAAAACAGGAGCATTTCCCAATCTTAGA 2421
2590 CGCAACGATATGCTGACGAGAAATGGCAATTCAGAGGGGAACTTTCCCAATCTCAGG 2649
2422 ACATTTTCGATTTACGATTTGGATCAGCTAAGAGAGATTTAGATTTGAGGAGCGCAGCTCG 2481
2650 TGCTCTGATATTTACTTGTCTGAAGCACTTAGAGAGATAAGATTTGAGGAGGCGACCTCG 2709
2482 CCCAGTTGGAAGATAGAAATCAGATCTGCAAGTTGGAATCAGGATTTATGGTATT 2541
2710 CCAACAATGGAAGATAGAAATTTATGGTTGCAAGTTGGAATCAGGATTTATGGTATC 2769
2542 ATCCACCTTCCAAGGCTCAAGGAGATTTCACTTCGATACGAAAGTAAAGTGGCTGGCTT 2601
2770 AAGCACTTCCAAGCTTAAGATTTATTTGCTTGAATATGATGTTAAGTCCGGAAGCTT 2829
2602 GCTCAGCTGGAGGAGAGTGCACACACACCCCAATCAACCCGCTGCTGCGAAAGAGGAG 2661
2830 GATGCTGCAAGAGGAGTGAATACACACCCCAATCATACTGAACCTGCAATGGCAGAG 2889
2662 GACCGAAGTATCAGACCTTGTGTGT 2688
2890 GATCGAAGTCATCATGACCTAGGAGGT 2916
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RESULT 14
US-10-437-963-41016
; Sequence 41016, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
```

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; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 41016
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1
US-10-437-963-41016

Query Match 43.0%; Score 1290.2; DB 18; Length 2925;
Best Local Similarity 70.5%; Pred. No. 0;
Matches 1753; Conservative 0; Mismatches 728; Indels 6; Gaps 2;

QY 205 GATTTCCTATGAGAGACATTCGCAATCAATCAGCTCGAAATGTTGGATGAAGCTTGAGCTT 264
DB 436 GATTTCCTACCTAGAAAGATGCTCGCAATCAATCAGGTAGCAACACTGACGAGTCAGAACTT 495
QY 265 GTTGGGTTTCTGACTCCAAGAAAAGGCTGCTTGAATGATCGATACCAATGCTTAATCAT 324
DB 496 GTGGGCTTTCGAAGACTAAAGATGAGTTGCTTAACTGATAGATGTCNACTACTAATGAC 555
QY 325 GGTCCGCCCAAGGTAATCTGTGTTGTTGGGATGGTGGTATTTAGGCAAGACAGCTCTTTTCG 384
DB 556 GGTCCAGCTAAAGTATATGTGTGTTGGTATGGTGGATTTAGGCAAGACTTACCCCTTGA 615
QY 385 AGGAGATCTTTGAAACGGAAGAGACATTAGGAAGAACTTCCCTTGCATGCTTGGATT 444
DB 616 AGGAAGCATAATGAAACAAAGGAACACAT---GAAGAACTTCTCGTGTGTTGGTGGATC 672
QY 445 ACAGTGTCACAATCATTTTCAAGGATTTGAGCTACTTAAAGATATGATACGCCAATCTTCT 504
DB 673 ACTGTGTCAGTCACTTTGACAGGAAAGAAATTCGAAACAAATGATCAGGCAACTTCTG 732
QY 505 GGCCCCAGTTCTCTGGATCAACTCTTGCAGAAATTTGCAAGGGAAGGTTGGTGGTCAAGTA 564
DB 733 GGTGCTGATTCATTAGACAAACTCTTGAAGAAATTTAGTGAGAAATTTGCTCGTGCAGCTC 792
QY 565 CATCATCTTTCTGAGTACCTGTATAGAGAGCTCAAGGAGAAAGAGGTACTTTGTTGTTCTA 624
DB 793 CAGCATCTCGCTGATCACTTTGGTTGAAGGGCTAAGGAGAAAGGTACTTTGTTGTTCTT 852
QY 625 GATGATCTATGGATTTTACATGATTTGGAATTTGGAATTAATGAAATTTGATTTTCCGAAGAC 684
DB 853 GATGACCTATGGACCATAGATGATGGAATTTGGATTCATGATATTTGCTTTTCCGAAGATT 912
QY 685 AATAAGAGGGCAGTCAAAATAGTAATACCACTTTGGAATTTGATCTTTGCGGAGAGTGT 744
DB 913 AACAAAGAGGTAGTCGCATAATAATAAAGCGAGATGCTGGCTTAGCTGGAAGGTGT 972
QY 745 GCACAGCCTCAGCTGGGTACCACTTGAATTTCTTGAGATGAACGATGCCATTAACATTG 804
DB 973 ACCTCTGAATCACTTATTTACCACCTTGAACCGTTACATATAGATGATGCTATACACTTG 1032
QY 805 CTACTGAGAAAACAAATAAATCATGAAGACATGGAATCAATCAATCAATCAATCAATCAAT 864
DB 1033 CTACTAGCAAGCAACAAACATAAGACTTTGAAGACATGGAATCAATCAATCAATCAATCAAT 1092
QY 865 ATGTTGAAAGCAATTTGTAATTAATATGTTGGTCTGCTACCATTTAGCAATCTTACCAATAGGA 924
DB 1093 ATAGTTACAAAATTTGGTAAAAAGGTGGTTATTTACCGCTGGCTATCTACCAATAGGA 1152
QY 925 GCTGTGCTTGCACCTAAACAGGTGTCAAGATGGAGAAAATTTCTATGAACACCTTCTTCA 984
DB 1153 GGCATTCTTGTCTACTAAGAGATAATGAGGTGGGAAAAATTTACAGAGAACTTCTTCA 1212
QY 985 GAACTAGAATAAACCACCGCTGGAGCTTTGAGGAGAAATGTTGACCCCTAGGTACTACAC 1044
DB 1213 GAGCTTGAGAGCAATCCAGCCCTAGAACCCATGAGGAGGATGGTGACCCCTAAGCTCAAT 1272
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Qy	2482	CCCAGTTGGAAAAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGGATTATTGGTATT	2541
Db	2713	CCAAAGATGGAAAGTATAGAAATTTATGGTTGCAGGTTGGAATCAGGGATTATTGGTATC	2772
Qy	2542	ATCCACCTTCCAAGGCTCAAGGAGATTTCACCTTGGATACGAAAGTAAAGTGGCTGGGCTT	2601
Db	2773	AAGCACCTTCCAAGACTTAAGATTATTTCGGCTTGAATATGATGTTAAAGTCGCGAAGCTT	2832
Qy	2602	GCTCAGCTGGAGGGAGAAGTGCACACACCCCAATCACCCCTGCTGCGAAAAGAGGAG	2661
Db	2833	GATGTGTGCAAGAGGAAGTGAATACACCCCAATCATACTGAATTGCAAAATGGCAGAG	2892
Qy	2662	GACCGAAGTGATCAGACCTTG	2683
Db	2893	GATCGAAGTCATCATGACCTAG	2914

Search completed: February 13, 2005, 20:04:27
Job time : 1065.02 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:34:07 ; Search time 106.253 Seconds
(without alignments)
3632.700 Million cell updates/sec

Title: US-10-656-394A-12

Perfect score: 5137

Sequence: 1 MAETVLSMARSLVGSATSKA.....LSGMNCFNLFSRDMLLVPA 998

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5137	100.0	998	8 ADM72249	Adm72249 O. minuta
2	4237	82.5	1032	8 ADM72245	Adm72245 O. minuta
3	4204	81.8	1031	8 ADI57172	Adi57172 Oryza min
4	4169.5	81.2	1091	8 ADI57176	Adi57176 Oryza min
5	4140	80.6	1032	8 ADM72241	Adm72241 O. minuta
6	2621	51.0	979	8 ADI57168	Adi57168 Oryza min
7	2616	50.9	993	8 ADM72239	Adm72239 O. minuta
8	2170.5	42.3	993	8 ADI57170	Adi57170 Oryza min
9	2103.5	40.9	1054	8 ADI57174	Adi57174 Oryza min
10	1748	34.0	660	8 ADM72243	Adm72243 O. minuta
11	1033	20.1	1205	3 AAY49434	Aay49434 Blast dis
12	1033	20.1	1205	8 ADM72280	Adm72280 O. minuta
13	1033	20.1	1251	3 AAY93135	Aay93135 Rice blas
14	996.5	19.4	451	8 ADI57178	Adi57178 Oryza min
15	857	16.7	953	3 AAY58854	Aay58854 sorghum r
16	772	15.0	901	2 AAW80251	Aaw80251 An antidi
17	772	15.0	901	2 AAY01966	Aay01966 A protein
18	772	15.0	901	2 AAY01965	Aay01965 A protein
19	772	15.0	901	3 AAY81926	Aay81926 Rice prob
20	772	15.0	901	3 AAY81925	Aay81925 Rice prob
21	751.5	14.6	958	4 ABB06875	Abb06875 Mla1 prot
22	745	14.5	967	4 ABB06878	Abb06878 Rgh1a pro
23	736	14.3	961	4 ABB06871	Abb06871 Barley Ml
24	736	14.3	961	4 ABB06869	Abb06869 Barley Ml
25	732.5	14.3	949	4 ABB06876	Abb06876 Mla1h pro

26	730	14.2	961	4 ABB06870	Abb06870 Barley Ml
27	722	14.1	2827	7 ADC08012	Adc08012 Rice prot
28	710.5	13.8	956	4 ABB06874	Abb06874 Mla6 prot
29	698.5	13.6	939	4 ABB06879	Abb06879 Rgh1e/f p
30	693	13.5	943	4 ABB06877	Abb06877 Rgh1bcd p
31	665.5	13.0	922	4 ABB06872	Abb06872 Barley Ml
32	664.5	12.9	937	4 AAU02144	Aau02144 Rx 28, mo
33	662	12.9	937	2 AAY52152	Aay52152 Potato re
34	661.5	12.9	937	4 AAU02143	Aau02143 Rx 25, mo
35	658	12.8	937	4 AAU02149	Aau02149 Rx 32, mo
36	655.5	12.8	937	4 AAU02145	Aau02145 Rx 72, mo
37	650	12.7	945	4 ABB06873	Abb06873 Barley Ml
38	649.5	12.6	937	4 AAU02148	Aau02148 Rx 7, mod
39	647.5	12.6	937	4 AAU02146	Aau02146 Rx 39, mo
40	647	12.6	912	3 AAY44818	Aay44818 Potato Gp
41	646	12.6	938	3 AAY45004	Aay45004 Protein e
42	641.5	12.5	937	4 AAU02147	Aau02147 Rx 193, m
43	627.5	12.2	1471	8 ADI45353	Adi45353 Rice isop
44	598.5	11.7	970	7 ADF17765	Adf17765 Solanum b
45	598.5	11.7	970	8 ADH51537	Adh51537 S bulboca

ALIGNMENTS

RESULT 1

ADM72249
ID ADM72249 standard; protein; 998 AA.

XX AC ADM72249,

XX DT 03-JUN-2004 (first entry)

XX DE O. minuta NBS6 polypeptide.

XX KW P12; NBS6; plant protectant; gene therapy; rice; disease resistance.

XX OS Oryza minuta.

XX PN WO2004022715-A2.

XX PD 18-MAR-2004.

XX PF 08-SEP-2003; 2003WO-US027913.

XX PR 09-SEP-2002; 2002US-0409216P.

XX PR 18-MAR-2003; 2003US-0455713P.

XX PR 05-SEP-2003; 2003US-00656394.

XX (OHIS) UNIV OHIO STATE.

XX Wang G;

XX WPI; 2004-257576/24.

XX N-PSDB; ADM72248.

New rice P12-like disease resistance nucleic acid molecule that confers disease resistance in plants, useful for creating or enhancing disease resistance in plants.
Claim 1; SEQ ID NO 12; 120pp; English.

The invention relates to novel broad-spectrum resistance gene P12 and the NBS(1-6) genes present in the P12 gene cluster region. The rice P12-like disease resistance nucleic acid molecules are useful for enhancing disease resistance in plants. The present sequence represents a rice NBS6 polypeptide.

XX SQ Sequence 998 AA;

Query Match 100.0%; Score 5137; DB 8; Length 998;

Best Local Similarity 100.0%; Pred. NO. 0;

Matches 998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAETVLSMARSLVGSATSKAASAAADETSLLLGVEKDIWYLFRRHGVGRSNGSPVVGWVAS 60
DB 1 MAETVLSMARSLVGSATSKAASAAADETSLLLGVEKDIWYLFRRHGVGRSNGSPVVGWVAS 60
QY 61 GNQSCLAIDSVAEIRNQSNARNVDEAEVLGSPDSKSKLLEMDITNANDGPAKVICVVGGMG 120
DB 61 GNQSCLAIDSVAEIRNQSNARNVDEAEVLGSPDSKSKLLEMDITNANDGPAKVICVVGGMG 120
QY 121 GLGKTALSRKIFESEEDIRKNFPCNAMIIVTSQSFRHIELLKDMIRQLLGPSSLDLLOL 180
DB 121 GLGKTALSRKIFESEEDIRKNFPCNAMIIVTSQSFRHIELLKDMIRQLLGPSSLDLLOL 180
QY 181 QGKVVQVHLSYELIEELKEKRYFVVDLWILHDNWNINEIAPPKNNKKGSIIVITW 240
DB 181 QGKVVQVHLSYELIEELKEKRYFVVDLWILHDNWNINEIAPPKNNKKGSIIVITW 240
QY 241 NVDLAECATASLVYHLDLFLQMDAITLLLRKTNKHEDMESNKNMQMVERIVNKCGR 300
DB 241 NVDLAECATASLVYHLDLFLQMDAITLLLRKTNKHEDMESNKNMQMVERIVNKCGR 300
QY 301 PLAILITGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMVTLGYNHLPSHLKPCFLY 360
DB 301 PLAILITGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMVTLGYNHLPSHLKPCFLY 360
QY 361 LSIPEPDEIKRNLVGRWIAEGFVRPKVGMVTTKDVGESYFNELINRSMIQRSVGIAGK 420
DB 361 LSIPEPDEIKRNLVGRWIAEGFVRPKVGMVTTKDVGESYFNELINRSMIQRSVGIAGK 420
QY 421 IKTCRIHDIIRDTIVTSIRQBNFVLLPMGDSGLVQENTRIAPHGSMCKTGLDWSIIR 480
DB 421 IKTCRIHDIIRDTIVTSIRQBNFVLLPMGDSGLVQENTRIAPHGSMCKTGLDWSIIR 480
QY 481 SLAIFGRPKSLAHAVCPDQLRMLRVLDLEVTFLITQKDPDRIALILCHLYSIGYSSS 540
DB 481 SLAIFGRPKSLAHAVCPDQLRMLRVLDLEVTFLITQKDPDRIALILCHLYSIGYSSS 540
QY 541 IYSLPRSIGKLGQIOTLNMPTSTYIALPSELSKQLCLHTLRCRKFVSDNPSLNHPMKCI 600
DB 541 IYSLPRSIGKLGQIOTLNMPTSTYIALPSELSKQLCLHTLRCRKFVSDNPSLNHPMKCI 600
QY 601 TNTICLPKVFPLVSRDDRAIQIAELHMAKSCWYKSGFKVVKPGIGIKLRDLQVLEYVDI 660
DB 601 TNTICLPKVFPLVSRDDRAIQIAELHMAKSCWYKSGFKVVKPGIGIKLRDLQVLEYVDI 660
QY 661 RRTSSRAIKELQSLKRLGVTNGSTKECKTILCAAIEKLSLOYLYNNAAGISDGGT 720
DB 661 RRTSSRAIKELQSLKRLGVTNGSTKECKTILCAAIEKLSLOYLYNNAAGISDGGT 720
QY 721 LECUDSISSPPPLRLTLVYGSLEMPNWIQLTHLKKIYLLRSKLEKGTMLILGALPN 780
DB 721 LECUDSISSPPPLRLTLVYGSLEMPNWIQLTHLKKIYLLRSKLEKGTMLILGALPN 780
QY 781 LMVLDLYRKAYGLBKLVFKTGAFPNLRTLSTYIDLQREIRFEDGSSPQLEKIBIRFCRL 840
DB 781 LMVLDLYRKAYGLBKLVFKTGAFPNLRTLSTYIDLQREIRFEDGSSPQLEKIBIRFCRL 840
QY 841 ESGIIGIHLPRLKEISLGYESKVAGLAQLBGEVTRTHNHPVLRKREDRSDHDLACDAEG 900
DB 841 ESGIIGIHLPRLKEISLGYESKVAGLAQLBGEVTRTHNHPVLRKREDRSDHDLACDAEG 900
QY 901 SPVEVETDPLPEQEGESSQRDRKHSSSWFQVNMISGIGISGRPCGCAHLAVPRGA 960
DB 901 SPVEVETDPLPEQEGESSQRDRKHSSSWFQVNMISGIGISGRPCGCAHLAVPRGA 960
QY 961 DLRLPLSSISHALDSSLGSMCNFNLTFSRDMLLVPA 998
DB 961 DLRLPLSSISHALDSSLGSMCNFNLTFSRDMLLVPA 998
QY 961 DLRLPLSSISHALDSSLGSMCNFNLTFSRDMLLVPA 998
DB 961 DLRLPLSSISHALDSSLGSMCNFNLTFSRDMLLVPA 998
RESULT 2
ADM72245
ID ADM72245 standard; protein; 1032 AA.
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XX ADM72245;
AC 03-JUN-2004 (first entry)
DT O. minuta NBS4 polypeptide.
DE P12; NBS4; plant protectant; gene therapy; rice; disease resistance.
XX Oryza minuta.
XX WO2004022715-A2.
XX 18-MAR-2004.
XX 08-SEP-2003; 2003WO-US027913.
XX 09-SEP-2002; 2002US-0409216P.
XX 18-MAR-2003; 2003US-0455713P.
XX 05-SEP-2003; 2003US-00656394.
XX (OHIS ) UNIV OHIO STATE.
XX Wang G;
XX WPI; 2004-257576/24.
XX N-PSDB; ADM72244.
XX New rice Pi2-like disease resistance nucleic acid molecule that confers
XX disease resistance in plants, useful for creating or enhancing disease
XX resistance in plants.
XX Claim 1; SEQ ID NO 8; 120pp; English.
XX The invention relates to novel broad-spectrum resistance gene Pi2 and the
XX NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
XX disease resistance nucleic acid molecules are useful for enhancing
XX disease resistance in plants. The present sequence represents a rice NBS4
XX polypeptide.
XX Sequence 1032 AA;
Query Match 82.5%; Score 4237; DB 8; Length 1032;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 854; Conservative 17; Mismatches 47; Indels 96; Gaps 4;
QY 1 MAETVLSMARSLVGSATSKAASAAADETSLLLGVEKDIWY----- 40
DB 1 MAETVLSMARSLVGSATSKAASAAADETSLLLGVEKDIWYIKDELKTMOAPLRAAELMKK 60
QY 41 -----LPRHGV----- 46
DB 61 KDELKLVABQIRDLSDYDIEDSLDEFKHHIESQTLFQLVKLRHRHRIARIHNLKSRVE 120
QY 47 ---GRSNGGVPVGVASGNQSCLAIDSVAEIRNQSNARNVDEAEVLGSPDSKSKLLEMD 103
DB 121 EVSSRNTRYSLVAKPISSGTB--IDMSYAEIRNQSNARNVDEAEVLGSPDSKSKLLEMD 178
QY 104 TNANDGPAKVICVVGGMGLGKTALSRKIFESEEDIRKNFPCNAMIIVTSQSFRHIELLKDM 163
DB 179 TNANDGPAKVICVVGGMGLGKTALSRKIFESEEDIRKNFPCNAMIIVTSQSFRHIELLKDM 238
QY 164 IROLLGPSSLDLLOLQELQGVVQVHLSYELIEELKEKRYFVVDLWILHDNWNINEI 223
DB 239 IROLLGPSSLDLLOLQELQGVVQVHLSYELIEELKEKRYFVVDLWILHDNWNINEI 298
QY 224 AFPKNNKKGSIIVITWNVDLAECATASLVYHLDLFLQMDAITLLLRKTNKHEDMESN 283
DB 299 AFPKNNKKGSIIVITWNVDLAECATASLVYHLDLFLQMDAITLLLRKTNKHEDMESN 358
QY 284 KNNQKQVERIVNKCGRPLAILITGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMV 343
DB 359 KNNQKQVERIVNKCGRPLAILITGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMV 418
```

QY 344 TLGYNHLPSHLKPCFLYLSIFPEDFEIKRNPLVGRWIAEGFVRPKVGTTHKDVGESYFNE 403
 DB 419 TLGYNHLPSHLKPCFLYLSIFPEDFEIKRNPLVGRWIAEGFVRPKVGTTHKDVGESYFNE 478
 QY 404 LINRSMIQRSRVGAGIKTCRIHDIIRDITVTSIROENFVLLPMWGDSDLVQENTRHIA 463
 DB 479 LINRSMIQRSRVGAGIKTCRIHDIIRDITVTSIROENFVLLPMWGDSDLVQENTRHIA 538
 QY 464 FHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDDVTFITQKDFDR 523
 DB 539 FHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDDVTFITQKDFDR 598
 QY 524 IALLCHLKYLISIGYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSISKLOLHTLRCS 583
 DB 599 IALLCHLKYLISIGYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSISKLOLHTLRCS 658
 QY 584 RKFDVSNFSLNHPMKCITNTICLPKVTPLVSRDDRAIQIAELHMAKSCWYKSGFKVP 643
 DB 659 GQFHYDNFSLNHPMKCITNTICLPKVTPLVSRDDRAIQIAELHMAKSCWSESGFKVP 718
 QY 644 KGIGKLRDLQVLEYVDIRRTSSRAIKELGQSLKRLKLGVTNGSTKECKILCAAIEKLS 703
 DB 719 KGIGKLRDLQVLEYVDIRRTSSRAIKELGQSLKRLKLGVTNGSTKECKILCAAIEKLS 778
 QY 704 SLQYLYNNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLSEEMPNTWIEQLTHLKKIYLLR 763
 DB 779 SLQSLHYDAAGISDGGTLECLDSISSPPPLRLTLVLDGILSEEMPNTWIEQLTHLKKIYLLR 838
 QY 764 SKLKEGKTMILGALPNLMVLDLYRKAYLGEKLVFKTGAPNRLTSLYDLDQLEIRFE 823
 DB 839 SKLKEGKTMILGALPNLMVLDLYRKAYLGEKLVFKTGAPNRLTSLYDLDQLEIRFE 898
 QY 824 DGSSPOLKEIEIRCRLESIGTIGIHLPLKKEISLGYESKVAQLAQLGEVTRHPNHPVL 883
 DB 899 DGSSPLEKEIEGCRLESIGTIGIHLPLKKEIPRYGSKVAGLQLEGEVNAHPNRPVL 958
 QY 884 RKREDRSHDPLACDAEGSPVE-----VETADPLPQEGESSQ 920
 DB 959 LMYSDDRYHDLGAEGSGSTEVQADPVPDAEGSVTVVAETADPLPQEGESSQ 1012

RESULT 3
 ADI57172
 ID ADI57172 standard; protein; 1031 AA.
 AC ADI57172;
 XX
 DT 22-APR-2004 (first entry)
 DE Oryza minuta P19 locus nucleotide binding site (NBS) protein #3.
 XX
 KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
 KW plant breeding; transgenic plant; plant.
 XX
 OS Oryza minuta.
 XX
 PN US2004006788-A1.
 XX
 PD 08-JAN-2004.
 XX
 XX 27-JAN-2003; 2003US-00352179.
 XX
 PR 25-JAN-2002; 2002US-0352106P.
 PR 01-FEB-2002; 2002US-0353304P.
 XX
 XX (WANG/) WANG G.
 PA (LIU/) LIU G.
 PA
 XX Wang G, Liu G;
 XX
 DR WPI; 2004-121064/12.
 DR N-PSDB; ADI57171.

XX
 PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
 PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
 PT infection.
 XX
 PS Claim 1; SEQ ID NO 89; 136pp; English.
 XX
 PS The invention comprises the amino acid and coding sequences of nucleotide
 CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
 CC blight and rice blast resistance genes). The DNA sequences may be used as
 CC markers for resistance to infection with Magnaporthe grisea in plant
 CC breeding programs. The present amino acid sequence represents an NBS
 CC protein encoded by a gene from the Oryza minuta P19 locus.
 XX
 SQ Sequence 1031 AA;
 Query Match 81.8%; Score 4204; DB 8; Length 1031;
 Best Local Similarity 83.9%; Pred. No. 0;
 Matches 851; Conservative 17; Mismatches 50; Indels 96; Gaps 4;
 QY 1 MAETVLSMARSLVGSASIKAAASAAADSTSLLGVEKDIWY----- 40
 DB 1 MAETVLSMARSLVGSASIKAAASAAANETSLLGVEKDIWYIKDELKTWQAFRAAEVMMK 60
 QY 41 -----LPRGV----- 46
 DB 61 KDBLLKVMAEQIRDLSYDIEDSLDEFKVHIESOTLFLQVLKLRHRHRAIRIHNLSRVE 120
 QY 47 ---GRSNGPVGVWAGSNQCLADISYARDINQSNARNVDEAELVGFSDSKKLELMD 103
 DB 121 EVSRNRYNLVPIPSGTED--DMDSYABDIRNQSARNVDEAELVGFSDSKKLELMD 178
 QY 104 TNANDGPAKVICVVGMGGLKTALSRKIFSEEDIRKNFPCNAWITVSQSFHRIELKDM 163
 DB 179 TNANDGPAKVICVVGMGGLKTALSRKIFSEEDIRKNFPCNAWITVSQSFHRIELKDM 238
 QY 164 IROLLGPSSLDLQELQGVVQVHLSYIELKEKRYFVVDLWLDLWLDWNNWINEI 223
 DB 239 IROLLGPSSLDLQELQGVVQVHLSYIELKEKRYFVVDLWLDLWLDWNNWINEI 298
 QY 224 AFPNNKKGSIQVITTNVNDLAEKCATASLVYHLDLQMDAITLLLRKTNKHEDMESN 283
 DB 299 AFPNNKKGSRIVITTRNVDLAEKCATASLVYHLDLQMDAITLLLRKTNKHEDMESN 358
 QY 284 KNNQKQVERIVNKCGRPLALITIGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMV 343
 DB 359 KNNQKQVERIVNKCGRPLALITIGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMV 418
 QY 344 TLGYNHLPSHLKPCFLYLSIFPEDFEIKRNPLVGRWIAEGFVRPKVGTTHKDVGESYFNE 403
 DB 419 TLGYNHLPSHLKPCFLYLSIFPEDFEIKRNPLVGRWIAEGFVRPKVGTTHKDVGESYFNE 478
 QY 404 LINRSMIQRSRVGAGIKTCRIHDIIRDITVTSIROENFVLLPMWGDSDLVQENTRHIA 463
 DB 479 LINRSMIQRSRVGAGIKTCRIHDIIRDITVTSIROENFVLLPMWGDSDLVQENTRHIA 538
 QY 464 FHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDDVTFITQKDFDR 523
 DB 539 FHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDDVTFITQKDFDR 598
 QY 524 IALLCHLKYLISIGYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSISKLOLHTLRCS 583
 DB 599 IALLCHLKYLISIGYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSISKLOLHTLRCS 658
 QY 584 RKFDVSNFSLNHPMKCITNTICLPKVTPLVSRDDRAIQIAELHMAKSCWYKSGFKVP 643
 DB 659 GQFHYDNFSLNHPMKCITNTICLPKVTPLVSRDDRAIQIAELHMAKSCWSESGFKVP 718
 QY 644 KGIGKLRDLQVLEYVDIRRTSSRAIKELGQSLKRLKLGVTNGSTKECKILCAAIEKLS 703
 DB 719 KGIGKLRDLQVLEYVDIRRTSSRAIKELGQSLKRLKLGVTNGSTKECKILCAAIEKLS 778
 QY 704 SLQYLYNNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLSEEMPNTWIEQLTHLKKIYLLR 763

Db 779 SLOSLYNAAALLSDIETLECLDSISSPPPLRLTLGLNGSLEEMPWTEQTLHLKKIYLLR 838
Qy 764 SKLKEGKTMILGALPNLMVLDLYRKAYLGEKLVFKTGAPPNLRTLSIYDLQDLREIRFE 823
Db 839 SKLKEGKTMILGALPNLMVLYWYNAYLGEKLVFKTGAPPNLRTLSIYDLQDLREIRFE 898
Qy 824 DGSSPOLKEIEIRFCRLSEGIIGIHLPRLKEISLGYESKVAGLAQLEGEVTRHPNRPVL 883
Db 899 DGSSPLLEKIEISCCRLESGIIGIHLPRLKEISLGYESKVAGLAQLEGEVTRHPNRPVL 958
Qy 884 KRDRSDHDLACDAEGSPVE-----VEATDPLPQEGESSQ 920
Db 959 RMDSDRRDHLGAEAGESSIEVQTADFPVDAEGSVTVAVEATDPLPQEGESSQ 1012

RESULT 4
AD157176
ID AD157176 standard; protein; 1091 AA.
XX AC AD157176;
XX DT 22-APR-2004 (first entry)
XX Oryza minuta P19 locus nucleotide binding site (NBS) protein #5.
XX nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
XX plant breeding; transgenic plant; plant.
XX Oryza minuta.
XX US2004006788-A1.
XX 08-JAN-2004.
XX 27-JAN-2003; 2003US-00352179.
XX 25-JAN-2002; 2002US-0352106P.
XX 01-FEB-2002; 2002US-0353304P.
XX (WANG/) WANG G.
XX (LIU/) LIU G.
XX Wang G, Liu G;
XX WPI; 2004-121064/12.
XX N-PSDS; AD157175.
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX and NBS3, useful for producing plants resistant to Magnaporthe grisea
XX infection.
XX Claim 1; SEQ ID NO 93; 136pp; English.
XX The invention comprises the amino acid and coding sequences of nucleotide
XX binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
XX blight and rice blast resistance genes). The DNA sequences may be used as
XX markers for resistance to infection with Magnaporthe grisea in plant
XX breeding programs. The present amino acid sequence represents an NBS
XX protein encoded by a gene from the Oryza minuta P19 locus.
XX Sequence 1091 AA;
XX Query Match 81.2%; Score 4169.5; DB 8; Length 1091;
XX Best Local Similarity 79.0%; Pred. No. 0;
XX Matches 848; Conservative 21; Mismatches 49; Indels 155; Gaps 4;
Qy 1 MAETVLSWASLVCASLSKASAAADETSLLLGVEKDIWY----- 40
Db 1 MAETVLSWASLVCASLSKASAAADETSLLLGVEKDIWYIKDELKIMQAFLEAEVWKK 60
Qy 41 ----- 40

Db 61 KDELKKVWAEQIRDLLDYDIEDSLDEFKVVHVESQTLFRQYIKDELKTMQAFLEAEALMKKK 120
Qy 41 -----LFRHGV----- 46
Db 121 DELLKVMAEQIRDLSDYDIEDSLDEFKVVHVESQTLFRQLVKLREHRHIAIRIHNLSRVVEE 180
Qy 47 --CRSNGGPPVGVVAGSNQSCLAIDSYAEDIRNQSARNVDEAEELVGSFSDSKRLEMDIT 104
Db 181 VSSRTRYSLVKPISSGTE--IDMSYAEDIRNQSARNVDEAEELVGSFSDSKRLEMDIT 238
Qy 105 NANGGPAKVICVVGMLGKGTALSRKIFSEEDIRKFPNCPNAMIYVSQSPHRIELLKDMI 164
Db 239 NANGGPAKVICVVGMLGKGTALSRKIFSEEDIRKFPNCPNAMIYVSQSPHRIELLKDMI 298
Qy 165 ROLLGSSSLDQLLQELQGVVQVHLSYLIIBELKEKRYFVVLDDLIWILHDMWNINEIA 224
Db 299 ROLLGPNSLKQLLQELQGVVQVHLSYLIIBELKEKRYFVVLDDLIWILHDMWNINEIA 358
Qy 225 FPKNNKKGSOIVITWNVDLAECATASLYTHLDLFQMNDAITILLKTKTNKHEDMESNK 284
Db 359 FPKNNKKGSRIVITTRNVDLAECATASLYTHLDLFQMNDAITILLKTKTNKHEDMESNK 418
Qy 285 NMOKMVERIVNKGRLPLAILITIGAVLATKQVSEWEKPYEHLPSLEINPSLEALRRMVT 344
Db 419 NMOKMVERIVNKGRLPLAILITIGAVLATKQVSEWEKPYEHLPSLEINPSLEALRRMVT 478
Qy 345 LGYNHLPKSHLKPFCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMVTKDVGSYFNEL 404
Db 479 LGYNHLPKSHLKPFCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMVTKDVGSYFNEL 538
Qy 405 INRSMIQRSRVGIAGIKTKCRIHDIIRDIIVTSISROENFVLLPMGDGSDLVQENTRIHAF 464
Db 539 ISRSMIQRSRVGIAGIKTKCRIHDIIRDIIVTSISROENFVLLPMGDGSDLVQENTRIHAF 598
Qy 465 HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTLITQKQFDRI 524
Db 599 HGSMSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTLITQKQFDRI 658
Qy 525 ALLCHLKYSIGYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSEISKLOCLHLRCR 584
Db 659 ALLCHLKYSIGYSSSIYSLPRSIGKLOGLQTLNMPSTYIAALPSEISKLOCLHLRCR 718
Qy 585 KFYVDNPSLNMHMKCINTTICLPKFTPLVSRDDRAIQIAELHMAIKSCWKSPGVKVPK 644
Db 719 KFYVDNPSLNMHMKCINTTICLPKFTPLVSRDDRAIQIAELHMAIKSCWKSPGVKVPK 778
Qy 645 GIGKLRDLQVLEYVDIRRTSSRAIKELGOLSKRLKGLVMTNGSTKCKKILCAIEKLSS 704
Db 779 GIGKLRDLQVLEYVDIRRTSSRAIKELGOLSKRLKGLVMTNGSTKCKKILCAIEKLSS 838
Qy 705 LQVLYNNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEMPNWIQLTHLKKIYLLRS 764
Db 839 LQVLYNNAALLSDIETLECLDSISSPPPLRLTLVLYGSLEMPNWIQLTHLKKIYLLRS 898
Qy 765 KLKEGKTMILGALPNLMVLDLYRKAYLGEKLVFKTGAPPNLRTLSIYDLQDLREIRFE 824
Db 899 KLKEGKTMILGALPNLMVLYWYNAYLGEKLVFKTGAPPNLRTLSIYDLQDLREIRFE 958
Qy 825 GSSPOLKEIEIRFCRLSEGIIGIHLPRLKEISLGYESKVAGLAQLEGEVTRHPNRPVL 884
Db 959 GSSPLLEKIEISCCRLESGIIGIHLPRLKEISLGYESKVAGLAQLEGEVTRHPNRPVL 1018
Qy 885 KRDRSDHDLACDAEGSPVE-----VEATDPLPQEGESSQ 920
Db 1019 RMDSDRRDHLGAEAGESSIEVQTADFPVDAEGSVTVAVEATDPLPQEGESSQ 1071

RESULT 5
ADM72241
ID ADM72241 standard; protein; 1032 AA.
XX AC ADM72241;
XX ADM72241;

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DT XX 03-JUN-2004 (first entry)
DE XX O. minuta NBS2 polypeptide.
KW XX P12; NBS2; plant protectant; gene therapy; rice; disease resistance.
XX OS Oryza minuta.
XX XX WO2004022715-A2.
XX XX 18-MAR-2004.
XX XX 08-SEP-2003; 2003WO-US027913.
XX XX 09-SEP-2002; 2002US-0409216P.
XX XX 18-MAR-2003; 2003US-0455713P.
XX XX 05-SEP-2003; 2003US-00656394.
XX XX (OHIS ) UNIV OHIO STATE.
XX XX Wang G;
XX XX WPI; 2004-257576/24.
XX XX N-PSDB; ADM72240.
XX XX New rice Pi2-like disease resistance nucleic acid molecule that confers
XX XX disease resistance in plants, useful for creating or enhancing disease
XX XX resistance in plants.
XX XX Claim 1; SEQ ID NO 4; 120pp; English.
XX XX The invention relates to novel broad-spectrum resistance gene Pi2 and the
XX XX NBS(1-6) genes present in the Pi2 gene cluster region. The rice Pi2-like
XX XX disease resistance nucleic acid molecules are useful for enhancing
XX XX disease resistance in plants. The present sequence represents a rice NBS2
XX XX polypeptide.
XX XX Sequence 1032 AA;

Query Match 80.6%; Score 4140; DB 8; Length 1032;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 837; Conservative 23; Mismatches 58; Indels 96; Gaps 4;

Qy 1 MAETVLSMARSLVGSALSKAASAADETSLLGVGEKDIWY----- 40
Dy 1 MAETVLSMARSLVGSALSKAASAADETSLLGVGEKDIWYKDELKTMQAFRAAEVWKK 60
Qy 41 -----LFRHGV----- 46
Dy 61 KDELKVMAEQIRDLSDYDIEDSLDFKVIHBSQTLFRQLVKLRHRHRAIRIHNLSRVE 120
Qy 47 ---GRSNGGPVGVWASGNQSLAIDSVAEDIRNQSARNVDEAELVGFSDSKKELLEMD 103
Dy 121 EVSRNRYNLVEFISGCTED--DMSVAEDIRNQSARNVDEAELVGFSDSKKELLEMD 178
Qy 104 TNANDGPAKVICVVMGGLGKTALSRKIFSEEDIRKNFPCNAWITVSQSFHRIELLDKM 163
Dy 179 TNANDGPAKVICVVMGGLGKTALSRKIFSEEDIRKNFPCNAWITVSQSFHRIELLDKM 238
Qy 164 IROLLGPSSLDQLLOELQGVVQVHLSLEYLIBELKEKRYFVVLDDLWILHDWNWINEI 223
Dy 239 IROLLGPSSLDQLLOELQGVVQVHLSLEYLIBELKEKRYFVVLDDLWILHDWNWINEI 298
Qy 224 APPKNNKGSQIVLTWNVDLAEKCATASLVYHLDLFQMDAITLLARKTNKHEDMESN 283
Dy 299 APPKNNKGSRIVITRNVDLAEKCATASLVYHLDLFQMDAISLLLRKTNKHEDMESN 358
Qy 284 KMQQKQVERIVNKGRLPLAILTTGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMV 343
Dy 359 KMQQKQVERIVNKGRLPLAILTTGAVLATKQVSEWEKFEYHLPSELEINPSLEALRMV 418
Qy 344 TLGYNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNE 403

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Db 419 TLGYNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMTTKDVGESYFNE 478
Qy 404 LINRSMIQSRVGIAGIKTCRIHDIIRDITVTSISROENFVLLPMGSGSDILVQENTRHIA 463
Dy 479 LINRSMIQSRVGTAGIKTCRIHDIIRDITVTSISROENFVLLPMGSGSDILVQENTRHIA 538
Qy 464 FHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDDVFTLITKQKDFR 523
Dy 539 FHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLDDVFTLITKQKDFR 598
Qy 524 IALLCHLKYSIGYSSSIYSLPRSIGKLGQLOTLNMPSTVIAALPSSISKQLCHLTLRCS 583
Dy 599 IALLCHLKYSIGYSSSIYSLPRSIGKLGQLOTLNMPSTVIAALPSSISKQLCHLTLRCS 658
Qy 584 RKFDVNDNFSLNHPMKCITNTICLPKFTPLVSRDDRAIQIAELHMAWKSCWYKSGFKVVP 643
Dy 659 RELEFDNFSLNHPMKCITNTICLPKFTPLVSRDDRAIQIAELHMAWKSCWYKSGFKVVP 718
Qy 644 KGIGKLRDLQVLEVDIIRRTSSRAIKELGQSLKRLGVMTNGSTKCKKILCAIEKLS 703
Dy 719 KGIGKLRDLQVLEVDIIRRTSSRAIKELGQSLKRLGVMTNGSTKCKKILCAIEKLS 778
Qy 704 SLOLYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEEMPNWIEQLTHLKKIYLLR 763
Dy 779 SLOLYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEEMPNWIEQLTHLKKIYLLR 838
Qy 764 SKLKEGKTMILGALPNLMVLDLYRKAYLGEKLVFKTGAPFNRLTLTDLDQLREIRFE 823
Dy 839 SKLKEGKTMILGALPNLMVLDLYRKAYLGEKLVFKTGAPFNRLTLTDLDQLREIRFE 898
Qy 824 DGSSPQLEKIEIRFCRLSISGIIHILPRLKEISLGYESKVAGLAQLEGEVTHPNRPVL 883
Dy 899 DGSSPQLEKIEIRFCRLSISGIIHILPRLKEISLGYESKVAGLAQLEGEVTHPNRPVL 958
Qy 884 RKREDSDHDLADAEKSPVY-----VEATDPLPQEGESSQ 920
Dy 959 RMDSDRRDHLDAEAGESSIEVQTADPVPDAQSGSVTVAEATDPLPQEGESSQ 1012

RESULT 6
ADI57168
ID ADI57168 standard; protein; 979 AA.
XX
AC ADI57168;
XX
XX 22-APR-2004 (first entry)
XX
DE Oryza minuta Pi9 locus nucleotide binding site (NBS) protein #1.
KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant.
XX
OS Oryza minuta.
XX
XX US2004006788-A1.
XX
XX 08-JAN-2004.
XX
XX 27-JAN-2003; 2003US-00352179.
XX
XX 25-JAN-2002; 2002US-0352106P.
XX
XX 01-FEB-2002; 2002US-0353304P.
XX
XX (WANG/) WANG G.
XX (LIUG/) LIU G.
XX
XX Wang G, Liu G;
XX
XX WPI; 2004-121064/12.
XX N-PSDB; ADI57167.
XX
XX Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
XX and NBS3, useful for producing plants resistant to Magnaporthe grisea

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PT infection.
XX Claim 1; SEQ ID NO 85; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present amino acid sequence represents an NBS
CC protein encoded by a gene from the Oryza minuta P19 locus.
XX
XX Sequence 979 AA;

Query Match 51.0%; Score 2621; DB 8; Length 979;
Best Local Similarity 55.3%; Pred. No. 7.8e-237;
Matches 539; Conservative 134; Mismatches 217; Indels 84; Gaps 6;

Qy 1 MAETVLSMARSLVGSATSKAASAADETSLLLGVEKDIWYL----- 41
Db 1 MAETVSMAMSVLGSVAGKAAASAADEATLLGVQKEIWIYIKDELKTIQAFRAAEVTKK 60
Qy 42 -----FR-HGVGRSNGGPPVGMVASGNQSCLA----- 68
Db 61 KDDLLKVAEQVRLSYNIEDCLDFKVVHVESQSLAKQLMKL---GSRHRIAVQILNLS 117
Qy 69 -----DSYAEDIRNQSARNVDEAEVLGFSDSKKRLLEM 101
Db 118 RIEVSNRNTFYSLIKLISSTTDEDRDSELYEDARNRSGSNTDESELVGFATKDELLKL 177
Qy 102 IDTNANDGPAPKVICVGMGGIGKLTALSRKIPESBEDIRKNPPCNAMITVSQSFRIBLK 161
Db 178 IDVNTNDGPAPKVICVGMGGIGKLTALARKAYENKEHM-KNFSCCAWITVSQSPDRKEILK 236
Qy 162 DMIRQLLGPSSLDQLLOELQGVVQVHLSLEYLIEELKEKYFVVLDDLWILHDWNIW 221
Db 237 QMIRQLLAGSLDKLKEFSEKJLVQVQHLADHLVEGLKEKYFVVLDDLWTDAMWNIH 296
Qy 222 EIAFPKNKKGQSVITVNNVDLAEKATASLVHLDPLOWNDAITLLLRKTNKNHEDME 281
Db 297 DTAPFKINNRSRIITTRDGLAGRCTSESLIVHLEPLHIDDAIHLLAKTNIRLEDME 356
Qy 282 SNKNMQKXVERIVNKCGRPLAIIITGAVLATKQVSEWEKPYEHLPSLEINPSLEALRR 341
Db 357 NDEDLGSIVTKLVKRCGVPLAIIITGIGLATKIMEMGKPYRELPSLEINPSLEAMRR 416
Qy 342 MVTLYNHLPSHLKPCFLYLSIFPEDFEIKNRLVGRWIAEGFVRPKVGMTTKDVGSEYP 401
Db 417 MVTLSYNHLPSHLKPCFLYLSIFPEDFEIQGRVLVDRWIAEGFVRATDGVNIEDVGNSHF 476
Qy 402 NELINRMIOQRSVGIAGKIYCTRIHDIITDITVISISROENFVLLPMGDGSDLVQENRTH 461
Db 477 NELINRLIQPSKVSTGVVRCRHHIMRDIIVISIREENFVLLTREKITTVADESIRH 536
Qy 462 IAFHGSCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTLITQKDF 521
Db 537 LAFHGSCKTGLEWNLRSVTLFGDRPAGTRPALCSPQFRLVRLVLDLEDAAKPKFTQNDI 596
Qy 522 DRIALLCHLKYSITGYSSSYSLPRSTKGLQLOTLNMPSTYIAALPSSEISKLOCLTLR 581
Db 597 RNIGLLRHMYKLNPARASTIYTLPRSIGKLOCLQLLNREANIISALATVETKLNQLSLR 656
Qy 582 CSRKFVSDNES-LNHPMKCIINTTCLPKVFTPLVSRDDRAIQIAELHMAKSCYKSGV 640
Db 657 CSRRSGSGYFIIIDNPKECMLIMWCLPWFSTSFNSDRVKLPEICMCSCTRWSDTKGV 716
Qy 641 KVPKGIGKRLQVLEYVDIRTSRAIKELGQLSKLRKLGVMNTNGSTKCKILCAAE 700
Db 717 RVPKGINLRELQILEVVDINRTRSKALEELGELIQLRKLSTTKGATNKYQIFCAAIE 776
Qy 701 KLSLQVLYNNAAGISGGTLECLDSISSPPPLRTLVLYGSLEEMPNWIEQLTHLKKIY 760
Db 777 KLSLSQSLRVDAGFSDTGTLEWLNISACPPFPFLTKLNGSLADTPNWFNGLKQLVKMC 836
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Qy 761 LLRSKLEKGTMLILGALPNLMVLDLYRKAYLQEKLVFTGAPFNLTSLIYDLQIREI 820
Db 837 LSRCLVQDGKTMELGALPNLMVLRNAYADEKMAFRGTTPFNACLDIYLLKQLREI 896
Qy 821 RFDGSSPOLKEIETPCRLSESGIIGIHLPRLKEISLGYESKVAGLAQLEGEVTRHPNH 880
Db 897 RFEGTSPTWESIYIGCRLESIGIIGIHLPRLKIISLEYDGVKAKLDVLQSEVNTHPNH 956
Qy 881 PVLKREDRSDHDL 894
Db 957 TELQMAEDRSHDL 970

RESULT 7
ADM72239
ID ADM72239 standard; protein; 993 AA.
XX
AC ADM72239;
XX
DT 03-JUN-2004 (first entry)
XX
DE O. minuta NBS1 polypeptide.
XX
KW P12; NBS1; plant protectant; gene therapy; rice; disease resistance.
XX
OS Oryza minuta.
XX
PN W02004022715-A2.
XX
PD 18-MAR-2004.
XX
PF 08-SEP-2003; 2003WO-US027913.
XX
PR 09-SEP-2002; 2002US-0409216P.
PR 18-MAR-2003; 2003US-0455713P.
PR 05-SEP-2003; 2003US-00656394.
XX
PA (OHIS ) UNIV OHIO STATE.
XX
PI Wang G;
XX
WPI; 2004-257576/24.
DR N-PSDB; ADM72238.
XX
PT New rice P12-like disease resistance nucleic acid molecule that confers
PT disease resistance in plants, useful for creating or enhancing disease
PT resistance in plants.
XX
PS Disclosure; SEQ ID NO 2; 120pp; English.
XX
CC The invention relates to novel broad-spectrum resistance gene P12 and the
CC NBS(1-6) genes present in the P12 gene cluster region. The rice P12-like
CC disease resistance nucleic acid molecules are useful for enhancing
CC disease resistance in plants. The present sequence represents a rice NBS1
CC polypeptide.
XX
SQ Sequence 993 AA;

Query Match 50.9%; Score 2616; DB 8; Length 993;
Best Local Similarity 55.1%; Pred. No. 2.4e-236;
Matches 542; Conservative 129; Mismatches 229; Indels 84; Gaps 5;

Qy 2 AETVLSMARSLVGSATSKAASAADETSLLLGVEKDIWYL----- 41
Db 3 AETVSMAMSVLGSVAGKAAASAADEATLLLGQKEIWIYIKDELKTIQAFRAAEVTKK 62
Qy 42 -----FRHGVGRSNGGPPVGM 57
Db 63 DDLKVAEQVRLSYNIEDCLDFKVVHVESQSLAKQLMKLGERHRIAVQIRNLKSREE 122
Qy 58 VASGNQSCLA-----DSYAEDIRNQSARNVDEAEVLGFSDSKKRLLEMIDTN 105
Db 123 VSNRNTFYSLIKPISSTTDEDRDSELYEDARNRSGSNTDESELVGFATKDELLKIDVN 182
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QY 106 ANDGPAKVICVVGGLGKLTALSRKIPSEBEDIRKNFPCNAWITVSQSFHRIELDKOMIR 165
 DB 183 TNDGPAKVICVVGGLGKLTALSRKIPSEBEDIRKNFPCNAWITVSQSFHRIELDKOMIR 241
 QY 166 QLLGSSLDLLOELQGVVQVHLSYILBELKEKRYFVVDLTLHHDWNNINETA 225
 DB 242 QLLGADSLDKLLEFSEKLLVQVHLADHLVEGLKEKRYFVVDLTLHHDWNNINETA 301
 QY 226 PKNKKGSIQVITWNVDLAEKATASLVYHDLFQMNDAITLLLRKTNKNHEDMESKN 285
 DB 302 PKNNRSGRIITTRDAGLAGCTSESILYHLEPLHIDDAITLLLRKTNKNHEDMESKN 361
 QY 286 MQKVERIVNKGRLPLAILITIGAVLATKQVSEWEKPYEHLPSLEINPSLEARRMVT 345
 DB 362 LGSIVTKLVKRCGLPLAILITIGAVLATKQVSEWEKPYEHLPSLEINPSLEARRMVT 421
 QY 346 GYNHLPKPCFLYLSIFPEDFEIKRNLVGRMIAEGFVRPKVMTTKDVGESYFVELI 405
 DB 422 SYNHLPSHLPKPCFLYLSIFPEDFEIKRNLVGRMIAEGFVRPKVMTTKDVGESYFVELI 481
 QY 406 NRSMIQSRVGIAGKIKTCRIHDIITVTSISROENFVLLPMGDGSDLVQENTRHIAFH 465
 DB 482 NRSMIQSRVGIAGKIKTCRIHDIITVTSISROENFVLLPMGDGSDLVQENTRHIAFH 541
 QY 466 GMSCKTGLDWSITRSIAIFGDRPKSLAHAVCPDQLRMLRVLDLDTFLITQKDFRIA 525
 DB 542 GSKCSKICLWNHLRSVTLFGDRPVGRTPALCSPQFRLRVLDLDTFLITQKDFRIA 601
 QY 526 LLCHLKVLISYSSISYPSISGLQLOTLNMPSTVIAALPSEISKLOCLHTRCSRK 585
 DB 602 LLRMKYLNFARASTIYTLPSISGLQLOTLNMPSTVIAALPSEISKLOCLHTRCSRK 661
 QY 586 FVSNFNS-LNHPMKCITWITCLPKVFTPLVSRDRAIQIAELHMTATSCWYKSGVVKPK 644
 DB 662 SGSGVFSIIDNPKECLMTWCLPWVFLTSINFSRDKLIPICMSCSTRNSDTKGVVRP 721
 QY 645 GIGKRLDQVLEYDVRTSSRAIKELGOLSKLARKLVMTNGSTKCKKILCAAEIKLSS 704
 DB 722 GIDNLKELQILEVVDINRTSKAIEELGELTQLRKLSTVTKGATNKYQIFCAAEIKLSS 781
 QY 705 LOYLIVNAAGISDGTLECLDSISPPPLATLVLYGSLSEMPNWI BOLTHTKIYLLRS 764
 DB 782 LQSRVDAEGSDGTLEWLNLSIACPPFPFLKRLKNGSLADTPNFWGNLKVXVCLSRC 841
 QY 765 KLKGGKTMILGALPNLMVLDRKAYLGEKLVFKAFTGAPNLRITLSIYDLQLEIRIFED 824
 DB 842 GLKDKTMEILGALPNLMVLDRKAYLGEKLVFKAFTGAPNLRITLSIYDLQLEIRIFED 901
 QY 825 GSSPOLEKIEIRFCRLSEGIIGIHLPRKLEISLGYSKVAGLAQLEGEVTRHPNHPVL 884
 DB 902 GTSPTMESIEIYGCRLSEGIIGIHLPRKLEISLGYSKVAGLAQLEGEVTRHPNHPVL 961
 QY 885 KREDSDHDL-----ACDAEGSP 902
 DB 962 MAEDRSHDLGGLASDGDADNDP 985

RESULT 8

AD157170

ID AD157170 standard; protein; 993 AA.

XX AC

XX AD157170;

XX DT

XX 22-APR-2004 (first entry)

XX DE

XX Oryza minuta P19 locus nucleotide binding site (NBS) protein #2.

XX KW

XX nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;

XX plant breeding; transgenic plant; plant.

XX OS

XX Oryza minuta.

XX

PN

US2004006788-A1.

XX

PD 08-JAN-2004.

XX

PF 27-JAN-2003; 2003US-00352179.

XX

PR 25-JAN-2002; 2002US-0352106P.

XX

PR 01-FEB-2002; 2002US-0353304P.

XX

PA (WANG/) WANG G.

XX

PA (LIUG/) LIU G.

XX

PI Wang G, Liu G;

XX

XX WPI; 2004-121064/12.

DR

XX N-ESDB; ADI57169.

XX

Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2

PT

and NBS3, useful for producing plants resistant to Magnaporthe grisea

PT

infection.

XX

Claim 1; SEQ ID NO 87; 136pp; English.

XX

The invention comprises the amino acid and coding sequences of nucleotide

XX

binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial

CC

blight and rice blast resistance genes). The DNA sequences may be used as

CC

markers for resistance to infection with Magnaporthe grisea in plant

CC

breeding programs. The present amino acid sequence represents an NBS

CC

protein encoded by a gene from the Oryza minuta P19 locus.

XX

Sequence 993 AA;

SQ

Query Match 42.3%; Score 2170.5; DB 8; Length 993;

Best Local Similarity 49.1%; Pred. No. 2.4e-194;

Matches 478; Conservative 155; Mismatches 236; Indels 105; Gaps 17;

QY 1 MAETVLSMARSLVGSATSKAASAADETSLLGVEKDIWYL-----FRHGVGRSN 50

DB 1 MTETVLSMARSLVGSATSKAASAADETSLLGVEKDIWYL-----FRHGVGRSN 60

QY 51 GGPVVGWVAS-----GNQS-----C---LAI----- 68

DB 61 QDELVKVWASQVRDLAYDIEDCLOEPFVHVGHQSLMQLKLCRHRIAVIRNLKQKVE 120

QY 69 -----DSYAEDIRNQSNARVDEAEALVFSKSKRLLEMDITN 105

DB 121 EVSNRNRYNLKSVSPSSSTDDSQSNMELIRYQTAHYVNESELVGFDPVKEILELVSS 180

QY 106 ANDGPAKVICVVGGLGKLTALSRKIPSEBEDIRKNFPCNAWITVSQSFHRIELDKOMIR 165

DB 181 EN-AEAQTIWVGGGLGKLTALSRKIPSEBEDIRKNFPCNAWITVSQSFHRIELDKOMIR 238

QY 166 QLLGSSLDLLOELQGVVQVHLSYILBELKEKRYFVVDLTLHHDWNNINETA 225

DB 239 QLLGSSLDLLOELQGVVQVHLSYILBELKEKRYFVVDLTLHHDWNNINETA 297

QY 226 PKNKKGSIQVITWNVDLAEKATASLVYHDLFQMNDAITLLLRKTNKNHEDMESKN 285

DB 298 -GNMGRSVVTVTRNKNLAGSST-SPVCLTKLEKEDATKLLRKTKRSLHDIKDO- 354

QY 286 MQKVERIVNKGRLPLAILITIGAVLATKQVSEWEKPYEHLPSLEINPSLEARRMVT 345

DB 355 MKEIFEKILKCGGLPLAITITIGAVLATKQVSEWEKPYEHLPSLEINPSLEARRMVT 414

QY 346 GYNHLPKPCFLYLSIFPEDFEIKRNLVGRMIAEGFVRPKVMTTKDVGESYFVELI 405

DB 415 SYNLPKPCFLYLSIFPEDFEIKRNLVGRMIAEGFVRPKVMTTKDVGESYFVELI 474

QY 406 NRSMIQSRVGIAGKIKTCRIHDIITVTSISROENFVLLPMGDGSDLVQENTRHIAFH 465

DB 475 NRSMIQSRVGIAGKIKTCRIHDIITVTSISROENFVLLPMGDGSDLVQENTRHIAFH 534

QY 466 GMSCKTGLDWSITRSIAIFGDRPKSLAHAVCPDQLRMLRVLDLDTFLITQKDFRIA 523

CC resistance to blast fungi

XX

SQ Sequence 1205 AA;

Query Match 20.1%; Score 1033; DB 3; Length 1205;

Best Local Similarity 31.4%; Pred. No. 5.6e-87;

Matches 308; Conservative 184; Mismatches 354; Indels 136; Gaps 37;

Qy	9	ARSLVGAISKAASAAADETSLL-----LGVKDIWYLFPHG--VGRSNGGPV-----VGM 57
Db	252	SRIIVTSQVEVASLCAQSQASSELKQLSADQTLYAFYDKGSOIEDSVKPVSSIDVAI 311
Qy	58	VASNGQCL-----AIDSAYEDIRNQSARNV-----DEAELVGFSDSKRLLLEMI 102
Db	312	TSTNNHTVAHGEIIDDQSMADAEKKVARKSLTRTSGASEESQIGREKISEITHLI 371
Qy	103	DTNANDGPAKVICVWGNGGLKKTALSARKIPSEBEDIRKNFPCNAWITVSGSFHRIELKO 162
Db	372	-LNDNSQQVQVISVWGNGGLKKTLLVSGVQSPR-LSDKFDKYVVFVIMRPFILVELLRS 429
Qy	163	MIRQL-LGPSLDDOLQ-----ELQGVVQVQVHLSLEYLIBELKEKRYFVVLDDLWILHDM 217
Db	430	LAEQHLHGKSSKKELENNRVSSKKSASLAMEDTELQGLRLEKSKCLVILDDFSDTSEW 489
Qy	218	NWINEIAPPKNKKGSOIVITWNVDLAEKCATAS-LVYHLDFLOMNDAITLLRKTY--N 274
Db	490	DOIKPTLFFPL-LEKTSRLIVYTRKENTANHCSGKNGVHNKVLKNDALCLLSEKVFEE 548
Qy	275	KNHEDMESNKMOMKVERIVNKCGRPLAIILITIGAVLAT--KQVSEWEKFVHEHLPSELEI 332
Db	549	ATYLDQNNPELVKXEAQILKKDGLPLAIVVIGFLANRPKTPPEWRKKNENINAELEM 608
Qy	333	NPSLEALRWVTLGYNHLPKPCFLYLSIFPEDFEIKRNRLVGRWTAGFVPRKVGMT 392
Db	609	NPELGMTIRTVLEKSYDGLPHLKSCFLYLSIFPEDQIYISRRRLVHRWAAEGSYTAAHGKS 668
Qy	393	TKDVGESVFBNLINRSMI-----QRSRVGIAGK-IKTCRIHDIIRDITVSISQENFVLLPM 448
Db	669	AIEIANGYFVELKNRSMILPFQOS--GSSRSKIDSCKVHDLMRDIAISKSTEENLVPRVE 726
Qy	449	GDGSDLVQENTRHIA-----FHGWSCKTGL-DWSIIRSLAIFGRDRPKSLAHAVCPDQLRM 503
Db	727	EGCSAYITHGAIRHLAISNNWKGDKSEPEGIVDLRSIRLSLFGDWKPPFVVG-----KMRF 782
Qy	504	LRVLDELDVPTLIITQKDFDRIALLCHLKYLKYSIVSSSIYSPRSIGKLOGLOTINMPSTY 563
Db	783	IRVLDFEG-TRGLEVYHLDDQIWKLNHLKFLUSLRCGYRIDLLPDLGNLRQLOMIDIRGT 841
Qy	564	IAALPSSISKIQCLHTLRCSRK--FV-SDNFSLNHPMK--CITNTITCLP---KVFTPLV 614
Db	842	VKALPTKIIKLOKQYIHAGRKTDYVWEKHSLSMQRCKVGCICATCCLPLLCEMYGPL- 900
Qy	615	SRDRAIQIAELHWATKSCW-----YKSGFVKVPKGIKLRDLQVLEYVD 659
Db	901	-----HKALARADAWTFACCVKPPSMTGVHEBEGAMVSPGIRKLDLHTLRNIN 950
Qy	660	IRRTSSRAIKELGOLSKRLKLGWNTSGTEKCKILCAAIEKLSLOLYVYNAAGISDGG 719
Db	951	VGR-GNAIRLDIGMLTGLHKLVGA--GINKNGRAFRALATISNLKLSLSVSSGAMP--G 1005
Qy	720	TLECLDSTSSPPPLRLTLVLYGSLEEMPNWIEQTLHKKIYLLRSKLE-KGKTLMLICAL 778
Db	1006	LCGCLDDISSPENLQSLKLGSLKTLPWEIKELQHLVKLVSTRLLLEHVDVAMEFJGEL 1065
Qy	779	PNLMVLDLYRKAYIGEKLIVFK--TG-APPNRLTSLIVDQLREIRPEDGSSPOLEKIE 834
Db	1066	PKVEILVI--SPFKSEETHFPKPQTGTAFVSLRVKLKLAGLWGIKSVKPEGTMPKJRLQ 1123
Qy	835	IRPCELES--GIIGIHLPRKETSLSL-----GYESKVAGLAQ 869
Db	1124	VQ-GRINEIEFGSLGFQNLQINEVOLSVWPFDDHDIRAARAAGADYETAWEVEQBARR 1182
Qy	870	LEGEVR-----THPNHPVL 883

Db 549 ATYDDQNNPELVKEAKQILKCDGLPLAIVVIGFLANRPKTPPEWRKLNENINASLEM 608
Qy 333 NPSLEALRRMVTGLGYNHLPSHKPCFLYLSIFPDEFEIKRNLVGRMTAEFGVPRKVGMT 392
Db 609 NPELGMRTVLEKSYDGLPYHLKSCFLYLSIFPDEQIISRRRLVHRWAAGYSTAAHGKS 668
Qy 393 TKDVGESYFNELINRSMI---QSRVGIAGK-IKTCRIHDIIRITVSIQRQENFVLLPM 448
Db 669 AIEIANGYFMELNKRSMLPFQOS--GSSRSKSIDCKVHDLMRDIAISKSTEENLVPRVE 726
Qy 449 GDGSDLVQENTRHIA---FHGSMCKTGL-DWSIIRSLAIFGRPRKSLAHAVCPDQJRM 503
Db 727 EGCSAYIHGAIRHLAISNNWKGDSPEGIVDLRSIRSLFSGDWKPPFFVYG---KMRP 782
Qy 504 LRVLDEEDVTFLITQKDFDRIALCHLYLSIGYSSSIYSLPRSIGKLGQIGLOTLMPSY 563
Db 783 IRVLDFEG-TRGLEVYHLDQIKWLNHLKFLSLRCYRIDLLPDLGNLRQLQMLDIRGTY 841
Qy 564 IAALPSEISKLOLTLRCSRK--FV-SDNFSLNHPMK---CITNTICLP---KVFTPLV 614
Db 842 VKALPKTIILKLOQYIHAGKRTDYVWEKSHLMQRCKVGCICATCCLPILCEMYGPL- 900
Qy 615 SRDDRAIQIAELHMAKSCW-----YKSGVGVKPGIGKGLDLQVLEYVD 659
Db 901 -----HKALARRDAWTFACCVKPPSMTGVHEEGAMVPSGIRKLDLHLNRIN 950
Qy 660 IRTSSRAIKELGOLSKLRKLGVMNTGSTKECKILCAAEKLSLOLYVNAAGISDGG 719
Db 951 VGR-GNAILRDIGMLTGLHLGVA--GINKNGRAFLAISNLKLSLSSVSSAGMP--G 1005
Qy 720 TLECLDISPPPLRLTLVYGSLEMPNTEQTHLKIYLLRSKLKE-GKTMILILGAL 778
Db 1006 LCGCLDISPPENLQSLYGLSKTLPEWIKELQHLVKLKVSTRLEHDVAMEFLGEL 1065
Qy 779 PNLVLDLYKAYLGEKLVK---TG-AFNLRLTSLYDLDQLEIRFEDGSSPOLKIE 834
Db 1066 PKVEILVI--SPFKSEIHFPPQTGTAFVSLRVLKLGLWGIKSVKPEGTMPKJRLQ 1123
Qy 835 IRFCRLS--GIIGIHLPLKBSL-----GYESVAGLAQ 869
Db 1124 VQ-GRIENEIGFSGLEFLOINEVOLSVWFFTDHRTIRARAAGADYETAWEVEVQEAR 1182
Qy 870 LEQVR-----THPNHPLV 883
Db 1183 KGGELKIRQLARNPNOPII 1204

RESULT 13

AA93135
Xx AA93135 standard; protein; 1251 AA.

Xx AC AA93135;

Xx DT 08-NOV-2000 (first entry)

Xx DE Rice blast fungus-resistance protein Pi-b from rice.

Xx KW Rice blast fungus; Pyricularia grisea; Magnaporthe grisea;
Xx KW resistance gene.

Xx OS Oryza sativa.

Xx PN JP2000125885-A.

Xx PD 09-MAY-2000.

Xx PF 29-MAR-1999; 99JP-00087305.

Xx PR 21-AUG-1998; 98JP-00235884.

Xx PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Xx PA (NORU) NORINSUISANSO NOGO SEIBUTSU SHIGEN.

Xx WPI; 2000-379868/33.
DR N-PSDB; AAA11349, AAA11350.

Xx A blast-resistant gene and related genes, useful for creating a rice
Xx grade of high blast resistance.

Xx Claim 26; Page 20-23; 36pp; Japanese.

Xx The invention relates to the isolation of novel rice blast fungus
Xx (Pyricularia grisea; also known as Magnaporthe grisea) resistance genes
Xx from rice strain BL-1. The genes are designated Pi-b (AAA11349) and Pi-b'
Xx (AAA11351). The genes can be used for creating rice which has high blast
Xx fungus resistance. This sequence represents the protein encoded by the Pi
Xx -b gene

Xx SQ Sequence 1251 AA;

Query Match 20.1%; Score 1033; DB 3; Length 1251;

Best Local Similarity 31.4%; Pred. No. 6e-87;

Matches 308; Conservative 184; Mismatches 354; Indels 136; Gaps 37;

Qy 9 ARSLVGAISKAASAAADETSL---LGVKDIWYLFHRG--VGRSNGGPV---VGM 57
Db 298 SRIIVSTQVEVASLCAQESQASELKQLSADQTLAYFYDKGQIIEDSVKPVISDVAI 357
Qy 58 VASGNQSL-----AIDSYAEDIRNQSANV-----DEALVGFSDSKRLLEMI 102
Db 358 TSTNNHTVAHEIIDDQSDMADEKKVARKSLTRTSTVGASEESQLIGREKEISEITHLI 417
Qy 103 DTANDGPAKVICVVGMGGLGKTALSRKIPESEDIRKNPPCNAWITVSQFHIELKD 162
Db 418 -LANDSQOVVISVWVGMLGKTTLVSGVYQSPR-LSDKFKDYVFVTIMRPFILVELRS 475
Qy 163 MIROL-LGPSLQDLQ---ELQKVVQVHHLSLEYLIEELKEKRYFVVLDDLWILHDW 217
Db 476 LAEOLHGSSKGBELLENVSSRSKSLASMETEUTGQLRLEKSKCLIVLDDPSDSEW 535
Qy 218 NWINEIAFPKNNKKGQIVITWNVDLAEKATAS-LVYHLDLFQMDAITLLRKT--N 274
Db 536 DOIKPTLPFL-LEKTSRIIVTKENIANHCSGKNGVHNKLVKHNDAICLLSEKVFEE 594
Qy 275 KNHEDMESNKNMQMVERIVNKCGRPLAILITIGAVLAT--KQVSEWEKFFYEHLPSLEI 332
Db 595 ATYLDQNNPELVKEAKQILKCDGLPLAIVVIGFLANRPKTPPEWRKLNENINASLEM 654
Qy 333 NPSLEALRRMVTGLGYNHLPSHKPCFLYLSIFPDEFEIKRNLVGRMTAEFGVPRKVGMT 392
Db 655 NPELGMRTVLEKSYDGLPYHLKSCFLYLSIFPDEQIISRRRLVHRWAAGYSTAAHGKS 714
Qy 393 TKDVGESYFNELINRSMI---QSRVGIAGK-IKTCRIHDIIRITVSIQRQENFVLLPM 448
Db 715 AIEIANGYFMELNKRSMLPFQOS--GSSRSKSIDCKVHDLMRDIAISKSTEENLVPRVE 772
Qy 449 GDGSDLVQENTRHIA---FHGSMCKTGL-DWSIIRSLAIFGRPRKSLAHAVCPDQJRM 503
Db 773 EGCSAYIHGAIRHLAISNNWKGDSPEGIVDLRSIRSLFSGDWKPPFFVYG---KMRP 828
Qy 504 LRVLDEEDVTFLITQKDFDRIALCHLYLSIGYSSSIYSLPRSIGKLGQIGLOTLMPSY 563
Db 829 IRVLDFEG-TRGLEVYHLDQIKWLNHLKFLSLRCYRIDLLPDLGNLRQLQMLDIRGTY 887
Qy 564 IAALPSEISKLOLTLRCSRK--FV-SDNFSLNHPMK---CITNTICLP---KVFTPLV 614
Db 888 VKALPKTIILKLOQYIHAGKRTDYVWEKSHLMQRCKVGCICATCCLPILCEMYGPL- 946
Qy 615 SRDDRAIQIAELHMAKSCW-----YKSGVGVKPGIGKGLDLQVLEYVD 659
Db 947 -----HKALARRDAWTFACCVKPPSMTGVHEEGAMVPSGIRKLDLHLNRIN 996
Qy 660 IRTSSRAIKELGOLSKLRKLGVMNTGSTKECKILCAAEKLSLOLYVNAAGISDGG 719
Db 997 VGR-GNAILRDIGMLTGLHLGVA--GINKNGRAFLAISNLKLSLSSVSSAGMP--G 1051

QY 720 TLECLDISPPPLRLTLVLYGSLSEENPNWIEQUTHLKKIYLLRSKLKE-GKTMILILGAL 778
 DB 1052 LCGCLDDISPPENQSLKLYSLKTLPEWIKELQHLVKKLVSTRLEHDVAMEFLGEL 1111
 QY 779 PNLMLVLDLYKAYIGEKLVPK---TG-APNLRITLSIYDLDQUREIRFEDGSSPOLKIE 834
 DB 1112 PKVEILVI--SPFKSEBIHFPPQGTAFVSLRVLKLGLWGIKSVKFEETWPKLERLQ 1169
 QY 835 IRFCRLFS--GIIGIHLPRLKEISL-----GVESKVAGLAQ 869
 DB 1170 VQ-GRINEIGFSGLEFLQINVEQLSVWPFTHDHRIRARAAGADYETAWESEVQEARR 1228
 QY 870 LEGERV-----THPNHPVL 883
 DB 1229 KGBELKKIRIQOLARNPNQPII 1250

RESULT 14
 ADI57178
 ID ADI57178 standard; protein; 451 AA.
 XX AC ADI57178;
 XX DT 22-APR-2004 (first entry)
 XX DE Oryza minuta P19 locus nucleotide binding site (NBS) protein #6.
 XX KW nucleotide binding site; NBS; P19 gene; bacterial blight; rice blast;
 XX KW plant breeding; transgenic plant; plant.
 XX OS Oryza minuta.
 XX PN US2004006788-A1.
 XX PD 08-JAN-2004.
 XX PF 27-JAN-2003; 2003US-00352179.
 XX PR 25-JAN-2002; 2002US-0352106P.
 XX PR 01-FEB-2002; 2002US-0353304P.
 XX PA (WANG/) WANG G.
 XX PA (LIU/) LIU G.
 XX PI Wang G, Liu G;
 XX WPI; 2004-121064/12.
 XX DR N-PSDB; ADI57177.
 XX PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
 PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
 PT infection.
 XX PS Claim 1; SEQ ID NO 95; 136pp; English.
 XX CC The invention comprises the amino acid and coding sequences of nucleotide
 CC binding site (NBS) proteins from the Oryza minuta P19 locus (bacterial
 CC blight and rice blast resistance genes). The DNA sequences may be used as
 CC markers for resistance to infection with Magnaporthe grisea in plant
 CC breeding programs. The present amino acid sequence represents an NBS
 CC protein encoded by a gene from the Oryza minuta P19 locus.
 XX SQ Sequence 451 AA;

Query Match 19.4%; Score 996.5; DB 8; Length 451;
 Best Local Similarity 40.4%; Pred. NO. 3e-84;
 Matches 220; Conservative 60; Mismatches 93; Indels 171; Gaps 4;

QY 1 MAETVLSNARSLVGSATSKAASAADETSLLGVKEKDIWYL----- 41
 DB 1 MADTVLSIAKSLVGSASVSKVASVAADKRMILLGVQKEIWFIKDELQTIQAFMAAEASKK 60

QY 42 -----FRHGVGRSNGGPVVG 57
 DB 61 SILLKVVVQVQVRLSDYIEDICLDEFTVHVGSQTLRQLMKLKHRIAVQIRNLRTRIEE 120
 QY 58 VASGNQSCLAIDS-----YAEIRNQSRNVDEAEALVGFSDSKRKLLEMDITNA 106
 DB 121 VSRNTRYNLINDLSTTGERNFIMEDIRNESANNIEEAEALVGFSGPKRELLDLIDVHA 180
 QY 107 NDGPAPKVICVVGGMGLGKTALSRKIFESEEDIRKNPFCNAWITVSQSFHRIELKKOMIRQ 166
 DB 181 KDGPTKVVCVVGGMGLGKTIAKRIYESKEDIAKNFSCCAWITVSQSFVRLLELLKDLMKV 240
 QY 167 LLGFSSDLQLLELQGVVVVHLLSELYIEELKEKRYFVVLDDLTWILHWNWINEIAFP 226
 DB 241 LFGEEVLKKRLRELEK-VPQVDDLASLYRLTELNERRYFVVLDDVWSTDSWKWINSIAFP 299
 QY 227 KNNKGSQIVITTWNVDLAEKCATASLVVHLDPLQNDALTLLLRKTNKHEDMESKNM 286
 DB 300 RNNKGSRVIVTTRDVGLAKECTSELLTYRLKPLEITYAKELLRKANKKIEDMKSDK 359
 QY 287 QKMVERIVNKCGRPLAILTIGAVLATKQVSEWEKFEYHLPFSELEINPSLEALRMVTLG 346
 DB 360 SDIITKIVKCGVLPAILTIGGVLATK----- 387
 QY 347 YNHLPSHLKPCFLYLSIFPEDFEIKRNLVGRVIAEGFVRPKVGMTTYKDVGESYFNELIN 406
 DB 388 ----- 387
 QY 407 RSMIQSRVGIAGKIKTCRIHDIIRDITVSIROENFVLPMGDSGLVQENTRHIAPHG 466
 DB 388 ----DPSRAGVRGEFKSCRIHDIRDIAISISREENFILLPEGTGYDGVHGNTRHIAFHG 443
 QY 467 SMSK 470
 DB 444 SKYC 447

RESULT 15
 AAY58854
 ID AAY58854 standard; protein; 953 AA.
 XX AC AAY58854;
 XX DT 08-MAY-2000 (first entry)
 XX DE Sorghum resistance gene homologue S6-1-encoded protein.
 XX KW Sorghum; resistance gene homologue; RGH; transgenic plant;
 KW disease resistance; crop protection.
 XX OS Sorghum bicolor.
 XX PN WO200004155-A2.
 XX PD 27-JAN-2000.
 XX PF 16-JUL-1999; 99WO-US016168.
 XX PR 17-JUL-1998; 98US-0093290P.
 XX PR 15-JUL-1999; 99US-00354453.
 XX PA (PURD) PURDUE RES FOUND.
 XX PI Bennetzen JL;
 XX WPI; 2000-182422/16.
 XX DR N-PSDB; AAY588293, AAY588294, AAY588295.
 XX PT New nucleic acid molecule encoding a resistance gene homolog, useful for
 PT producing disease resistant transgenic plant.
 XX PS Claim 1(b); Page 88-90; 98pp; English.
 XX

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:37:57 ; Search time 27.7041 Seconds
(without alignments)
3466.067 Million cell updates/sec

Title: US-10-656-394A-12
Perfect score: 5137
Sequence: 1 MASTVLSMARSLVGSAISKA.....LSGMNCFNLFSRDMLLVPA 998

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: PIR.79.*
- 2: PIR1.*
- 3: PIR2.*
- 4: PIR3.*
- 4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	854	16.6	926	2 A57072	disease resistance
2	712	13.9	1584	2 F96573	protein F12M16.25
3	676.5	13.2	906	2 G96621	probable disease r
4	675.5	13.1	907	2 F96617	probable disease r
5	672	13.1	908	2 T48899	disease resistance
6	663	12.9	847	2 T12977	hypothetical prote
7	660.5	12.9	906	2 T48898	disease resistance
8	644.5	12.5	899	2 H96617	probable disease r
9	640	12.5	831	2 T51185	resistance protein
10	635	12.4	835	2 T45590	hypothetical prote
11	634	12.3	900	2 G96617	probable disease r
12	631.5	12.3	820	2 T51186	resistance protein
13	628	12.2	821	2 A86243	hypothetical prote
14	603.5	11.7	839	2 B96538	hypothetical prote
15	601.5	11.7	852	2 T08416	disease resistance
16	600	11.7	847	2 T12979	hypothetical prote
17	561	10.9	1240	2 T06404	resistance complex
18	544	10.6	1220	2 T06403	resistance complex
19	530	10.3	1824	2 T07589	disease resistance
20	526.5	10.2	571	2 T02213	NBS-LRR type resis
21	525	10.2	695	2 T52429	PRM1 homolog [mpo
22	511	9.9	560	2 T52438	PRM1 homolog [mpo
23	511	9.9	613	2 T52465	hypothetical prote
24	491.5	9.6	1255	2 T06267	nematodes resist
25	491.5	9.6	1257	2 T06269	root-knot nematode
26	462	9.0	941	2 B96533	hypothetical prote
27	446.5	8.7	483	2 T02226	NBS-LRR type resis
28	438	8.5	1802	2 T00020	bacterial blight-r
29	437.5	8.5	985	2 T06049	hypothetical prote

30	430	8.4	967	2 G96637	hypothetical prote
31	427.5	8.3	921	2 D86293	FH2.22 protein -
32	421	8.2	884	2 F96659	protein F2K11.26 [
33	414.5	8.1	889	2 F96637	hypothetical prote
34	408.5	8.0	893	2 H96651	protein T3P18.19 [
35	406	7.9	889	2 C86257	resistance to Paeu
36	402	7.8	892	2 T01899	disease resistance
37	400	7.8	885	2 B86257	NBS/LRR disease re
38	397.5	7.7	909	1 A54809	disease resistance
39	395.5	7.7	919	2 T05746	hypothetical prote
40	389.5	7.6	925	2 H96638	protein T1F9.20 [i
41	376.5	7.3	898	2 E96659	hypothetical prote
42	361	7.0	622	2 T52439	PRM1 homolog [mpo
43	348	6.8	389	2 T04390	NBS-LRR type resis
44	341	6.6	470	2 T52440	PRM1 homolog [mpo
45	331	6.4	266	2 T04393	NBS-LRR type resis

ALIGNMENTS

RESULT 1

A57072
disease resistance protein RPM1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A57072
R:Grant, M.R.; Godiard, L.; Straube, E.; Ashfield, T.; Lewald, J.; Sattler, A.; Innes, R
Science 269, 843-846, 1995
A:Title: Structure of the Arabidopsis RPM1 gene enabling dual specificity disease resist
A:Reference number: A57072; MUID:95365795; PMID:7638602
A:Accession: A57072
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-926 <GRA>
A:Cross-references: UNIPROT:Q39214; GB:X87851; NID:9963016; PIDN:CAA61131.1; PID:9963017
C:Genetics:
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat
F:582-604/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:605-627/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:628-650/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

Query Match 16.6%; Score 854; DB 2; Length 926;

Best Local Similarity 28.2%; Pred. No. 1.5e-46;

Matches 283; Conservative 174; Mismatches 343; Indels 202; Gaps 36;

Qy	8	MARSLVGSATSKAASAAADETSLLLGVKDIWYL-----FRIGVRSNGGP	53
Db	1	MASATVDFGIGRILSVLENETLLSGVHGEIDKMKELLIMKSFLEDTKHG--	57
Qy	54	VV-----GMVASGNQSLAIDSYAEDIRNQSAENVDAE	87
Db	58	TTTTQLFQTPTVANTRDLAYQIEDLDFGVHGYRSCAKIWRAPFPYMWARH-SIAQ	116
Qy	88	LVG-----FSDSKR-----LLEMIDTNDNDGPAK-----	112
Db	117	KLGVVWVWIOISDSMKRYHSENYQAALLPPID----DGDAKVWNISSSLFFSENSL	172
Qy	113	-----VICVVMGGLGKTALSRKIFSEEDIRKNPPCNWITV	150
Db	173	VGIDAPKGLIGRLLSPQRIVVAVVGMGSGKTTLSANIFKS-QSVRRHFESYAVVTI	231
Qy	151	SQSPHRELAKDMITRQLLGSSLDQLLOQLQGVVQVHLS-----EYLIELKEKEYF	205
Db	232	SKSY-----VIEDVFRTM-----IKEFYKEADTQIPALYSGLYRELVEKLVYQSKRYI	282
Qy	206	VLLDDLWLDWNNWNIAPFNKKNKGSQIVITTWNVDLAE-KCATASLVVHLDPLQWMD	264
Db	283	VLLDDVTTGLWREIS-IALP-DGIYGSRVWMTTRDMNVASFPYIGISTKHEILLKEDE	340
Qy	265	AITLLLRKTNKHEDMESNKNQMQRVERIVNKCGRPLAIIITIGAVLATKQV-SEWEKFY	323

Db 341 AWLFSNKAFFASLEQCRQNTQNLFIARKLVERCOGLPLATASLGSMSTKKFSEWKKVY 400
 Qy 324 EHLPSLELEINPSLEALRMVTLGNHLPKPCFLYLSIPPEDFEIKRNLVRGWIAG 383
 Db 401 STNLWLNHNLKIVASIMFLSFNDLPYPLKRCFLYCSLPVNYMRKRELIRMMWAQR 460
 Qy 384 FVRPKVMTKDVGESYFNELINRSMIORRGVAGIKTCRIHDIIRDTIVSISROENF 443
 Db 461 FVEPIRGVKAEEVADSYLNELYVRNMLQVILWNPFGPKAFKMDHVIWEIALSYSKLERF 520
 Qy 444 --VLLPMGDSGLVQ--EN--TRHIAFHGSMSCKTGLDWSIIRSLAIFGDRPKSLAHVC 497
 Db 521 CDVYNDSDGDAAETWENYGRSLCTQKEMT-PDSIRATNLHSLLLVCSSAKHKM--ELL 577
 Qy 498 PDQLRMRLVDLEVDVTLTIQKODRIALLCHLYLSIGYSSSYLSIPRSTGKIQIGLQTL 557
 Db 578 P-SNLIRALDLESSI---SKLPDCLVTMPNLKYNLS-KTQVKELPKPHKLVNLETL 632
 Qy 558 NMPSTYIAALPSEISKLQCLHTLRCSRKFVSDNFSLNHPMKCIINTICLPKVFTPLVSRD 617
 Db 633 NTKHSKIEELPLGMWKLKRLYLITFR----- 660
 Qy 618 DRAIQIAELHMAWTSCHYKSGVVKPGIGKRLDLOVLEYVDIRRTSSRAIKELGOLSKL 677
 Db 661 -----NEGHDNNYNYLGTTRVPKIQWOLQVW---DCFNAEDELKNGCMTQL 708
 Qy 678 RKLGMVTNGSKCKKILCAIEKLSLOYLYVNAAGISDGTLECLDSISSPPPLRLTL 737
 Db 709 TRISLVM--VREHGRDCLSNKIKIRPL--SLTSDIEEPELIDDLIATAS--TEKL 762
 Qy 738 VLYGSLEMPNWIQLTHLKKIYLLRSKLKRGKTMILGALPNLMVLDLYRKAYLGEKLV 797
 Db 763 FLAGKLERVSWFNTQLNLTIVGLRGSOLQ--NAILSQTPLRLVWLSFY-NAYMGPRLR 820
 Qy 798 FKTAGFNLRTLSYDLDQIREIRFEDGSSPOLSKIEIRPCR-LESGIIGIHLPLKEI 856
 Db 821 FAQC-FQNLKILEIVOMKHLTEVVIEDGAMPELOKLYVACRGLYVYPRGIENLINLQEL 879
 Qy 857 SLGYES-----KVAGLAQLEGV-RTHPNHPLVRKREDRSDH 892
 Db 880 HLHVSQNLVERIRG-----EGSVDRSRVKHPIPAIKHYFRIDN 917

RESULT 2
 F96573
 Protein F12M16.25 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: F96573
 R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F96573
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1584 <STO>
 C;Cross-references: UNIPROT:Q9WAG6; GB:AE005173; NID:g7769860; PIDN:AAF69538.1; GSPDB:GN
 C;Genetics:
 A;Gene: F12M16.25
 A;Map position: 1

Query Match 13.9%; Score 712; DB 2; Length 1584;

Best Local Similarity 26.1%; Pred. No. 4.2e-37;

Matches 265; Conservative 172; Mismatches 349; Indels 230; Gaps 39;

RESULT 3

G96621

C;Species: Arabidopsis thaliana (mouse-ear cress)
 probable disease resistance protein F23H11.10 [imported] - Arabidopsis thaliana

Qy 45 CVGRSNGSPVGM-----VASNQSCLAIDSVAEDIRNQSARNVDAAELVGFSDSKCR 97
 Db 427 GITKRISVEVGMQSLGIGHIADGGGRSLSRQREIROTFSRN-SESDLVGLDQSVE- 484
 Qy 98 LLEMIDTNDMGPAKVICVVMGGLGKTALSRKIFEESEDIRKNFPNCNAVITVQSQFHRI 157
 Db 485 --ELVDHLVENDSVQVVSVMGGIGKTTLARQVHF-HDIVRRHFDGFSWVCVQQFTR- 540
 Qy 158 ELLKDMIRQLLGPSSLDQLLQEL-----QGVVVQVHHLSBYLIELKBEKRYFVVLDDLWI 213
 Db 541 --KDV-----WQRIQLDLRPPYDEGIQIMDEYTLQELPELLESGRYLLVLDVWK 588
 Qy 214 LHDWNWINEIAPKNNKKSQIVITWVVDIAEKATASVLYHLDLFQMDAIYLLLRKT 273
 Db 589 EEDWDRIKAV-FP--HKRGWMLLTSRNEGLGLHADPTCFAPRPIILTPBQSWKLPFRIV 645
 Qy 274 KKNHEDMESKNKQKMYRIVNKGRLPLAITITIGAVLATKO-VSEWEKFFVEHLPSELEI 332
 Db 646 SSRDKTEP-KVDEAMGKEMVTCGGULPLAVKVGLGLAKHTVLEWKRVHSNIVTHIVG 704
 Qy 333 NPSL-----BALRRMVTLYNHLPSHLKPCFLYLSIFEPDEFIKRNLVGRWIAEGFVRP 387
 Db 705 KSGLSDDNSNVYVLSLYEDLPQMKHCFYLAHPEDYKIDVKILFNYYVAEGITP 764
 Qy 388 -KVGMTTKDVGESYFNELINRSMIORRGVAGIKTCRIHDIIRDTIVSISROENF--- 443
 Db 765 FHDGSTTQDTGESYLEELVRRNMVVBESYLSRIEYCOMHDMREVCLSKAKEENIRV 824
 Qy 444 VLLPMGDSGLVQEN---TRHIAFH--GSMCKTGLDWSIIRSLAIFGD-----RPSLA 493
 Db 825 VKVPTTSTTINAQSPCSRRLVHSGNALHMLGHKDNKKARSVLIIFGVEKFWKPGFQ 884
 Qy 494 HAVCPDOLRMRLVDLEVDVTLTIQKODRIALLCHLYLSIGYSSSYLSIPRSTGKIQIG 553
 Db 885 ---C---PLRLVLDLSYVQF-EGGKLPSISGDLIHLRFLSL-YEAGVSHLPSSLGNLKL 936
 Qy 554 LQTLNM--PSTYIAALPSEISKLQCLHTLRCSRKFVSDNFSLNHPMKCIINTICLPKVFT 611
 Db 937 LCLNLGVADRLLVHVPNLKEMQELAYLRPSM-----PAK----- 974
 Qy 612 PLVSRDDRATQIAELHMAWTSCHYKSGVVKPGIGKRLDLOVLEYVDIRRTSSRAIKEL 671
 Db 975 -----TKL-----ELGDLVNLESITNFTSKHGSVTDL 1001
 Qy 672 GOLSKLRKLGVMTNGSTKEKC--KILCAAIEKLSLOYL-----YVNAAGISDGTLECLD 725
 Db 1002 LRMTKLSLVNVIQSG---ECTFTLLSLRELNLSTLSPHDFOKYSVANHGGELLVLD 1057
 Qy 726 SISPPPLRLRLVLYGSLEMPNWIQLTHLKKIYLLRSKLKRGKTMILGALPNLMVLD 785
 Db 1058 FIH-----LKDLTLSMHLPRFPDQYRFPPLAHILWLGCRMEE-DPMPILEKLLHLSVY 1111
 Qy 786 LYRKAYLGEKLVFKTAGFNLRTLSYDLDQIREIRFEDGSSPOLSKIEIRFPLESGII 845
 Db 1112 LSSGAFIIGRMVCSKGGFPOLLAKMSYKXKELVEMRVBEGSMPCRLTLTDNCK----- 1165
 Qy 846 GIHLPLKELISLGVESKVLGALQLEGEVTRHPNHPVLRKREDSDHDLACDAEGSPVEV 905
 Db 1166 -----KLKQLPDGLK-YVTCLEKLEI-----RMKRE----- 1191
 Qy 906 EATDPLPEQEGESSQRDRKHSSWMFYQVMISSSISGRCPCFCGCAHLAVPR-RGADLRR 964
 Db 1192 -----W-----TERLIVIGGEDYKGLKHLCKLEKSRGAPLRR 1222
 Qy 965 -----LPLSSIA-----SHALDSSLSCGMN-CFNLTFSRDL 994
 Db 1223 SIDIIFELVPAKSIARFCVSESIHRRPVDTEQSLTKSMSRPRLLFALEYNKOLL 1278

Db	552	DINNPKLSLVVLDHDLWVENWKLGLGTSFTRKLLRLVLDLFPYDFEG--MKLPFGIGNLI	609
Qy	553	GLQTLNMPSTVIAALPSEISKLOCLHTLRCSRK----FVSNFSLNHPMKITNTICLPK	608
Db	610	HLRVLSLDQAKVSHLPISGLNMLLIYLNLDVDTFIFVPDVFVRMHELAYLK-----LP-	664
Qy	609	VFTPLVSRDRDRAIOIAELHMATKSCWYKSGFVKPGKIGKLRDIOVLVEYDIRTSSRAI	668
Db	665	-----LHMHKT-----RLSLRNLVKLETLYVFTWHS--	694
Qy	669	KELQOLSKLRKLGWMTNGSTKECKILCAATEKLSSLOLYLV--NNAGISDGTLECLD	725
Db	695	KDLGGMTRMLTAIRLFRVT--STETLSASISGLRNLLEYLYIVGTHSKQREBEGIV--LD	750
Qy	726	SISPPPLRLTLVLYGLEEMPNIQIOLTHLKYIYLLRSKLKECKTWLIIGALPNLMVLD	785
Db	751	FIH-----LKHLLDLIYMPROQHPFSLTFVK---LSECGLEE-DMPPILEKLHLHGVI	801
Qy	786	LYRKAYLGEKLVFKTGAPNRLTISYDLQDLREIFEDGSSPOLEKIEIRFCRLESGII	845
Db	802	LLKGSYCGRRMVCSGGFPQLKKLEIVGLNKEWEMLVEGSMPLLETLSILDCE-----	855
Qy	846	GIHLPRKLEISIG	859
Db	856	-----ELKEIPDG	863
RESULT 5			
T48899			
disease resistance protein rpp8 [similarity] - Arabidopsis thaliana			
C/Species: Arabidopsis thaliana (mouse-ear cress)			
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000			
C/Accession: T48899			
R/McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl			
Plant Cell 10, 1861-1874, 1998			
A/Title: Intragenic recombination and diversifying selection contribute to the evolution			
A/Reference number: 224999; MUID:99030193; PMID:9811794			
A/Accession: T48899			
A/Status: preliminary; translated from GB/EMBL/DBJ			
A/Molecule type: DNA			
A/Residues: 1-908 <MCD>			
A/Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AAC78631.1; PID:g3901294			
A/Experimental source: Columbia			
C/Genetics:			
A/Gene: rpp8			
A/Introns: 293/1; 342/1			
C/Function:			
A/Description: susceptible allele of a gene that promotes resistance to Peronospora para			
Query Match			
Best Local Similarity			
Matches			
Qy	74	DIRNQSARNVDEAELVGFSDSKKELL-EMIDTNANDGPAKVIVCGMGGLKTALSRKIF	132
Db	152	EIR-QTPDSSSDLVGVEQSKVELVGHVENDVH----QVWSIAGNGGIGKITLARQVF	206
Qy	133	ESBEDIRKPNPCNANITVSSQSFHRIELKDMIRQLLGFSSLDQLLEIQ---GKVV-VQV	188
Db	207	H-HDLVRRHFDGFAWVCVSOQFTQKHVWQ-----RILQELQPHDGDILQWDE	252
Qy	189	HLSEVLIIEELKEKRYFVVLDDMLHDMWNINEIAFPKNNKGSQIVITWNVDLAEKC	248
Db	253	YALQRKQLLEAGRYLVLDVDMVKEDVDIKAV-FPR--KRGWKMLTSRNEGVIHA	309
Qy	249	ATASLVVHLDFLOWNDAILTLIRKT--NKNHEDMESNKNQKQWVERIVNRCGRPLAILT	306
Db	310	DPTCLTFRASILNPEESWKLCEIRVFRPRDETEVRLDEEMANGKEMVTHCGGLPLAVKA	369
Qy	307	IGAVLATQK-VSEWEKYEYHLPS-----LEINPSLEALRMVTLGYNHLPSHLKPCFL	359
Db	370	LGGLLANKHTVPEWKRVFDNIGSQIVGSGWLDDN-SLNSVYRILSLSYEDLPTHLKHCFL	428

Qy	360	YLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMVTTKDVGESYFNELINRSIMQSRGVGIAG	419
Db	429	NLAHPPEDEISVTSVLYWAAEGIDY---GSTIEDSGEYVLELVRNLVADNVLWSM	485
Qy	420	KIKTCRTHDIRDITVTSIQENF---VLLPMGDSGLVQENTR-----HTAF	464
Db	486	QSKYCOMHDMVREYCLSKAKEENFLQIIIDPTCTTINAQSPSRSLRSHSGKAFILG	545
Qy	465	HGSMCKTGLDWSIIRSLAI-----FGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLLITQ	518
Db	546	HKN---KTK-----VRSLIVPRFEEDWIRASVFH-----NLTLRLVLDLSWKFEGCK	592
Qy	519	KQFDRIALLCHLKYLISYSSISYSLSPRSIGKLGQLTNMNPSTYIAALPSEISKLOCLH	578
Db	593	LPCS-IGGLIHLRYLSL-YEAKVSHLPSTWRNLKLLLYNL-----RVDTBEPFH	640
Qy	579	TLCSRKFVSDNFSNHPMKITNTICLPKVFVTLVSRDDRAIOIAELHMATKSCWYKSF	638
Db	641	VPNVLKEMIQLRY-LSLPLK-----MDDK-----TKL-----	666
Qy	639	GVKVPKGIGKLRDLQVLEYVDIRRTSSRAIKELGOLSKLRKLGWMTNGSTKEKC--KILC	696
Db	667	-----ELGDLVNLEYLGFSTQHSVVTDLURMTKRLYAV-----SLSERCNFETLS	713
Qy	697	AAIEKLSLQ-----YLYVNAAGISDGTLECLDSISSPPPL	733
Db	714	SSLRELNLLETNPLFSLETYVMDYMGFEFVLDHFIHLKQLGLAVRMS-KIPDQHPFPHL	772
Qy	734	LRTLVLVYGLSEMPNWI-EQIETHLKKIYLRSKLKEGKTMILGALPNLMVLDLYRKAYL	792
Db	773	VHLFLYICGMEEDPMPILEKLLHLKSVRLA-----RKAFL	807
Qy	793	GEKLVFTGAFPNRLTISYDLQDLREIFEDGSSPOLEKIEIRFC-RLESIGIIGIHLPL	851
Db	808	GSRMVCSGKGFQPCVIEISKESELEEWIVEEGSMCLRTLTIDDDCKKLKELPGLKYYT	867
Qy	852	RLKEISL	858
Db	868	SLKELKI	874
RESULT 6			
T12977			
hypothetical protein T6H20.240 - Arabidopsis thaliana			
C/Species: Arabidopsis thaliana (mouse-ear cress)			
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004			
C/Accession: T12977			
R/Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa			
submitted to the Protein Sequence Database, July 1999			
A/Reference number: 217586			
A/Accession: T12977			
A/Molecule type: DNA			
A/Residues: 1-847 <CHO>			
A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240			
A/Experimental source: cultivar Columbia; BAC clone T6H20			
C/Genetics:			
A/Gene: ATSP:T6H20.240			
A/Map position: 3			
C/Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat			
Query Match			
Best Local Similarity			
Matches			
Qy	73	EDIRNOSARN-----VDEAEL-VGFSDSKRL--EMIDTNANDGPAKVIVCGMGGLGK	124
Db	140	ENITNVVRQLRRAPPVDQELVGLDDVKILLVLLSDNEKD-KSVIISIFCMGGLGK	198
Qy	125	TALSRKIFESEEDIRKPNPCNANITVSSQSFHRIELKDMIRQLLGFSSLDQLLEOGLQK	184
Db	199	TALARKLYNS-GDKRRFDCRAWTVYSQYKTRDILIRIRS-LGIVSABE-MEKI--KM	253

Qy	185	VQVHLLSEYLIELKEKRYFVVDLDDWLHDMWINEIAPPKNNKKGSIQIVITTNVDL	244
Db	254	FEDEELVLYGLLEGKQNVVDDVDWDPAWESLKR-ALPCDH-RGSKVITITRIIRAI	311
Qy	245	AEKATASLVYHLDPLQNDATITLLRKTNNHDMESNNKMMQKVERIVNKCGRPLAI	304
Db	312	AEGVEGTYAHKLAFITFEESWTLFERKAFSNIKVD--EDLQRTGKEMVKCGGLPLAI	369
Qy	305	LTIGAVLATQVSWKEFYEHLPELEINPSLEALRRMVTGYNHLSHLKPCFLYISIF	364
Db	370	VWLSGLLSRKRTNEWHEVCASLWRLLKDN-SIH-ISTVFDLSFKEMRHELKCLPYFSVF	427
Qy	365	PEDEFEIKRNLVGRWIAEGFVRPVGMVTKDVGESYFNELNRSMIQRSRVGIAGIKTC	424
Db	428	PEDYEIKVEKLTHULLVAEGFTQDEEMMEDVACYIDELVDRSLKAERIE-RGKWNSC	486
Qy	425	RIHDIIRDITVISRQENFVLL--PMGDGSLDVQENTRHIAFHGSMSCKTGLDWSIIRSL	482
Db	487	RIHDLRLDAIKKAKELNFVNVYNEKHQSSDI CREVVHLMWYDYLCDRRVN-KRMRSF	545
Qy	483	AIFGDRPKSLAHAVCPD-QLRMLAVLOLEDVTFLL---ITQKDFDRIALLCHLKYSIGYS	538
Db	546	LFIGER-RGFGYVNTTNLKLRLVLANMEGLLFVSKNISNTLPDVGELIHLRLVGLIA-D	603
Qy	539	SSIYSLPRSICKLOQLTL----NMPSTYIAALPSEISKLOCL-HTLRCSRKFVSDNPSL	593
Db	604	TYVILPASISNRLFLTLDASGNDPFQY-----TTDLSKJTSLRHVI---GKFVGE----	652
Qy	594	NHPMKCITNTICLPKVTPLVSRDRAIQIAELHMAKSCWKYFGVKVPGIKGLRDLQ	653
Db	653	-----CLIG-----EGVNLQTLRSISYSWSK-----LNHELLRNLO	684
Qy	654	VLE-----YVDIRTSRAIKELGOLSKURKLGMVNTGSTKECKILCAAIEKLSSLOY	707
Db	685	DLEIYDHSKWVQRRVPLNFV---SFSKPKNLRLV-----KLEMRNFKLSSESRTTIGL	735
Qy	708	LYNNAAGISDGTLECLDSISSPPPLRLTLVLYG-SLEEMPNWIEQIHLKKIYLLRSKL	766
Db	736	VDVNF-----PSLESLLVGTTLLE-----	755
Qy	767	KEGKTMILIGALPNMLVLDLYRKAYLGEKLV-FKTGAPPNLRITLSI-----YLDQLRE	819
Db	756	---NSMPALQKLPLEDVLVKDCNYSGVKMISIAQGFGRLLKNLEMSMERGHGLD---E	809
Qy	820	IRPEDGSSPOLEKTEIRFCRLLE 841	
Db	810	LRTEEEAMPSLIKLVK-GRLE 830	

RESULT 7

T48898

disease resistance protein Rpp8 [validated] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000

C;Accession: T48898

R;McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl

Plant Cell 10, 1861-1874, 1998

A;Title: Intragenic recombination and diversifying selection contribute to the evolution

A;Reference number: 224999; PMID:99030193; PMID:9811794

A;Accession: T48898

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-906 <MCD>

A;Cross-references: EMBL:AF089710; NID:g3928861; PID:AAC83165.1; PID:g3928862

A;Experimental source: Landsberg erecta

C;Genetics:

A;Gene: Rpp8

A;Introns: 293/1; 342/1

C;Function:

A;Description: promotes resistance to Peronospora parasitica

Query Match 12.9%; Score 660.5; DB 2; Length 906;

Best Local Similarity 26.6%; Pred. No. 3.6e-34;

Matches	237;	Conservative	171;	Mismatches	311;	Indels	171;	Gaps	33;
Qy	33	GVEKDIWYLF-----RHVGSRNGG-----PVG-VVASGNQSQL-AIDSYAEDIRNQS	79						
Db	90	GVKQVRLARFLTRHKVASDIEGITKRISDVIGEMQSGFIQIIIDGVRSLSLQERQV	149						
Qy	80	ARNV-----DEAELVGFSDSKKRL--EMIDTNANDGPAKVICVVGWGGKGLKLTALSRI	131						
Db	150	QREIRQYTPDSSSDLVGVQSKVELGHLVENDVH---QVVSIAAGMGIGKTTTLARQV	205						
Qy	132	FESEBEDIKAPPCNAWITVSQSFHRIELLKDMIRQLLGPSSLDLQLLQELQ---GKVV-VQ	187						
Db	206	FH-HDLVRHFDGFAWCVSQOFTQKHVQ-----RILQELQPHDGDILQMD	251						
Qy	188	VHHLSEYLIBELKEKRYFVVDLDDWLHDMWINEIAPPKNNKKGSIQIVITTNVVDLAK	247						
Db	252	EYALQRLKFLLEAGKYLVLDDVWKCKEDWDVIKAV-FPR--KRGWKMLLTSRNEGVGIH	308						
Qy	248	CATASLVYHLDPLQNDATITLLRKT--NKNHEDMESNNKMMQKVERIVNKCGRPLAIL	305						
Db	309	ADPTCLTFRASILNPEESWKLCEIRVFPFRDTEVRLDDEEMAEKGMVTHCGGLPLAVK	368						
Qy	306	TIGAVLATQ-VSEWEKFYEHLPE-----LEINPSLEALRMVTLGYNHLSHLKPCF	358						
Db	369	VLCGLLANKHTVPWKRVSDNIGSQIVGSGCLDDN-SLNSVYRILSLSYEDLPTHLKHP	427						
Qy	359	LYLSIPPEDFEIKRNLVGRWIAEGFVRPVGMVTKDVGESYFNELNRSMIQRSRVGIA	418						
Db	428	LFLAHPEYSKISAYDLFNWAVEGIYD--GSTIQDSGEYVLEELVRNLVIADNRVLS	484						
Qy	419	GKIKTCRHDIIRDITVISRQENFVLLPMGDGSLDVQENTRHIAFHGSMSCKTGLDWSI	478						
Db	485	SHSKNCKMDHMDREVCLSKAKENFLQI-INKDPTSTSTINAQSPSRRLSIHSGKAPHL	543						
Qy	479	-----IRSLAI---FGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLLITQKDFDRIAL	526						
Db	544	LGHKNNTKVASLIVWDEDFGIRASVFN-----NLTLRVLDLYWVF-----	586						
Qy	527	LCHLKYSIGYSSSIYSLPRSICKLOQLTNMPSYIAALPSISIKLQCLHTLRCSRKF	586						
Db	587	-----EGGKLPSISIGGLIHLRLVSLFLAGVSHLPSTMRNLKLLYL-----	627						
Qy	587	VSDNFSLNHPMKCITNTICLPKVTPLVSRDRAIQIAELHMAKSCWKYSGVKVPGKI	646						
Db	628	---NLSVNN---KEPIHVPNVLKEM-----IQLRYLSLPLK-----KDDTK	663						
Qy	647	GKLRDLQVLEVYDIRRTSSRAIKELGOLSKLRKLGMVNTNGSTKEK--KILCAAIEKLSS	704						
Db	664	LELGDVLNLEFLFGFSTQHSVTDLLHMTKURLYAV---SLSRCHNPFETLSSSLRELXN	719						
Qy	705	LQVLYNNAAGISDGTLECLDSISSPPPL-----LRTLVLVYGSLEEMPVW	749						
Db	720	LETLYV-----LFSPEIFWVDYNGEFLVDHFIHLKELGLAVRMSKIPDQ	763						
Qy	750	IEQLTHLKLIYLRSLKSEKTMILIGALPNMLVLDLYRKAYLGEKLVFKTGAFNLRITL	809						
Db	764	HQLPPLHQAIIYICNRMBS-DMPMILEKLLHLKSVKLTFRKAFAGRMVYCSKGGTQCAL	822						
Qy	810	SIYDLDOLRIEIRFEPDSSPOLEKIEIRFC-RLESGIIGIHLPLRKEISL	858						
Db	823	EISEQSELEEWIVEEGSNMPCRLTITHDCEKUKELPDGLKYITSLKELKI	872						

RESULT 8

H96617

probable disease resistance protein P9K23.6 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: H96617

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De

anssen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96617
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-899 <SPO>
A;Cross-references: UNIPROT:Q9C646; GB:AEO05173; NID:g11034973; PIDN:AAG27128.1; GSPDB:C;Genetics:
A;Gene: F9K23.6
A;Map position: 1

Query Match 12.5%; Score 644.5; DB 2; Length 899;
Best Local Similarity 25.1%; Pred.No.3.ee-33;
Matches 228; Conservative 192; Mismatches 365; Indels 123; Gaps 30;

Qy	6	LSMARSLVGSASIKAAASAAADETSL-----LLGVEKDIMYLFPRHGVSNGSGPVVGMVASGN	62
Dd	83	VEMKGIM-KRIKEPASTINDRELASDIGGISKRISKVIQD--MQSFQ--VQIIITDGS	137
Qy	63	QSCLAISDAEDIRNQSNRVDEALVGFSDSKKRLEMTDTNANDGPAKVICVWGGL	122
Dd	138	RSSHPLQERQRMHRTPSRD--SENDFVGMENVKLVGYL---VEKDDYQIVSLTGWGL	193
Qy	123	GKTALSRSKIPESEDIRKNFPCHAWTVYSOSFHRIELDKDMIRQLLPSSLDQLLOEQ	182
Dd	194	GKTTLARQVP-NHDDVVKDRFDGFAMSVSQEFTRISVMOTILQNLTSKERKD----EIQN	248
Qy	183	KVVQVHHLSYLIEELKEKRYFVLVDLWLTHDWMNINEIAPPKNKGSGQIVITWNV	242
Dd	249	MKEADLH---DDLFRLESSEKTLVLDDIWEEDWDLIKPI-PPP--KKGWKVLLTSRTE	302
Qy	243	DLAEKATASLVYHLDFLOMNDAITLL--LRKTNKHEDMESNNQMOMVERINVKGRL	300
Dd	303	SIAMRGDTTVISPCKCLSDPSWTLPQSTAMPKRTSEPKVDEEMENMGKMCHKCGGL	362
Qy	301	PAILTTIGAVLATK-QVSEWEKFEYHLPSEL--EINPSLEALRRWVTLYGNYHLP SHLKPC	357
Dd	363	SLAVKVLGGGLAAKYTHLDWKRISENESHIVERTSGNNSSI DHVLSVSFEELPNYLKHC	422
Qy	358	FVLISPEPDEFKRNRLVGRWTAEGFV--RPKVGMTTKDVGSYFNELNRNMIOKRSRV	415
Dd	423	FLYLAHPDPBEDHDVEKLHYWAABGISERRYDGETIRTGDSYTEELVRNNVTSERD	482
Qy	416	GIAGKITCRHDIIRDITVISIQRQNFVLL-----PMGDGSDIJVOEN--TRHI	462
Dd	483	VMTSRPETCLRHDMMREICLPKAKEENFLQIVSNHSPTSNPQTLGASRRFVLENPTLHV	542
Qy	463	AFHGSMECKTGLDWSITRSIAI-----FGDRPKSLAHAVCPDQLRMLRVLDLEDVTFLITQ	518
Dd	543	ERYKN-----PKLRSLVWVYDDIGNRWMLSGSIF--TRVKLLRVLDLVAQXF----	589
Qy	519	KDPRIALLCHLYLSIGYSSIVLSPRSITGKLOGLOTLANMPSTYAALPSETSKLCQLH	578
Dd	590	-----KGGKPSD LGKL IHLRYLSLKOAKVSHLPSSLRNLVLLI	628
Qy	579	TLRCSRKFVSNFNSLNHPMKCITNTICLPKVFTPLVSRDDRRAIQIAB-LHMATKS CWYKS	637
Dd	629	YLDIRTDFTD-----IFVPNVFMGM--RELRYLELPRFMHEKTKL-----	666
Qy	638	FGVKVPGIKGLRDQLVLEVVDIRTSRAIKELGQLSKURLGWMGTNGSTEKKCILCA	697
Dd	667	-----ELSNELEKALEANFSTKSSSLEDLRGMVRLTRLVIIISLSECT--SLQTLISA	714
Qy	698	AIEKLSLIQ-YLYVNAAGISDGGTLECLDSISPPPLRLTLVLVGSLEEMPNIQHTL	756
Dd	715	SVCCLRHLRHNFKMENAGVNMRGEERVMVLDFT-----YLKKLTLTISIENPRUPKTIQHLPSHL	770
Qy	757	KKIYLLRSKLKGEKTMILILGALPNLMVLDIYRKAYLGEKLVFKTAGFPNRLTSLSYDLOQ	816

Qy 557 LNPSTYIAALPSRISIKLOLTLRCSRKFVSDNFSNLNHPMKCTNTICLPKVFPLVSR 616
Db 612 LEV-STY-----SEPIYDTIDL-RKLT-----SRHVIGQVGGELLI----- 647
Qy 617 DDRAIQIAELHMAKSCWYKSGVKGKGLRDQLVLEVDIRRTSSRAIKELGOLSK 676
Db 648 -GDAANLQTLRFIISDSNWK-----LKPPELLNLRLDLIYEDYD-EDFRRVSVSWASLTK 701
Qy 677 LRKLGVTNGSTKEKCKILCAAEIKLSLSQVLYNNAAGISDGGTLECLDSISSPPPLRLT 736
Db 702 LRSRLVL-----KLYYL-----RLESEEAVERS-----T 724
Qy 737 LVLYGSLEEMPNWIEQLTHLKKIYLLRSKKEGKTMILLGALPNLMVLVLYRKAYLGEKL 796
Db 725 DVISLSLESVT--LEGITF-----EEDMPFLQKMPRLDELILHLCNYSGGKM 770
Qy 797 VFKTGAFPNRLTLIYDLQDLREIRFEDGGSPQLEKIEIRCRLESIGIIGIHLPRLKEI 856
Db 771 SVSQGGFGLRKLQIFHNSLDELQIEEAMPNLEIKITPEVKYKLI-----PNRLRA 825
Qy 857 SLGYES 862
Db 826 CMSYES 831

RESULT 10
T45590
hypothetical protein F12A12.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Mar-2000
C;Accession: T45590
R;Choiane, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A;Reference number: 223008
A;Accession: T45590
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-835 <CHO>
A;Cross-references: EMBL:AL13314
A;Experimental source: cultivar Columbia; BAC clone F12A12
C;Genetics:
A;Map position: 3
A;Note: F12A12.50
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Qy 400 YFNELINRSM---LQSRVGIAGKIKTKRIHDIRITVTSISROENFVLLPMWGDGSLVQ 456
Db 463 YIEELIDRSLEAEVRRR---GKVMSCRIHDLRLDVAIKKSKELNF-----VN 507
Qy 457 ENTRHIAFHGSMSCKTGL-----DWSIIRSLAIFGDRPKSLAHAVCPD--QL 501
Db 508 VYNDHVAQHSTTCRREVHHQPKRYSEKKNKMRSEFLYFGE-----FDHLVGLDPETL 563
Qy 502 RMLRVLDLEVDVLIITOKDFRIALLCHLKYLISI-GYSSSIYSIPRSIGKQGLQTLNMP 560
Db 564 KLLRVLDLFGSLWL-----PFKINGDLIHLRYLGDGNSINDFDIAAIIKSLRFLQTL--- 615
Qy 561 STYIAALPSEISKLOLTLRCSRKFVSDNFSNLNHPMKCTNTICLPKVFPLVSRDDRA 620
Db 616 -----FVSDNY-----PIETIDLRKL----- 632
Qy 621 IQIAELHMAKSCWYKSGVKGKGLRDQLVLEVDIRRTSSRAIK-ELGOLSKLRK 679
Db 633 -----TSLRHVIGNFFGGL-----IGDVANLQTL--TSISFDSWNLKPEL--LINLRD 678
Qy 680 LGVMTNGSTKE-KCKILCAAEIKLSQVLYNNAAGISDGGTLECLDSISSPPPLRLT- 737
Db 679 LGISEMSRSKERRVHVSWASLTKLESRLVLT-ATPTEVHLSLESEEAVERSMOVSRSLE 737
Qy 738 --VLYG-SLEEMPNWIEQLTHLKKIYLLRSKKEGKTMILLGALPNLMVLVLYRKAYLGE 794
Db 738 SVTLVGITPEEP-----MPFLQKMPRLDELILHLCNYSVGK 773
Qy 795 KLVFKTGAFPNRLTLIYDLQDLREIRFEDGGSPQLEKIEIRFCRLESIGI 845
Db 774 MSVSEQ-FGLRLKLDLL-WRSLDELQIEEAMPNLEIELSUSKRETKLI 822

RESULT 11
G96617
Probable disease resistance protein P9K23.7 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G96617
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G96617
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-900 <STO>
A;Cross-references: GB:AE005173; NID:g11034962; PIDN:AAG27117.1; GSPDB:GN00141
C;Genetics:
A;Gene: P9K23.7
A;Map position: 1
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 12.3%; Score 634; DB 2; Length 900;
Best Local Similarity 25.3%; Pred. No. 1.8e-32;
Matches 220; Conservative 163; Mismatches 330; Indels 156; Gaps 29;
Qy 33 GVEKDIWYLF--HGVRSGNGGPPVGVGVASGNQSLAIDSVAEDIRNQSRNVDEAEVLG 90
Db 114 GISKRISKVIQDMHSGF-----VQQMISDGSOSHLQEREMRQTFSGRY-ESDFVG 166
Qy 91 FSDSKKLELMDITNDANGPAKVICVVGMLGKLTALSRKIFESEEDIRKNFPCNMITV 150
Db 167 LEVNVKLVGYL---VEEDIQIVSVTGMGLGKTLTLARQVF-NHEDVKHQDFRLAVCV 222
Qy 151 SQSFHRIELKDMIRQLLPSSLDQLLQELQGVVQVHHLSEYLIBELKEKRYFVVLDD 210

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Db 223 SQEFTRNQVMQILONLTSRETKDEILQ-----MEEAELHDLFOLLTSKSLIVFDD 275
Qy 211 LWILHDNWNINEIAFPKNNKKSQIVITWNVDLAEKATASLVYHLDPLQMN---DAIT 267
Db 276 IKWEDDGLNIPPIPPKKE-----TIAMHGNNRYVNFPECLT 313
Qy 268 LL-----LRKTNKHEDMESKNQKQKVERIVNKGCRPLAILITIGAVLATQV-SE 318
Db 314 ILSWILFORIAMPRVDESEFKVDKEMGMQKMIKYGGLPLAVKVLGGLAAKYTFHD 373
Qy 319 WEKPYE----HLPSELEINP-SLEALRRMVTGLYNNHLPKPCFLYLSIFPEDFEIKRN 373
Db 374 WKRLSENIGCHIVGRTDFSGNNSSVHVLSLSPEELPSVLKHCFLYLAHFPEDHNIKVE 433
Qy 374 RLVRGRTAEGFVRPK--VGMTTKDVGESYFNNELNRSMIQBSRVGIAGKTKCRIHDIIR 431
Db 434 KLSYCAAGGLEPRHYHGOTIRDVGESYIEELVRRNNVIAERDVTTLRFEACHLHDMR 493
Qy 432 DITVSIHQENFV---LLPMGDSGLVQENTRHIA-----FHGSMCKTGLDWSIIRSL 482
Db 494 EVCLLKAEENFVOIASILPPTANSQYPGTSRRRFVSQNPPTLHVRDINNPKQSL---L 550
Qy 483 AIFGDRPKS---LAHAVCPDQRLMRVLDDLDVDTFLITQKDFDRIALCHLKLYLSIGYSS 539
Db 551 IVWENRRKSKWLLGSSFI--RLELRVLVDLYKAF-----583
Qy 540 STVSLPSRSGKLOGLQNTNMPSTVIAALPSEISKLOCLHTLRCRKVFSDNFSLNHPKC 599
Db 584 EGRNLPISGIGKLIHLRYNLDLARVSRPSSGLNRLRLIYL-----DIN-----627
Qy 600 ITNTICLPKVTPLVSRDDRAIQIAELHMAKTSQWYKSGVKVPGKIGKLRDLQVLEVD 659
Db 628 ----VCKTSLFVPCNLMGMHELRYLRLPFTSK-----EIKLGICNLVNLETNFS 675
Qy 660 IRTSSRAIKELGOLSKRLKLGVTNGSTKEKCK-ILCAAIEKLSLQYLYVNAAG---714
Db 676 ---TENSLEDLRGMVSLRTL---TIGLFKHI SKETLFASTLGRHLENLSIRTPDGSSK 729
Qy 715 ----ISDGTLECLDSTSSPPPLRTVLVYGSLEEMPNWIEQLTHLKVIYLRSLKKEGK 770
Db 730 FKXIMEDGVLDAITH-----LKQLNRLYMPKLPDEQHPFSPHLTSLSDGCLVE-D 780
Qy 771 TMLILGALPNMVLDIRKAYLGRKLVFKTAGFAPNRLATLSIYDLDQLEIRFEFGSSPOL 830
Db 781 PLPLEKLELKEVRLDFRACGRMVSSDGGFPQLHRLIYIWLGAEMEIVIEGSMFRL 840
Qy 831 EKIEIRFC-RLESIGIIGI IHLPRLKEISL 858
Db 841 HTLTWNCQKLKQLPDGLGRFIYSIKOLDM 869
```

RESULT 12

T51186
resistance protein Rpp13 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
R/Accession: T51186
R/Bittner-Biddy, P.D.; Crute, I.R.; Holub, E.B.; Beynon, J.L.
Plant J. 21, 177-188, 2000
A/Title: Rpp13 is a simple locus in Arabidopsis thaliana for alleles that specify downy
A/Reference number: 225333
A/Accession: T51186
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-820 <BIT>
A/Cross-references: UNIPROT:Q9M667; EMBL:AF209732; PIDN:AAF42832.1
C/Genetics:
A/Experimental source: cultivar Neiderzens
A/Gene: RPP13
A/Map position: 3
C/Superfamily: disease resistance protein Rps2; leucine-rich alpha-2-glycoprotein repeat

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Query Match 12.3%; Score 631.5; DB 2; Length 820;  
Best Local Similarity 27.7%; Pred. No. 2.2e-32;  
Matches 225; Conservative 143; Mismatches 295; Indels 149; Gaps 34;  
Qy 44 HGVG---RSGGPPVGMVAGSNQSCLAIDSAYEDIRNQSARNVDEAE-LVGFSDSKRLLL 99  
Db 129 YGIGGLKEPQGG-----GNTSSLVRQL-----RRARSVDQEEVVVGLADADAKILL 174  
Qy 100 EMIDTNDANDGPAKVICVVGGMGLGKTALSRKIPESBDIRKNPFCNAWITVQSQFHREL 159  
Db 175 EKL-LDYDEKRRFIISIFGMGLGKTALARKLYNS-GDVRRFERYRAWTVYSQYTKGDI 232  
Qy 160 LKDMIRQLLQSSLDQLLOBLQKVVQVHVHLSYLLIEELKEKRYFYVLDLTLHDWNW 219  
Db 233 LMRIISLIGTSG-----EELEKIRMFABELEVHLHGLLEGKLYLVVDDIWEREAWES 287  
Qy 220 INEIAPPNNKKSQIVITWNVDLAEKATASLVYHLDPLQMNDAITLLLRKTNKHED 279  
Db 288 LKR-ALPCNH-EGSRVITITRIKAVAEGLDGRFYAHKLRFLTFFESWELFEQRAFRNIQ- 344  
Qy 280 MESKNQKQKVERIVNKGCRPLAILITIGAVLATQVSEMEKFYEHLPSLEINPSLEAL 339  
Db 345 -RKDEDLTKTGKEMQVCKRGPLCIVVLAGLLSRKTPSEWNVCSNLWRRLLK-DDSLHVA 402  
Qy 340 RRMVTLGYNNHLPKPCFLYLSIFPEDFEIKRNRLVGRMIAEGFVRPKVGMITTKDYGES 399  
Db 403 PIVFDLSFKELRHESKLCFLYLSIFPEDYEIDLEKLRLVAGCFIQDEEMMEDVARY 462  
Qy 400 YFNELINRSM---IQRSRVGIAGIKTKCRIHDIIRDTVISROENFVLLPMGDSGLVQ 456  
Db 463 YIBELIDRSLEAVRRER---GKVMSCRIHDLRLDVAIKSKELNF-----VN 507  
Qy 457 ENTHTIAFHGSMCKTG-LDWSI-----IRSLAIFGDRPKSLAHAVCPDQLRMLRVL 507  
Db 508 VYNDHVSQHSSTTCRRQVNVHQIKRFARNKRMRSFLYFGEL-KPLVR-LDVEKLUKLRLVL 565  
Qy 508 DLEDVTFLIQKQDFDRIALCHLKLYSI-GYSSSIYSLPRSIGKLOGLQNTNMPSTVIAA 566  
Db 566 DLEALL-----GFPASNGDLIHLRYLRFDFGSLRVFDIAAISKSRLQTLD--ADHVP 618  
Qy 567 LPSEISKLOCLHTLRCRKVFSDNFSLNHPKCITNTICLPKVTPLVSRDDRAIQIAEL 626  
Db 619 IYDTID-----LRKET---SLRH-----VICKFVGELLIGD--AANLQTL 653  
Qy 627 HMAKTSQWYKSGVKVPGKIGKLRDLQVLEIRDTSSRAIK-ELGOLSKRLKLGVTN 685  
Db 654 RSISSDSWSK---LKHELLI-NLRDLEI--YEDYNKSKERRVTVSWASLTKRLSLRV--- 704  
Qy 686 GSTKECKILCAAIEKLSLQYLYVNAAGISDGTLECLDSTSSPPPLRLTLVLYG-SLE 744  
Db 705 -----LKLVDRLRYLSESE-----EAVRSMQVISLESVTLVGITFE 743  
Qy 745 EMPNWIQLTHLKVIYLRSLKKEGKTMILGALPNLMVLDIRKAYLGEKLVKPTGAPP 804  
Db 744 EDP-----MPFLQKMPRLLEDLIFENCYDYGWGMVSEQGF 779  
Qy 805 NLRTLSTYDLDQLEIRFEFGSSPOLKEIR 836  
Db 780 RLRLKLLF-INRLDELQIEEAMPNLIELVQ 810
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RESULT 13

A86243
hypothetical protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R/Accession: A86243
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86243
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-821 <STO>
A:Cross-references: UNIPROT:004093; GB:AE005172; NID:gi931650; PIDN:AAB65485.1; GSPDB:GN
C:Genetics:
A:Map position: 1

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Query Match      12.2%; Score 628; DB 2; Length 821;
Best Local Similarity 27.5%; Pred. No. 3.7e-32;
Matches 215; Conservative 152; Mismatches 292; Indels 124; Gaps 28;

Qy 73 EDIRNQARNVDEAEVLGFSKRLLEMDITNANDGPAKVICVGMGLGKLTALSRKIP 132
Db 126 KEIR-QTFANSESEDVGVESVEALAGHLVENDY---IQVVISGMGIGKTLARQVP 181

Qy 133 ESEEDIRKNFPCNAWITVSQSFHRIELKDMIRQLLGPSSLDQLLQELQGRKVVVQVVRHLS 192
Db 182 H-HDMVQRHFGFAWVFVSQFTQKHVWQ-RIWQELQPQGD-----ISHMD 226

Qy 193 EYLIEE-----LKEKRYFVVLDDWLHDMWNWINEIAPPKNKKGSIQVITVNWVDLAEK 247
Db 227 EHILQGLFKLLETGRVYLVDVWKEBDMDRIKAV-FPR--KRGWKMLLTSRNEGVGIIH 283

Qy 248 CATASLVYHLDPLQWNDATITLLRKTNKNHEDMESNKNQKQWVERIYNKCCGLPLAILTI 307
Db 284 ADPKSFGKTRILTPESWKLCEKIVFHRRDETGTLSDEAMGKEMVTCGGLPLAVKL 343

Qy 308 GAVLATKQ-VSEWEKFEY---HLPSELEINPSLEALRRMVTYTLGNHLPShLPCFLYLS 362
Db 344 GGLLATKHTVPEWKRVYDNIPLHLAGRSSLDNLNSIVVLSLSYENLPCLKHCFLYLA 403

Qy 363 IFFDEFEIKRNLVGRWIAEGFVRPK-VGMTTKDVGSYFYNELINRSMIOBSRVGIAGKI 421
Db 404 HFPEYIEHVXRLFNLYAAEGIIITSSDDGTIQKGEDYLEELARRNMITIDKNVFLRK 463

Qy 422 KTCRIHDIIRDIWISIQENFV-LLPMGDGSDLVQ-----ENTRHIAFGSMSCKTGLDW 476
Db 464 KHCQMDHMRREVCLSKAKEENFLBIFKVSTATSAINARSLSKRSLVHGG-NALPSLGQ 522

Qy 477 SI-----IRSLAIFGDRPKSL---AHAVCPDQLRMLRVLDLEDVTLITQKDPDRIALLCHL 530
Db 523 TINKVRSLLYFAFEDEFECILESTTPCPSLPLRLVLDLSRVKF-----566

Qy 531 KYLSIGYSSSYISYPSRIGKLGLOTLNMPSTYIAALPSEISKLOCLHTLRCSRKFVSDN 590
Db 567 -----EGGKLPPSSIGDLIHLRFLSLHRAWISHLPPSSLRNLKLLYL-----N 608

Qy 591 FSLNHPMKCINTITCLPKVFTPLVSRDRAIQI-AELHMAKSCWYKSFVKVPKGIKGL 649
Db 609 LGFN-----GMVHVNVLKEM---QELRYLQLPMSMDTKL-----EL 644

Qy 650 RDLQVLEYVDIRRTSSRAIKELGOLSKRLKGV-MTNGSTKECKKILCAATEKLSSLOYL 708
Db 645 SDLVNLESIMNFTKYASVMDLHMTKLELSLFTDSS-----DTLSSSLGQRLSLEVL 700

Qy 709 YV-----NAAGISDGG--TLECLDSISGPPPLRLTLVLYGSLEEMPNWIEQTHLKKIYLL 762
Db 701 HLYDQRPVAYHGGIEVLNCIH-----LKELEIAHMPRPDQVLPFPHLSHYLVW 752

Qy 763 RSKLKEGKTMILGALPNLMVLDLYRKAYLGEKLVFTGAPNLRITLSYDLDQIREIRP 822
Db 753 CCSMBE-DPIPIERLLHLKSVILTFGAFVGRMVCSGGPQLCFLKLELEEBEWIV 811

Qy 823 EDG 825
Db 812 EEG 814
```

RESULT 14

B96538

hypothetical protein F14I3.19 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: B96538

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huiztar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafci, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96538

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-839 <STO>

A:Cross-references: UNIPROT:Q9SK38; GB:AE005173; NID:95734781; PIDN:AAD50046.1; GSPDB:GN

C:Genetics:

A:Gene: F14I3.19

A:Map position: 1

Query Match

Best Local Similarity 11.7%; Score 603.5; DB 2; Length 839;

Matches 222; Conservative 155; Mismatches 285; Indels 245; Gaps 32;

Qy 5 VLSMARSL--VGSIAI-----SKAASAADETSLLIGVEKDIWYLFPHGVGRSNGPVPV 55

Db 101 ILNEAVSLHVSGBIRBITSRLSKIAAAMLD-----FGIKESM-----138

Qy 56 GWASGNQSCLAIDSVAEDIRNQSRNVDEAEVLGFSKRLLEMDITNANDGPAKVIC 115

Db 139 -----GREGLSLSDLRE--QRQSFPPVVEHNLVGLSQSLEKLVN--DLVSGGSKLRVTS 189

Qy 116 VVGMGLGKLTALSRKIPESBEDIRKNFPCNAWITVSQSFHRIELKDMIRQLLGPSSLDQ 175

Db 190 ICGMGLGKLTAKQIFHHK-VRRHDFRFAWVVSQDCRRHVVQDIFNL-----S 241

Qy 176 LLOELQKVVVQVHLSLEYLIBELKEKRYFVVLDDWLHDMWNWINEIAPPKNKKGSIQ 235

Db 242 YKDNQRILSLRDBQLGEELHRLKRNKCLIVLDLWGDADWCLKHV-FP--HETGSEI 298

Qy 236 VITTNVVDLAEKCATASLVYHLDPLQWNDATITLLRKTNKNHEDMESN--KMQKQWVERI 293

Db 299 ILTTRNKEVALYADPRGVLPHEPQLLTCEESWELLEKI SLSGRENIEPMLVKQMBEIGKQI 358

Qy 294 VNKGRPLAILITIGAVLATKQV-SEWEKFFVEHLPSLEINPSLEALRRMVT-----LGY 347

Db 359 VVRCGGLPLAITVGLGLLATKSTWNEQRCENTIKSVYSGSGSSNGSKNMLVADVLCUSY 418

Qy 348 NHPLSHLKPCFLYLSIPFDEFKIKRNLVGRWIAEGFVRP-----KVGMTTKDVGESYFNE 403

Db 419 EYLPPHVKQCFLYFAHPYEDYEVHVGTLVSVYCIAEGMVPVKHTEAGTTVEDVG DYLEE 478

Qy 404 LNRSMIQRVRGT-AGKIKTCRIHDIIRDIWISIQENFVLSQENFVLLPMGDGSD-----LV 455

Db 479 LVKRSVMVVRDIDVTSEVMTCRMHDLMRVCLQAKQESFVQVIDSRDQDEAEAFISLS 538

Qy 456 QENTRHIA--PHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVT 513

Db 539 TINTSRRLSVQLHG-----GAEHHIKSLs---QEPB-----REIDKREGT 575

Qy 514 FLITQK----DFDRIALLCHLKYLSIGYSSSIYSLPRSIGKLGLOTLNMPSTYIAALPS 569

Db 576 YIIYWKLVDDYSRL-----VREKATVYS-----599

Qy 570 EISKLOCLHTLRCSRKFVSDNFSLNHPMKCINTITCLPKVFTPLVSRDRAIQIAELHMA 629

Db 600 ----- 599
Qy 630 TKSCWYSGVGVKPGIGKLRDLQVLEYVDIRRTSSRAIKELGQLSKRLKGVMTNGSTK 689
Db 600 -----KHLDPKTKLDLSTLRNLQQLWDPFVGKCNPR---DLLAMTSLRLSI--NLSSQ 648
Qy 690 EKCKILCAAIK-LSSIQLYLVNAGISDGGTLECLDSISSPPL-----LRTL 737
Db 649 NTDFPVVSSLSKVLKRLGLTN-----VPCPEML---PPVDVTQLVSAFTNLCEL 696
Qy 738 VLYCSLEMPNWIQLTHLKKIYLLRSKLEKGTMLILGALPNLWLDLRKAYLGEKLV 797
Db 697 ELFLKLEKLPGEQSFSSDLGRLWQCGLVDDPFM-VLEKLPNLKILQLFEGSVGSKLC 755
Qy 798 FKTCGAFFNLRTLSYDLDLREIRFEDGSSPOLKIEIRFC-RLESGIIGIHLPLRKEI 856
Db 756 CSK-----NLENLEWTVEDGAMWRLVTVELKCNKLSVPEGTRFLKNLQEV 803
Qy 857 SLGYESK 863
Db 804 EIGNRTK 810

RESULT 15
T08416
Disease resistance protein homolog F18B3.230 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 26-May-2000
C:Accession: T08416; S71195
R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub
submitted to the Protein Sequence Database, May 1999
A:Reference number: 216409
A:Accession: T08416
A:Molecule type: DNA
A:Residues: 1-852 <QE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.230
A:Experimental source: cultivar Columbia; BAC clone F18B3
R:Rouse, D.T.; Heazlewood, J.L.
submitted to the EMBL Data Library, January 1995
A:Description: Incomplete sequence of an Arabidopsis gene with similarities to myosin he
A:Reference number: S71195
A:Accession: S71195
A:Molecule type: DNA
A:Residues: 'LKNNPFILWLLFRYSRWLIDFMVKQSDDTNRLNCLVIVYQLEIFLEVAGSEK',1-36,'K',38-128,131
A:Cross-references: EMBL:U19616; NID:G699494; PID:G699495
C:Genetics:
A:Gene: ATSP:F18B3.230
A:Map position: 3
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 11.7%; Score 601.5; DB 2; Length 852;
Best Local Similarity 25.0%; Pred. No.2e-30;
Matches 213; Conservative 150; Mismatches 297; Indels 191; Gaps 32;

Qy 28 TSLILGVKEQDIWYLFHGVGRSNGSPVGVWASGNQSLAIDSVAEDIRNQSARNVDEAE 87
Db 123 TKIKSQVEPYPEFITPNSVGRDNG-----TDRWSPV-----YDHTQ 159

Qy 88 LVGFSDSKRLLEMDTNDANDPAKVICVGMGGLGKTALSRKIPESEEDIRKNPFCNAW 147
Db 160 VVGLGDKRKIKEWL-FRSNDSQLIMAFVGMGGLGKTTIAQEVF-NDKEIEHRFERRI 217

Qy 148 ITVSQSFHRIELLKDMIRQLGSPSLDQLLOELQGVVQVHLSVIELKEKRYFV 207
Db 218 VVSQTFTEEQIMRSILRN-LGDASVGDDIGTLRKI-----QQYLL-----GKRYLIV 265

Qy 208 LDDLWILHDWN--WINEIAPFPKNNKGSQIVITTVNVDLAEC-ATASLVVHLDLQWMD 264
Db 266 MDDVW---DKNLSWDKIYQLPRGQGSVIVTTSSSEVAKRVQARDKTHRPPELLSPDN 322

Qy 265 AITLLLRKTNKQHEMESNKQMKQKRIYVKNCGRLPLAULTIGAVLATQ--VSEWEKF 322
Db 323 SWLLFCNVAFANDGTCERPELEDVGKEIVTKCKGLPLTIKAVGGLLLCKDHVYHEWRI 382

Qy 323 YEHLPSLEINPS-LEALRMVTLGYNHLPKPCFLYLISIPPEDEFEIKRNLVGRWIA 381
Db 383 AEHFQDELRGNTSETDNVMSLQLSYDELPSHLKSCILTLSLYEDCVIPKQQLVHGWI 442
Qy 382 EGFVRPKVGMTTKDVGESYFNEINRSMIORSRVGIAGKIKTCRIHDIIRDITVISIROE 441
Db 443 EGFVWRNGRSATESGSDCFSLNRLCIIEVDKTYSGTTITCKIHDMVRDLVIAKDD 502
Qy 442 NFVLLPBGDGLVQENTRIHAFHGS-----SCKTGLOWSIIRSLA-I 484
Db 503 SF-----SNPEGLNCRHLGISGNFDEKQIKVNHKLRGVVSTTKTEVKNLMSDLAKK 554
Qy 485 FGDPRKSLAHAVCPDQRLMLRVLDDLEVDVTLITOKD-FDRIALCHLKLYLSIGYSSSIYS 543
Db 555 FTD-----CKYLRVLDDISKSIFDAPLSEILDEIASLQHLACLISLNTPLIQ 601
Qy 544 LPRSIGKLOGLQTLNMPSTYIAALPSEISKLOCHLTLRCSRKFVSDNPSLNHPMKCITNT 603
Db 602 FPRSMEDLHNLQILD-----ASYQNKLKQLQ-----PCIV-- 631
Qy 604 ICLPKVFTPLVSRDDRAIQIAELHMAKSCWYKSGVGVKPGIGKLRDLQV-LBYVDIR 662
Db 632 -----LFRKLLVLD-----MTNCGSLECF-----PRGIGSLVKLEVLGFKPARS 671
Qy 663 TSSRAIKELGQLSKRLKLV-MTNGSTKRCCKILCAAIKELSSLYLVNAAGISDGGTL 721
Db 672 NNGCKLSEVKNLTLNRLKLGSLTRGDOIEBEEL--DSLINLSKLMSISINCYDSYGDDLI 729
Qy 722 ECLDSISPP-----PLLRTL-VLYGSLEEM--PNWIEQLT 754
Db 730 TKIDALTTPPHQLHELSSLQFYPGKSSPSWLSPHKPLMLRYMSICSGNLVYQMQEPFGNENT 789
Qy 755 HLAKIYLLRSKLEKGTMLILGALPNL-MVLDLYRKAYLGEKLVFKTGAPPNLRATLSYD 813
Db 790 HWR-----IEG---LMLSSLSLDDMDWEVLQQ-----SMPYLKRTVTANW 825
Qy 814 LDQLREIRPED 824
Db 826 CPELESFAIED 836

Search completed: February 9, 2005, 08:54:50
Job time : 33.7041 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 08:34:07 ; Search time 121.246 Seconds
(without alignments)
4215.017 Million cell updates/sec

Title: US-10-656-394A-12
Perfect score: 5137
Sequence: 1 MAETVLSMARSLVGSALSKA.....LSGMNCFNLFSRDMLLVPA 998

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

- 1: uniprot_sprot.*
- 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2319	45.1	1014	2	Q84KC5 hordeum vul
2	2184	42.5	1007	2	Q9LW77 oryza sativ
3	1172	22.8	1485	2	Q69U98 oryza sativ
4	1101.5	21.4	1226	2	Q84Q10 oryza sativ
5	1101.5	21.4	1226	2	Q9MBF2 oryza sativ
6	1068	20.8	953	2	Q65159 oryza sativ
7	1043.5	20.3	954	2	Q65172 oryza sativ
8	1042	20.3	1169	2	Q6WSR3 oryza sativ
9	1040.5	20.3	1169	2	Q947C8 oryza sativ
10	1033	20.1	1251	2	Q9ZNV6 oryza sativ
11	1023.5	19.9	1494	2	Q8H5A7 oryza sativ
12	1005	19.6	935	2	Q9LJ13 oryza sativ
13	982.5	19.3	989	2	Q65170 oryza sativ
14	987.5	19.2	963	2	Q69MT5 oryza sativ
15	965	18.8	1011	2	Q9LJ10 oryza sativ
16	963	18.7	894	2	Q6ZB12 oryza sativ
17	948	18.5	1280	2	Q6Z574 oryza sativ
18	932.5	18.2	1205	2	Q84Q14 oryza sativ
19	914	17.8	774	2	Q84MG3 oryza sativ
20	914	17.8	917	2	Q6PKX5 prunus pers
21	912	17.8	1404	2	Q9LJ11 oryza sativ
22	908	17.7	906	2	Q7X119 oryza sativ
23	895.5	17.2	949	2	Q6Z397 oryza sativ
24	884	17.2	947	2	Q6YVX3 oryza sativ
25	883.5	17.2	926	2	Q9ZSH1 oryza sativ
26	880.5	17.1	921	2	Q9XHG0 arabidopsis
27	873.5	17.0	945	2	Q6EST1 oryza sativ
28	869.5	16.9	927	2	Q7XH20 oryza sativ
29	869.5	16.9	927	2	Q9AYH9 oryza sativ
30	869	16.9	927	2	Q9ZSH2 brassica na
31	866.5	16.9	1006	2	Q6ZBT2 oryza sativ

32	859	16.7	907	2	Q84Q56	Q84Q56 oryza sativ
33	854	16.6	926	1	RPML_ARATH	Q39214 arabidopsis
34	852	16.6	693	2	Q8S7Q5	Q8S7Q5 oryza sativ
35	850	16.5	880	2	Q8LSR9	Q8LSR9 oryza sativ
36	849.5	16.5	933	2	Q8W2U9	Q8W2U9 oryza sativ
37	849.5	16.5	933	2	Q7G732	Q7G732 oryza sativ
38	849.5	16.5	954	2	Q6Z392	Q6Z392 oryza sativ
39	848	16.5	959	2	Q6Z572	Q6Z572 oryza sativ
40	835	16.3	996	2	Q8LM68	Q8LM68 oryza sativ
41	835	16.3	1018	2	Q6ZBT0	Q6ZBT0 oryza sativ
42	831	16.2	935	2	Q6H4T9	Q6H4T9 oryza sativ
43	808	15.7	913	2	Q6YUT7	Q6YUT7 oryza sativ
44	805.5	15.7	900	2	Q6K4R1	Q6K4R1 oryza sativ
45	804.5	15.7	961	2	Q6Z569	Q6Z569 oryza sativ

ALIGNMENTS

RESULT 1

Q84KC5	Q84KC5	PRELIMINARY;	PRT; 1014 AA.
AC	Q84KC5;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DB	NBS-LRR disease resistance protein homologue.		
GN	Name=xga S-9202;		
OS	Hordeum vulgare (Barley).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;		
OC	Triticeae; Hordeum.		
OX	NCBI_TaxID=4513;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22600637; PubMed=12715163;		
RA	Madsen L.H., Collins N.C., Rakwaliska M., Backes G., Sandal N.,		
RA	Krusseil L., Jensen J., Waterman E.H., Jahoor A., Pryor A.J.,		
RA	Langridge P., Schulze-Lefert P., Stougaard J.;		
RT	"Barley disease resistance gene analogs of the NBS-LRR class:		
RT	Identification and mapping."		
RL	Mol. Genet. Genomics 269:150-161(2003).		
DR	EMBL; AJ507094; CAD45030.1; -.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0006915; P:apoptosis; IEA.		
DR	GO; GO:0042829; P:defense response to pathogen; IEA.		
DR	InterPro; IPR000767; Disease resist.		
DR	InterPro; IPR002182; NB-ARC.		
DR	InterPro; IPR009058; Wing_hlx_DNA_bnd.		
DR	Pfam; PF00931; NB-ARC; 1.		
DR	PRINTS; PR00364; DISEASERISIT.		
SQ	SEQUENCE 1014 AA; 114280 MW; 62C3PESF04657332 CRC64;		

Query Match	45.1%;	Score 2319;	DB 2;	Length 1014;
Best Local Similarity	49.8%;	Pred. No. 8.1e-133;		
Matches 509;	Conservative 149;	Mismatches 263;	Indels 102;	Gaps 14;
Qy	1	MAETVLSMARSLVGSALSKAASAADETSLLGVKEDIWYL-----FRHGVSNG 51		
Db	1	MAETVLSMARSLVGSALSKAASAADETSLLGVKEDIWYL-----FRHGVSNG 51		
Qy	52	-----GPVGVGNVAGNSQCL-----		
Db	61	KNMLLKVAEQVRDLAYGIEDCLDFMHHVGSQSRRLKLDKRYRIASQIRDLKARVE 120		
Qy	67	-----AIDSYAEDIRNGARVNDVDEALVGFSDSKRRLLEMDTN 105		
Db	121	EVSNNRARNYLINADASSNTDENVNMDIRSHSAGNIDVDEALVGFVKPKGELINMYDVN 180		
Qy	106	ANDGPAKVICVGMGGIGKTLARKIFESREDIRKNPCNAWITVSQSFRIELLDKDIR 165		
Db	181	SRDLGSKVICVGMGGIGKTLARKVYESKEDIVNKFACCANWITVSQFSKIEMKEMIR 240		


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Db      834 KQLRKFELRSEL-DGRAIELGLTLPNMLNLDGRAYVGNELAKKHEPNLXELRISM 892
Qy      814 LDQLREIRFEGSPQLEKIEIRFCRLGSGIIGIHLPRLEKISGLYESKVGAGLAQEGE 873
Db      893 LSELRGIRFERKDALPHMERBIECQLRSGIVGIGKLEQLNEISLGCD--VAGLDLLEQE 950
Qy      874 VRTHPNHVLKREDRSDHDLACDA-----EGSPVEVENTDPLPEQGESQ 920
Db      951 VKAHPKTPTALRLQLDRSKIDGLPVLVTYKOGSNVEBEAKESVHDDAGESSQ 1002

RESULT 3
Q69U98
ID Q69U98 PRELIMINARY; PRT; 1485 AA.
AC Q69U98;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative Pi-b protein.
GN Name=P0666G10.130;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC
RT Cloned:P0666G10.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004592; BAD33147.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002029; Pept_s8_s53.
DR Pfam; PF00560; LRR_1; 2.
DR PRINTS; PR00364; DISEASERISIT.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
SQ SEQUENCE 1485 AA; 167594 MW; 181AB09C7BAB8006 CRC64;

Query Match 22.8%; Score 1172; DB 2; Length 1485;
Best Local Similarity 33.9%; Pred. No. 1.6e-62;
Matches 326; Conservative 163; Mismatches 312; Indels 162; Gaps 33;

Qy      40 YLFRHGVGRNGGPPVGM-----VAGNQSCLA-----DSYAEIDRNGARNV-- 83
Db      566 YTYNKLGSQNDGTAVGSEWVGLDSNINSETKPSMASSSTGGDNHPEGLRESSSPSLNK 625
Qy      84 -----DEAEL-VGFSDSKKRLLEMDITNANDGPAKVICV 116
Db      626 DPNAAVKLRTCTAMVPKRSRTVVAEEAQLMIGRNEKDLKMLDGGC-DAKHRVISV 684
Qy      117 V---GMGGLGKTALSRKIFESEEDIRNFFCNAMITVSQSFRIELKDMIRQLGPSL 173
Db      685 ISVWGMGIGKTLVKSIYQSSELEKLGFFERRAVVPSRPFRIELRLAQ----- 736
Qy      174 DQLLQELQGVVQVHHL-----SEYLIELKE-----KRYFVVLDLILHLDNWI 220
Db      737 -RLVKDSFGKKVSTPGRLARSGLSMGSKELIDKQLDGTGKKYLIVLDDLSTTTEWDFI 795
Qy      221 NETAFPNKNGKSGIIVLTWNVDLAEKATASLVYH-LDFLQWMDATLLLR----- 272
Db      796 KTI--FPENS--SSRIIVTRPKVAQHCSEEEYMHHRIGDLKOKDALDLFDLXFLIYLF 852
Qy      273 ----TNKNHED-----MESKNQMKQVVERVVKRCGRPLAILAIGAVLATK--QVS 317
Db      853 NYKVKCKGDSSELKPDMDILKQNPDMIAEALIVKCGRLPLAIVAGVGFSLTRPPNIR 912
Qy      318 EWEKFYEHLFSELEINPSLEALRRNMTLVGNHPLSHLKPCLFLYLSIPPEFETKRNRLVG 377

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Db      913 EWKFSDFHISTEDENPSLEMIKKILISSYEGLSYHLKSCFLYLSIFPEDHDIRYGLLR 972
Qy      378 RTWIAEGVRPKVGMWTKDVGESYFNELINRSMTQSRVGIAGIKTKCRIHDIIRDITVSI 437
Db      973 RTWIAEGYSRAKRNNAEKEAEQFTALLNKSMTQQSRVTTTGKTFQCVQVHDLMEISIAK 1032
Qy      438 SROENFVLLPMKDGSDLVQENTRHIAFHGMS-----CKTGLDWSIIRSLAIFGRDP 489
Db      1033 SEENLVLLDEHISISSKDKVRHLVISQSWRSREQKQNDMQNVIVDVSHRSLRVFGEW- 1091
Qy      490 KSLAHAVCPQLRMLRVLDLEDVTLITQKDFORIALLLCHLKYSIGSYSSSIYSLPSIG 549
Db      1092 KSP---PLSKKRMRLRVLDLED-TDGLSDHDIPIGKLHLKYLSLRGSATILNLPSSFG 1147
Qy      550 KLOGLQTLNMPSTYIAALPSEISIKLOCLHLTRC-----SRKFVSDNPSLNMHPMKCI 600
Db      1148 NLNLETLDIRGTWVTWKLPATIGRLQNLKYLHAGMPDDEDDTRSWVP----- 1195
Qy      601 TNTICLPKVTPLVSRDDRAIQIAELHMYK-----SCHYKS---FGVKVPKGIG 647
Db      1196 TTPSAILEAFREYWTNQ-----EVGMGIKLFVSVLMFLISGLWRNMDLFGVKVPRRIG 1249
Qy      648 KLRLDLQVLEVVDIRRTSSRAIKELGQLSKLKLGVMTNGSTKCKKILCAAEIKLSSLOQ 707
Db      1250 RLRSIHTLSVNISSR-GKAMLKMLKLTQRLKLV--TGINKNCEELCSVIVKHGCLQS 1306
Qy      708 LYVNAAGISDGTLE-CLDSISSPPPLRLTLVLYGSLEEMPNIETQLTHLKKIYLLRSKL 766
Db      1307 LLRAEG-KDG--LEGCLDGLSPPKDLSSLQVNLVLPKPEWKELNQLSLRSTNL 1363
Qy      767 KEGKTMILIGALPNLMVLDLYRKAYLGEKLVFTGAPFNRLRTLSIYDLQDLREIRFEDGS 826
Db      1364 EADATMQVGLGLEMLDILRLQDKACENELRFPDCFTNLRALELISWGLSKSVIFEEGA 1423
Qy      827 SPOLKIEIRFCRL--ESGIIGIHLPRLEKISL-GY---ESKVAGLAQLEGEVTRHPNH 880
Db      1424 TPKEVLLVDHCSSIDEAGPFGIENLATLKEVSLQGIYYTEFK-KKLQQQLNMIEPRNL 1482
Qy      881 PVL 883
Db      1483 RIL 1485

RESULT 4
Q84QL0
ID Q84QL0 PRELIMINARY; PRT; 1236 AA.
AC Q84QL0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative Pi-b protein.
GN Name=P0666G10.123;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC
RT Cloned:P0666G10.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004592; BAC75861.1; -.
DR Gramene; Q84QL0; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 3.

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Db 782 KPFFLS-----DKMRLARVLDLEDTTGLVNH-HLEHIGKFLHLRLVLSLRGCESICHLPDT 835
Qy 548 IGKLOGLOTAMPSTYIAALPSEISKLOCLHTLR-----CSRKFVSDNFSNLNHPM 597
Db 836 LGNLRQLETLDIRGTSIVMLPQTIIKLOKLOHLHAGFTKGNLYLCTRHLH-HTYGFENOLD 894
Qy 598 KCIYNTICLPKVFPVPLVSRDRDRAIOIAELHMAKSCWKSP-GVKVPKGIGKLDLQVLE 656
Db 895 AC-TSLCC--GAATPCIMMD-----KYGGVVLPGGARKLKSHTIR 933
Qy 657 YVDIRRTSSRAIKELGQSLKRLKLGVMGTNGSTKCKKILCAAIKLSLOYLYVNAAGIS 716
Db 934 GVHV-AYGDAVIOEIGRLSGLRKLGV--GINKNDVKFCSAINLSRLESLSVQ----S 986
Qy 717 DGGTLECLDSTSSPPPLRLTLVLVGSLEEMENWIEQLTHLKKI---YLLRSLKHEGKTM 773
Db 987 DKG---CLDDITSPPNLRSKLEGLVLPWIKLQNLVKLSLFTTSSQVEQDAAME 1043
Qy 774 ILGALPNLWLDLYRKAVLGEKLVFKTGAFFNLRATLSIYDLDQREIRFEDGSSPOLEKI 833
Db 1044 VZGHLNPLNLSIURLPCCSPFGELHFPQDAFRSIVVDFVEGLGGIKSVNFDQGAPELEQL 1103
Qy 834 EIRFCRLSEGI--IGIHLPLKELISGYESKV--AGL-----AQLEGEVRT----HPNH 880
Db 1104 KVTACKREGGIGFGGLDILPSIKEVLLSVHFEMDRAGTELEAREALKEQFTQLARNPKK 1163
Qy 881 PVLR 884
Db 1164 PILK 1167

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RESULT 9

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Q947C8 ID Q947C8 PRELIMINARY; PRT; 1169 AA.
AC Q947C8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Putative resistance protein.
GN Name=RGA-2;
OS Triticum monococcum (Einkorn wheat) (Small spelt).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4568;
RN [1]
RP MEDLINE=21332852; PubMed=11439119;
RX Wicker T., Stein N., Albar L., Feuillet C., Schlagenhauf E.,
RA Keller B.;
RT "Analysis of a contiguous 211 kb sequence in diploid wheat (Triticum
RL monococcum L.) reveals multiple mechanisms of genome evolution.";
DR ENBL; AF326781; AAK84082.1;
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 3.
DR Pfam; PF00931; NB-ARC; 2.
DR PRINTS; PR00364; DISEASERISIT.
SQ SEQUENCE 1169 AA; 131599 MW; 0563D1ABC6D7B891 CRC64;

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Query Match 20.3%; Score 1040.5; DB 2; Length 1169;
Best Local Similarity 32.7%; Pred. No. 1.2e-54;
Matches 304; Conservative 174; Mismatches 330; Indels 123; Gaps 37;
Qy 5 VLSMARSLVSGAISKAAASAADETSLLLGVEKDIWLFHGVGRSNGSGPVVGVMAAGNQ 64
Db 309 IVSTKQVEVASLCAGPQNVAPDHQK--LSIDQDTLYIAFFEKSGDQGSTVEGS-SSTNST 365

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Qy 65 CLADSVAEDIRNOSARNVD-----EAEVLGFSDSKRLLEMDTNDNPGPAKVICW 117
Db 366 TTASHIL---VNNKILTRMETTLAAFKFQIIGREKSEKSEIIQLV--TNGDGRQFVLSVC 421
Qy 118 GMSGIGKTALSRKIFESEEDIRKNPFCNNAWITVSQSFHRIELLDKMDIRQLLGPSSLDOLL 177
Db 422 GMSGIGKTTVRDVYQSOB-LRGKFEKACACVTIMRPNCEDELLKNLQAG--FGYEDVADMV 479
Qy 178 QELQGVVQVHHLSEYLI BELKEKRYFVVDLDDWLHDMWINEIAIAPPKNNKKGSIQVI 237
Db 480 RHLEG-----KKCLIVLDDLSSTREWDAI--IPHTALETSSRIIV 518
Qy 238 TTNVNLAEKCA-TASLVYHLDLFLQMDAITLLRKTNNKHEDM-ESNKNQKQKVERIVN 295
Db 519 TTRVEDIGKCKSKRKNYIKLQGLELNDADHDF-OKYFVDKTMDDQEPPELVEQTNMILK 578
Qy 296 KCGRLPLAITIGAVLAT--KQVSEWEKFEHL--PSELEINPSLEALRMVTLGYNHLPS 352
Db 579 KCKGLPLAIVTIGGFANQPKTALEWKKLNEHISAELQNNPELEAITVLNKSVDGLPY 638
Qy 353 HLKPCFLYLSIFPPDFEIKNRLVGRWIAEGF---VRPKVGMTTKOVGESYFENBLINRSM 409
Db 639 HLKSCFLYLSIFPPDYNIKLRLLRWIAEGYPGVWRNK---STEEVAESYFMDLISRM 695
Qy 410 IQRSRVCIAG--KIKTCRIHDIIRDITVSIRQENFVLLPMGDSGL--VOENTRHIAFHG 466
Db 696 LLPQRSICDGKRGSCQVHDLIREIGISKSMGNLV-LRLEEGCSLNTQGTARHLAIS 754
Qy 467 S-----MSCKTGLDWSIIRSLAIFGD-RPKSLAHAVCPDOLRLRLVLDLDTVFLITQKD 520
Db 755 NWERDQSAPEISIVDMRSRITVFGEWKPFLLS-----DKMRLRVLDLDTTGLVNH-H 808
Qy 521 FDIRALLCHLYLSIGYSSISYSLRPSIGKLGQIOTLNPSTYIAALPSEISKLOCLHTL 580
Db 809 LEHIGKFLHLRLYLSRGCESICHLPDPLGNLRQLETLDIRGTSIVMLPQTIIKLOKLOHL 868
Qy 581 R-----CSRKFVSDNFSNLNHPMKCITNTICLPKFTPLVSRDDRAIOIAELHMA 630
Db 869 HAGFPTKGNLYLCTRHLH-HTYGFENQDLC--TSLCC--GAATPCIMMD----- 911
Qy 631 KSCWYKSF-GVKVPKGIGKLDLQVLYVDIRRTSSRAIKELGQSLKRLKLGVMGTNGSTK 689
Db 912 -----KDYGVVLPGGARKLKSHTIRGVHV-AYGDAVIOEIGRLSGLRKLGVN--GINE 963
Qy 690 EKCKILCAAIEKLSLOYLYVNAAGISDGGTLECLDISISSPPPLRLTLVLVGSLEEMP 749
Db 964 KNDVKFCSAINLSRLESLSVQ---SDKG--CLDDITSPPNLRSKLEGLRGLVLPW 1016
Qy 750 IEQLTHLKKI---YLLRSLKHEGKTMILGALPNLWLDLYRKAYLGEKLVFKTGAPN 806
Db 1017 IKKQLNVLKLSLFTTSSQVEQDAAMEVLGHLNLSILRLSGCSFKGGELHFKDAFRSI 1076
Qy 807 RTLSIYDLDOLREIREFGSSPOLEKIEIRFCRLSEGI--IGIHLPLKELISGYESKV 864
Db 1077 VFDVEGLGGIKSVNFDQGAPELEQKJVTDAKVRGGIGFGGLDILVSIKEVLSVHFQK 1136
Qy 865 --AGL-----AQLEGEVRT----HPNHPLVR 884
Db 1137 DRAGTELEAREALKEQFTQLARNPKPILK 1167

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RESULT 10

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Q9ZNV6 ID Q9ZNV6 PRELIMINARY; PRT; 1251 AA.
AC Q9ZNV6; Q9SSY0;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Pib.
GN Name=Pib; Synonyms=Pi-b;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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OC Ehrhartoideae; Oryzeae; Oryza.
 RN NCBI_TaxID=4530;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Tohoku IL-9; TISSUE=Green leaf;
 RX MEDLINE=99348180; PubMed=10417726;
 RX Wang Z., Yano M., Yamanouchi U., Iwamoto M., Monna L., Hayaoka H.,
 RA Katayose Y., Sasaki T.;
 RA "The Pib gene for rice blast resistance belongs to the nucleotide
 RT binding and leucine-rich repeat class of plant disease resistance
 RT genes.";
 RT Plant J. 19:55-64 (1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BL-1; TISSUE=Green leaves;
 RC Jwa N., Tsunoda Y., Akiyama K., Nakamura S., Motomura T., Kamiyama K.,
 RA Kodama O., Kawasaki S.;
 RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB013449; BAA76282.2; -.
 DR EMBL; AB013448; BAA76281.2; -.
 DR EMBL; AB026839; BAA85975.1; -.
 DR Gramene; Q9SSY0; -.
 DR Gramene; O9ZNV6; -.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0042829; P:defense response to pathogen; IEA.
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR_1; 2.
 DR Pfam; PF00931; NB-ARC; 2.
 DR PRINTS; PR00364; DISEASERSIST.
 DR SEQUENCE 1251 AA; 141638 MW; 011F56630118AB98 CRC64;
 Query Match 20.1%; Score 1033; DB 2; Length 1251;
 Best Local Similarity 31.4%; Pred. No. 3.9e-54;
 Matches 308; Conservative 184; Mismatches 354; Indels 136; Gaps 37;
 QY 9 ARSLVGSATSKAASAAADETSL-----LGVEKDIWYLFPHG--VGRSNGGPV---VGM 57
 DB 298 SRLIVSSTOVEVASLCAQESQASELKQLSADQTYAPYDKGSIIEDSVFVPSIDVAI 357
 QY 58 VASGNQSL-----AIDSYAEDIRNQSARNV-----DEALVGFSDSKRLLEMI 102
 DB 358 TSTNNHTVAHEITDQSDMDAEEKVARKSLRITSVGASESGLIKREKEISEITHLI 417
 QY 103 DTVANDGPVKIVCVGMGLGKLTALSRKIFESSEEDIRKNFPCNAWITVQSQFRIELKD 162
 DB 418 -LNNDSSQVQVIVSVGMGGLGKTLTVSGVYQSPR-LSDKFDKVFVFTMRPFILVLR 475
 QY 163 MIRQL-LGPSLDDQLQ-----ELQGVVVQVHLSYLEELKEKRVFVLDLWILHDW 217
 DB 476 LAQLHKGSKKEELLENRVSSKSLASMEDTELQGLKRLLEKSCULIVDDFSDTSEW 535
 QY 218 NWINEIATFPKNNKSGQIVITWVNDLAEKCATAS-LVYTHLDFLQMDAITLLARKT--N 274
 DB 536 DQIKPTLPFL-LEKTSRIIVTTRKENIANHCCKGNVHNLKVLKHDALCLLSEKYPFE 594
 QY 275 KNHEDMESNNKQKQWVERIVNKGRLPLAILITIGAVLAT--KQVSEWEKFEYHLPSELEI 332
 DB 595 ATYLDQNNPELVKEAKQLKKCDGLPIAVVIGGFANRPKTPPEWRKLNENINAELEM 654
 QY 333 NPSLEALRWVTLGVNHLPSHLKPCFLYLISPEDFELKENVLGRWTAEGFVRPKVGMT 392
 DB 655 NPGLGMIRTVLEKSYDGLPYHLKSCFLYLISPEDOIISRRRLVHRWAEGYSTAAHGKS 714
 QY 393 TKDVGESYFNEILNRSMI---QRSRVGIAGK-IKTCRIHDIIRDITVTSISQENFVLPLP 448
 DB 715 ATEIANGYFWEKLNRSMLIPFOQS--GSRKSIDCKVHDLMDRLAISKSTEENLVPRVE 772
 QY 449 GQGSDLVQENTRHIA-----FHGSMCKTGL-DWSTIRSLAIPGDRPKSLAHAVCPDQLRM 503
 DB 773 EGSAYIHGAIRHLATSSNNKGDKEFEFIVDLRSIRLSIFGDKWKPFFVVG---KNRF 828

Matches	306;	Conservative	174;	Mismatches	347;	Indels	219;	Gaps	32;
Qy	1	MAETVLSMARSLVSGA	ISKAASAAADETSL	LLGVKDIWYL----	----	----	----	----	41
Db	514	MEHAVVSAAECAIHT	LLGKGTIVLQEAQ	LLAGGIRGELQHL	KDBLESMTAP	LQDLSGRDE	573		
Qy	42	----	----	FRHGVRSH----	GGPVV----	----	55		
Db	574	CGKQVKIWKXHVRE	IAYDIEDICIDEFK	HQLGDSSAGSGSV	GVVFRKATHILO	TRVRHQ	633		
Qy	56	----	----	GWASG----	NOSCLAIDSYAED	IRNQSARNV----	DE 85		
Db	634	IAKIQELKRTWNI	SARNSRYSANHLIS	GTAGNSMAAYDSQ	A--NLNVDTRI	TALPFR	692		
Qy	86	ABLYGSPDSKRLLE	MDTNANDPAKVIC	VVGVGGGLGKTAL	SRKIPESBEDIR	KNFPNC	145		
Db	693	ROLVIEPRQGNLV	HWHL-LEAHVQ	QLRVVSIFGFG	LKTKTLAMT	TYQSLSGRNGP	751		
Qy	146	AWITVSQSFHRIEL	LKDWIRQL-----	LGPSSLDQLQ	LBELQGVVVQV	HHLS 192			
Db	752	AFVTVSQSFVKVLR	MDILLQITQPVN	QSPSPSTGAGK	GMGEGSLK	MGMAWVVO----	LA 808		
Qy	193	EYLTELKEKRYF	VVLDDLTILH	DNWINEIAPKNN	KGSOIVITTV	NVDLAEKCATAS 252			
Db	809	SILRQLENKRYLV	DDIOWMTAWEG	I-RPSLPDSN	-NGSRIVVTRI	RAVATCC----	863		
Qy	253	LVHLDLQMDNDAI	TLLLRKTNKH	EDMESN-----	-----KMKQ	MVERIVNKCQ 298			
Db	864	-----PHEVDRA	VEI-----KPL	TDCESRDLFP	KRIFGSSICE	HELEDISAKILKCG 911			
Qy	299	RLPLAIIITGAVL	ATKQVSE---WEK	YEHLPSELEIN	PSLEALRRM	VTLYGNHLP	355		
Db	912	GTPLSVISVIA	GLASKPVHSD	LWEKLYSSLS	EIETNPSL	DRLLKILESL	971		
Qy	356	PCFLYLSIFPE	DEIKENRLVGR	NIAGFVRPKV	GMTTKDVGES	YFNELINRSI	415		
Db	972	TCFLYLSIYP	EDHNRKTIIL	LRVWASRFV	TGKGLSV	FVEAESYF	1031		
Qy	416	GIAGKICTRIH	DIIRDTYSIS	RQENFVLLP	MGDGDVLV	-QENTRIAHF	472		
Db	1032	SFTGKVTFRV	HDVMLEIIV	SKSIEDNFIT	-VGEQNTLP	QEKIRLTV	1090		
Qy	473	GLDWSIIRSLA	IFGDRPKSLA	HVCPQOLR	MLRVLDIED	VTLITQKDP	532		
Db	1091	REILCHVRSLS	IFAD-----	GETLQFGW	KMLRILDL	EGEYFL--RNRDL	1144		
Qy	533	LSIGYSSSIY	SLPRSIGKLO	QTIANP	SYIAALPSEI	SKLOCLHT	592		
Db	1145	LNL-RRTHIT	ELPAQIGNK	KLFLTRD	TAIKHLP	PGITNPL	1197		
Qy	593	LNPBMKCI	TNTICLPKV	FTPLVSR	DDRAIOIAEL	HMATKSWYKS--	650		
Db	1198	YNHTR-----	-----WP	SEFWGLH	IPNELRMD	1222			
Qy	651	DLOVLEYVD	IRRTSSRAIK	ELGOLSKLR	KLGVMTNG	STKECKITL	709		
Db	1223	SLTTLAQVEIT	TSHTSVISEL	SKLSRLRKL	GVLMFVDD	STWASLIS	1282		
Qy	710	VNAAGISDGG	-TLECLDSIS	PPPLLT	TVLYGSL	EMPNI	768		
Db	1283	L---WRPD	GAMNFIVN	SLNSPPI	FTTKSMN	RGOLTQPC	1339		
Qy	769	GKTMILIGAL	PNLMVLDR	KAYLGK	LVKFTGAF	NLRTLSIV	827		
Db	1340	EEDKVGUS	PLSLYLRL	HNAYIGT	FSASAGE	FPSSLRLV	1399		
Qy	828	POLEKIEIR	FCRLS--GIIG	IHLPRK	BEISL-GYES	KVAGLAQ----	880		
Db	1400	PKLARLESL	FEESAIOEIT	GIEPL	PSLKEVS	IRACHSN	1459		
Qy	881	PVLKRRED	-----RSD	HDLACD	AEBS 901				
Db	1460	PIVTFEEK	QWVPMRS	RTDPP	LDHGN 1485				

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Db 362 NGPLAIVSIGGMLARMKNTYAEMQKVCDRDLDCGLEINNTVGQWRKILSGYNDLPYHL 421
Qy 355 KPCFLYLSIPDEPEIKRNLVGRWIAEGFVRPKVGMTTKDVGSYFNELINRSMIOQRS 414
Db 422 KACFLYLSVPDEPEIKRNLVGRWIAEGFVRGSGNLEBIAKYDFDEFSRNVITPIR 481
Qy 415 VGIAGKIKTCTRIHDIIRDITVISIQENFVLLPGD-----GSDLVQENTRHI--AFHG 466
Db 482 IDSSEVRSCRVDHMLEIVSAISVQENFISL-LGNYSYSITGHDKIRRLSIHVGGGKEQ 540
Qy 467 SMSCKTGLDWSIRSLAIFGRPKSLAHAVCPDQLRMLRVLVDLTDVTLTKQDFDIAL 526
Db 541 DFSCR--NLSHLSLTLGCKEKPPIALA--DLTLRLVLDLEGCGWL--SDSLDKDICK 594
Qy 527 LCHLYLSIGVSSISYLSIPRSGIKLQIOTLNMPSYIAALPSISIKLOCL-HTLRCSRK 585
Db 595 LYLRYVSL-RSTNISKPRAGVNLKELLTUDVRSYTIRELPAITQRLCKHLLAGRYK 653
Qy 586 FVSNFSLNHPMKCITNTICLPKVFTPLVRDRAIQIAELHMATKSWYKSGVKVPKG 645
Db 654 Y----YRTRHVK-----HPASKE-----AVTIPAG 675
Qy 646 IGKRLDQVLEYVDIRTSRAIKELGOLSKRLKLGWNTNGSTKECKILCAAIEKLS-S 704
Db 676 LKNMSALQSIAPVNI-SSSFRAMELGELSQTLCAL-NRKGVKWRPFATSLKLSNS 733
Qy 705 LOYLVAAGISDGTLECLDSISSPPLLRTLVLSLEEMPNIWISQTLHKVILRS 764
Db 734 LRHLVSUIHDKMEHG-LEFLMDLSSPPLFKGVYFGRVSAIPWISSLNVLRL-SLRE 791
Qy 765 KLKRGKTLILGALPNLMVLDLYRKAYLGEKLVKTKGAPFNLRTLSDYLDQLREIRFED 824
Db 792 NYLSESLVKILGKLSLLSKLYNSYLGTELCFEHNLFPPLKQLMIDNLKNLDELSPK- 850
Qy 825 GSSPOLKEIRFCRL-ESGIIGIHLPRKEI---SLGYESKVAGLAQLEGEVTRTPNH 880
Db 851 GGAPDLRLTLAFKAPERGIGSIENLPKLKEVEFFGIIVDSVVEGVI---AAAKIHENH 907
Qy 881 PVLKREDRSDHDI--AC 896
Db 908 PRVTRDETIDPRSLTTAC 925

RESULT 13
Q651T0
ID Q651T0 PRELIMINARY; PRT; 989 AA.
AC Q651T0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to NBS-LRR type resistance gene.
GN Name=P0702F05.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone.p0702F05.16";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005828; BAD46437.1; -.
SQ SEQUENCE 989 AA; 109590 MW; 09BF11AAD9C3028A CRC64;

Query Match 19.3%; Score 992.5; DB 2; Length 989;
Best Local Similarity 30.5%; Pred. No. 8.2e-52;
Matches 290; Conservative 170; Mismatches 333; Indels 159; Gaps 30;

Qy 18 SKAASAAADETSLLGVEKDIWYIFRHGVGRSGNPGPVVGMVAGSNQSCLA-----IDSYAE 73
Db 95 SHPAAAAAGDEGLVASLRRFV-RLLAGALG-----VGGDRSVAAQRLKAR 143
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Qy 74 DIRNQARN-----VDAAELVGFSDSKRLLMIDT 104
Db 144 DAGERRTRYGSLAAAVRGSGSSGRDLRPLHALFTBEAQLVGIDGPREELVGVW-- 201
Qy 105 NANGDPKAVICVVMGGIGKLTALSRKIPSEEB-DIRKNFPCN-AWITVSQSFRIELKD 162
Db 202 MESEPRILVLAIVGFGGLGKTTILARMVCGSPRVKGAADFQCSPLVVSQTSFITALFQH 261
Qy 163 MIRQLL-----CPSSLDQLQER-LOGKVVVVHHLSE-----YLI 196
Db 262 LLRELQRPKMAVAAGGGGDLVAYDALQMERWETAALASKAEGIPAROKFVHIC 321
Qy 197 EELKEKRYFVVLDDTLILHDWNINETAIFPKNNKKSQIVITWNVDLAKCA--TASLV 254
Db 322 GTITLYRYIILDDINSSSAWESI-KCAFP-DNKKGSRIIVTTNEDVANTCCRPQDRI 379
Qy 255 YHLDPLQMDAITLL---RKTNNHEDMSNKNMQMQRIVNVKCRQLPLAILITIGAVL 311
Db 380 YKIQ--RLSDAASRELFFKRIFGMADAGAPDDDELKQVSDSILKKCGGLPLAIVSIGLL 437
Qy 312 ATK--QVSEWEXFYHLPSELINPSEALRRMVTLYGNHLPShLKPCTLYLSIPEDF 368
Db 438 ASKPNRSKEWQKVDNLGSELSNPTEGTQVLTLSYNDLPHYLKACFLYSIFPENH 497
Qy 369 EIKRNLVGRWIAEGFVRPKVGMTTKDVGSYFNELINRSMIOQRSVGIAGIKTCRIHD 428
Db 498 VIKRGPLVRWIAEGFVYQRHGLSMEQVGERYDFEFVRSRNVHLVRIDWSKVRSCKVHD 557
Qy 429 IIRDTVISIQENFVLLPMGDSDLV-QENTRHIAFHGSMCKTGLDWSIIRSLAIFGD 487
Db 558 IMLEVISKLEENFASPCDNGTELVSVDKIRRLSIRSS-----SYSSAQR 604
Qy 488 RPKSLAH-----VCPD-----QLRMLRVLDLEDVTLITQKDFRIALLCHLYLS 534
Db 605 TSNsvAHVTRFRMSPSIDNIPFFPQLRLRLVLDMDQG-SRCMGNKLDJCIRFFQLKLYS 663
Qy 535 IGVSSSIYSIPRSGIKLQIOTLNMPSYIAALPSISIKLOCLHTRLCRKFVSDNFSLN 594
Db 664 L-RNTSVSILPRLIGNLHLETLDIRETLIKUPSSAANTCLKHLLAGHK----- 713
Qy 595 HPMKCTNTICLPKVFTPLVSRDRAIQIAELHMATKSWYKSGVKVPKG-IGKLRDLQ 653
Db 714 ---EQLTRTSV-KFLRP-----SSGLKQSHGVIRNMAKLQ 745
Qy 654 VLEVDIRTSRAIKELGOLSKRLKLGWNTNG---STKECKILCAAIEKLSLOLYLV 710
Db 746 SLVHVEIKEHPS-VFQIALLQNLRLKLSVLFGYIEVNMKPFLELLNMLSGSVRSLSIDIF 804
Qy 711 NAAGISDGTLECLDSISSPPLLRTLVLYGSLEEMPNIWIEQLTHLKKIYLLRSKLKEGK 770
Db 805 DAQGNISISSELMSSLSVPIITSPSLTGKLSLPPVWASLSRSVSLTLRRSOLR-AD 863
Qy 771 TMLILGALPNLMVLDLYRKAYLGEKLVKTKGAPFNLRTLSDYLDQLREIRFEDGSSPOL 830
Db 864 AIHVGLGQLNLLCLKYHSYADRLVFPQGGFARVKLLIDDDNLVLEKLHFNESGMPNL 923
Qy 831 EKIEIRPCR-LESIGIIGIHLPRKEISLGYESKVAGLAQLEGEVTRTPNH 881
Db 924 ERLTSLFREPDKGISGLNLLKKEVEFFGNIVSSVSVKVSVCVKDHPNHP 975

RESULT 14
Q69MT5
ID Q69MT5 PRELIMINARY; PRT; 963 AA.
AC Q69MT5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative resistance protein.
GN Name=OSUNBB0034B12.23;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatoxphya; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
 clone:OSJNB0034812";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005735; BAD33830.1; -
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0042829; P:defense response to pathogen; IEA.
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR Pfam; PF00560; LRR_1; 3.
 DR PRINTS; PR00364; DISEASERSIST.
 DR SEQUENCE 963 AA; 109012 MW; 5E808C349CBFA3C6 CRC64;
 Query Match 19.2%; Score 987.5; DB 2; Length 963;
 Best Local Similarity 29.8%; Pred. No. 1.6e-51;
 Matches 303; Conservative 180; Mismatches 324; Indels 211; Gaps 38;
 Qy 1 MAETVLSWASRLVGSATSKAASAADETSLLGVEKDI----- 38
 Db 1 MEATVLSWASRLVGSATSKAASAADETSLLGVEKDI----- 38
 Qy 39 -----WYL-----FRGVG----- 47
 Db 61 ADDTVRTWVKQVRLAYDVESLDDLFALFADTLSSSSSSWMLPWAERHVAARIREL 120
 Qy 48 -----RNGGPPVGMVAGSNQSCLAIDSYAEDIRNQSAR-NVD 84
 Db 121 KASVEELNQRFLRYIVVEHPRARGGG-----ASDDQQL-----HHHDGGYYSAELAFQ 171
 Qy 85 EAEVLGFSDSKKRLLEMDITNANDGPA-----KVICVVGSGGLGKTALSRKIPESBED 138
 Db 172 ESDIIGRAREAEVATLVSLGCGGDDVGGGALGVSVWGMGKSLVRWVY-NDPEL 230
 Qy 139 RKNPCHAWITVQSFRHIELDKMIRQLLPSPSLDQLLQELQKVVV-----QVHLSY 194
 Db 231 LDAFDCAWVTP-----HPLD-----SADEFVRLRLHVAAGKDDVH----- 269
 Qy 195 LIEELKEKRYFVWLDLWILMDWNIENIAPPKNNKGSQIVITMNVDLAEKATA--- 251
 Db 270 --AYLREKRYVIVDDLHRSREWEHWPV-LHVDGGKGSRVVVTTRREDVARHCGVLRE 326
 Qy 252 --SLVYHLDPLQMNDAITLLRKTNNKHEDMESNNKNNQKQWVERIVNKCGRPLPLAILTIGA 309
 Db 327 GHGHVYELRPLGRESKDLFCQVYKSTEXI-LEKEMEDLAGPILKRCRGLPLAISTIGG 385
 Qy 310 VLATQVVS--EWKPYEHLSPLEINSLRMRMTLVGNHLPBHLKPCFLYLSIPPED 367
 Db 386 LLANRPKTGIEWIKLDEHGAELS-SSDLRNITVIVSSYDGLPYLKSIFLYLSIPPEN 444
 Qy 368 FEIKRNLVGRWIAEGFVRPKVGTMTKDVGSYFENELINSMIQ--RSRVCAGKIKTCR 425
 Db 445 HEICTRLRKNWMAEGFIKRNQDMVPEVGQRFYNELINRSMIQPKKRISPSVSDRCR 504
 Qy 426 IHDIIITVTSRQENFVLLPMGDGSDLVQENTRHIA---FHGSMSCKTGLDWSIIRSL 482
 Db 505 VHSVNLQILSKSIEENQLFIKKHCNEVPQSKIRHLVSVRKRDERLENINFSYVSL 564
 Qy 483 AIFGRPKSLAHVCPQLRMLRVLDDVETVLTQKDPRIALLCHLKYLSIGYSSIIY 542
 Db 565 TVFGDCPASL---ISP-KMRLRLVLDLED-SLNKNEDLRHVGLHRLYLCL-RGTEIS 618
 Qy 543 SLRPSIGKIQLOTLNWPSTVIALPSEISKQLCLHTRCSRKFVSNFSLNHPMKCITN 602
 Db 619 KLP-SFONRLYLETDIQTKVLTQDPGIAKLEKRLYL-----LAGVNFSE----- 664

603 TICLPKVPTPLVSRDDR-ATQIAELHMTKSCWY-----KSFVGVKVPKIGIKL 649
 665 --LLHKVEQP--ETDNKANQLGNM----LSCLYCNSSDYCGISSLSLRVSVRAPEGEVKL 716
 650 RDLQVLEVVDIRRTSSRAIKELGOLSKRLKLVGMTNGSTREKCKILCAAIKSLSSLOVLY 709
 717 RDLHMLGVINVGH-GNGVGVKIKKLTNRLRGV--SGVLKEGGQDLCKSIEKLSRLQRL 773
 710 VNAAGISDGGTLECL-DSISSPPPLRLTLVLYSGLEEMPNWIBOLTHLKKIYLLRSKIKE 768
 774 LRS-----DSLKFLAESFAAPKHLLSRLYGNLVRPKWIGSLNDLAKLILGTQLKQ 827
 769 GKTMLILGALPNLMVLDLYKAYLGEKLVFTKTAFFPNRLTSLIYDQLREIREDESSP 828
 828 GEIN-HLGLKRLNLAFLGLMDNSYVGSYLFHFGPGTFPKLKFIDLGLKNIETVATENGAMP 886
 829 QLEKIEIRFCR--LES--GIIGIHLPLKLEISIGYESKVAGLAQ--LEGEVTRHPNHP 881
 887 ELEQLWVNDCKGLDSDKGLSGVPHLTNLNELLVKCKEKENLMEILQTVQVSEHSKRP 944

RESULT 15
 Q9LJ10
 ID Q9LJ10 PRELIMINARY; PRT; 1011 AA.
 AC Q9LJ10;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similar to Oryza sativa gene for Pib.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatoxphya; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1247438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 Wu J., Niumura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayaashi M.,
 Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 Hijiishi S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
 Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 Nagaaki H., Nakaehima M., Nakama Y., Nakamichi Y., Nakamura M.,
 Naniki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
 Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 Zhao H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 DR EMBL; AP001073; BAA89580.1; -
 DR Gramene; Q9LJ10; -
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0042829; P:defense response to pathogen; IEA.
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR InterPro; IPR000630; Ribosomal_S8.
 DR Pfam; PF00560; LRR_1; 2.
 DR Pfam; PF00931; NB-ARC; 2.
 DR PRINTS; PR00364; DISEASERSIST.
 DR PROSITE; PS00053; RIBOSOMAL_S8; UNKNOWN 1.
 SQ SEQUENCE 1011 AA; 114012 MW; 14EDDB8A31A4835C CRC64;
 Query Match 18.8%; Score 965; DB 2; Length 1011;
 Best Local Similarity 31.3%; Pred. No. 4.1e-50;
 Matches 282; Conservative 164; Mismatches 315; Indels 140; Gaps 33;
 Qy 76 RNQARNVDEAEVLGVFSDSKK---RLLEMDITNANDGPA--KVICVVGSGGLGKTALSRK 130

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 08:38:22 ; Search time 26.4004 Seconds
(without alignments)
2821.919 Million cell updates/sec

Title: US-10-656-394A-12

Perfect score: 5137

Sequence: 1 MASTVLSMARSIVGSAISKA.....LSGNCNFNLTFSDMLLVPA 998

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1033	20.1	1205	3 US-09-330-330-1	Sequence 1, Appli
2	848	16.5	920	3 US-09-330-996A-8	Sequence 8, Appli
3	576	11.2	905	3 US-09-360-186-3	Sequence 3, Appli
4	576	11.2	905	4 US-09-864-680A-3	Sequence 3, Appli
5	561	10.9	1240	3 US-09-930-996A-4	Sequence 4, Appli
6	540	10.5	928	4 US-09-336-946B-4	Sequence 4, Appli
7	540	10.5	1220	3 US-09-930-996A-2	Sequence 2, Appli
8	539.5	10.5	928	4 US-09-336-946B-2	Sequence 2, Appli
9	539.5	10.5	928	4 US-09-933-170-58	Sequence 58, Appli
10	530	10.3	1824	2 US-08-680-327-3	Sequence 3, Appli
11	530	10.3	1824	3 US-09-228-246-2	Sequence 2, Appli
12	525	10.2	1247	4 US-09-803-286A-2	Sequence 2, Appli
13	512.5	10.0	1402	3 US-09-004-838-11	Sequence 11, Appli
14	500	9.7	1206	4 US-09-245-928A-19	Sequence 19, Appli
15	500	9.7	1243	4 US-09-245-928A-17	Sequence 17, Appli
16	500	9.7	1257	4 US-09-245-928A-18	Sequence 18, Appli
17	491.5	9.6	1255	3 US-08-947-823-3	Sequence 3, Appli
18	491.5	9.6	1257	3 US-08-947-823-5	Sequence 5, Appli
19	450	8.8	784	3 US-09-004-838-12	Sequence 12, Appli
20	399.5	7.8	885	2 US-08-310-912A-2	Sequence 2, Appli
21	399.5	7.8	885	3 US-08-841-089-2	Sequence 2, Appli
22	399.5	7.8	885	3 US-09-301-085-2	Sequence 2, Appli
23	399.5	7.8	885	5 PCT-US95-04570-2	Sequence 2, Appli
24	399.5	7.8	885	5 PCT-US95-04589-2	Sequence 2, Appli
25	397.5	7.7	909	2 US-08-310-912A-142	Sequence 142, App
26	397.5	7.7	909	3 US-09-301-085-142	Sequence 142, App
27	397.5	7.7	909	5 PCT-US95-04589-142	Sequence 142, App

28	389.5	7.6	907	3 US-08-930-996A-7	Sequence 7, Appli
29	385.5	7.5	553	3 US-09-004-838-16	Sequence 16, Appli
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32	330	6.4	1854	3 US-09-004-838-108	Sequence 108, App
33	310.5	6.0	1074	3 US-09-004-838-111	Sequence 111, App
34	302	5.9	250	4 US-09-803-286A-7	Sequence 7, Appli
35	292.5	5.7	429	2 US-08-310-912A-109	Sequence 109, App
36	292.5	5.7	429	3 PCT-US95-04589-109	Sequence 109, App
37	292.5	5.7	429	5 PCT-US95-04589-109	Sequence 109, App
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41	289.5	5.6	1143	5 PCT-US95-04589-108	Sequence 108, App
42	289.5	5.6	1144	1 US-08-261-663A-2	Sequence 2, Appli
43	289.5	5.6	1144	1 US-08-261-663A-4	Sequence 4, Appli
44	289.5	5.6	1144	3 US-09-357-206A-3	Sequence 3, Appli
45	289.5	5.6	1144	4 US-09-813-742A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-330-330-1

; Sequence 1, Application US/09330330

; Patent No. 6274789

; GENERAL INFORMATION:

; APPLICANT: Yano, Masahiro

; APPLICANT: Iwamoto, Masao

; APPLICANT: Katayose, Yuichi

; APPLICANT: Sasaki, Takuji

; APPLICANT: Wang, Zi-Xuan

; APPLICANT: Yamanouchi, Utako

; APPLICANT: Ishimaru, Lisa

; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/330,330

; FILING DATE: 11-JUN-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 10-181455

; FILING DATE: 12-JUN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Ph.D., J.D., Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 06501/032001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1205 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-09-330-330-1

Query Match 20.1%; Score 1033; DB 3; Length 1205;
Best Local Similarity 31.4%; Pred. No. 3.7e-92;

Qy 325 HLPSELEINPSLEALRMVTLGYNHLPSHLKPCFLYLSIPPEDFEIKRNLVGRWIAEGF 384
Db 400 TLNWLNNHNLKTVRSIMPLSFNDLPYPLKRCFLYCSLPVNYRMKRLIRMMMAQRF 459
Qy 385 VRPKVGMTTKDVGSYFNELINRSMIOKRSRGIAGKIKTCRIHDIIRDITVTSIQENF- 443
Db 460 VEPKRGVKAEEVADSYNELVYRNLQVILWNPGRPKAFKMDHVIWIALSVSLKRF 519
Qy 444 -VLLPMGDGSDLVQ--EN--TRHIAFHGSMCKTGLDWSIIRSAIAFGRPKSLAHAVCP 498
Db 520 DVYNDSDGDDAAETMENYGRHLICIKEMT-PDSIRATNLHSLVLCSSAKHKM--ELLP 576
Qy 499 DOLBMLRVLDLDDVTFPLITQKDFRIALLCHLKYSIGYSSSYLSRSGCKLOGLTLN 558
Db 577 -SLNLLRALDLEDDSI---SKLPDCLVTMFLNKLKYNLS-KTQVKELPKNFHKLNLNLTN 631
Qy 559 MPSTYIAALPSEISKLOCLHTRCSRKFVSDNFSNLNHPMKITNTICLPKVFTEPLVSRDD 618
Db 632 TKISKIEELPLGMWMLKRLYLITFR----- 658
Qy 619 RAIQIABLHMATKSCWYKSGVYKPGIGKLDLQVLEYVDIRRTSSRAIKELGQLSKLR 678
Db 659 -----NEGHDNMYVLTGRVVPKIQWQKDLQVMDCFN----EBELIKNLGCMTQLT 706
Qy 679 KLGWMTNGSTKECKKILCAIEKLSLOYLYVNAAGISDGGTLECLSSISPPPL----- 733
Db 707 RISLVM--VRRHGRDCLDSLNKIKRIFL-----SLTSIDEEPLEIDDL 750
Qy 734 ----LRTLVLVYLSLEEMPNMIEQLTHLKKIYLLSKLKEGKTMILGALPNLMLVLDLYRK 789
Db 751 ATASIEKFLAGLKVLPVSPNTQNTYGLRGSQLOE-NAIUSIOTLPLVWLSFY-N 808
Qy 790 AYLGKLVFTKGPAPNRLTISIYDQDREIFRFDGSSPQLEKIEIRFCR-LESIGIIGII 848
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RESULT 3
US-09-360-186-3
; Sequence 3, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staekawicz, et al.
; TITLE OF INVENTION: B62 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Capsicum annuum
US-09-360-186-3

Query Match 11.2%; Score 576; DB 3; Length 905;
Best Local Similarity 24.6%; Pred. No. 3.7e-47;
Matches 218; Conservative 172; Mismatches 310; Indels 186; Gaps 37;
Qy 88 LVGFSKSKRLELMIDTNANDPAKVICVGMGGIGKTLRSKIFESSEDIRKNPPCNW 147
Db 152 MVRGDRDQKLEDL-TRSYSGEPKVPVPMGMGIGKTLAKEVY-NDESLTCRFDVHW 209
Qy 148 ITVSQSFRITELLKDMIRQLGPSLQLOLQELQGVVQVHHLSVLEBELKEKRYFV 207
Db 210 ATISQQHNKKEILLGLLHSTIKMDRVRKMGIEAB-----LADMLQSLKRRKRYLV 260

Qy 208 LDDLWILHDNWINETAPPKNNKKGSOIVITWVNDVLAEKCATASLYVHLDFLOMDAIT 267
Db 261 LDDIWSCEVWDGVR--CFPTEDNAGSRILLTRNDEVACYAGVENFSLRSMFMDDESSWS 319
Qy 268 LLRLKTKNKHEDNESKNMOKWVERIVNKGRLPLAILTIGAVLATKQ-VSEWEKFPVEHL 326
Db 320 -LPKSAAPSEALP--YEFETVGKQIADCHGLPLTIWVAGLLKSKRTTIEDTKTAKDV 376
Qy 327 PSELEINPSLEALRMVTLGYNHLPSHLKPCFLYLSIPPEDFEIKRNLVGRWIAEGFVR 386
Db 377 KSFVTNDPD-ERCSRVLGLSYDHLTSDLKTLCHLFGIFPDSDDIPVKNLRSMAEGFL- 434
Qy 387 PKVGMTTKDVGSYFNELINRSMI---QRSRVGTAGIKTCRIHDIIRDITVTSIQENF 443
Db 435 -KLENDLEGEVEKQLQELVDRCLVLSKRSRDGT--KIRSCKHDLIYDLCVREVQRENI 491
Qy 444 VLLPMGDGSDLV-----QENTRHIAFHGSMCKTGLDWSII----- 479
Db 492 FIM-----NDIVDVSYPECSYLCWYKQKPFKVTGDEINYPYGLYRALLTPVNRQLRD 546
Qy 480 -----RSLAIFGDRPKSLAHAVCPD--QLRMLRVLDLEDVTLITQKDFD----RIA 525
Db 547 HDNNLLKXTHSVFSEFHLPLYYVVKSEVHFLLKVLRLR-----HRQIDGFPREIL 599
Qy 526 LLCHLKYSIGYSSSYLSRSGCKLOGLTLNMP--STYIAALPSEISKLOCLHTRCS 583
Db 600 SLIWLRYLSL-FSYGNFDPPEICRLWNLOTFIVQFRSDIIIPAEIWMELMQLRHLKLP 658
Qy 584 RKVSDNFSNLNHPMKITNTICLPKVFTEPLVSRDDRAIQIAELHMATKSCWYKSGVQVP 643
Db 659 RFLPD-----CFSGSV-----DKGRHL----- 676
Qy 644 KGIGKLRDQVLEYVDIRRTSSRAIKELGQLSKLRKLGVMNTNGSTKECKILCAAIEKLS 703
Db 677 -----DFSNLTQISVLSPRCCTKEVI--MG-IQNVKKLGISGKD----- 713
Qy 704 SLOYLYVNAAGISDG-----GTLECLDSISSPPPLRLTLVLVYLSLEEMPNMIEQLTHLKKI 759
Db 714 --DYKSPRDSGLPNLVLQLOLEILSLISVDYSLP--VIISAKAFATLKKL-KLERT 768
Qy 760 YLLRSLKKEGKTMILGALPNLMLVLDLYRKAYLGEKLVFKTGAPPNRLTISI-YDLQDLR 818
Db 769 YLSWYLD-----IAELPNLEVLKMDACCSEWHPIVMGNRNLKLLIKYSP--LK 820
Qy 819 EIRFEDGSSPQLEKIEIRFCRLRSGIIGIIHLPLKIEISLGYESKVAGLAQLE-GEVRTH 877
Db 821 FWKATNDNFPVLERLMIRSK-----NLKEIPIEF-----ADIHTLQLELREC 864
Qy 878 PNHPLVRK---RDRSDHDLACDAEGSPVEATDPLPEGEGSSQ 920
Db 865 P--PKLGESAARIQKEQEDLG---NNPVDVRISNPLKESDSDSEE 904

RESULT 4
US-09-864-680A-3
; Sequence 3, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staekawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B62 Resistance Gene
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 3

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; LENGTH: 905
; TYPE: PRT
; ORGANISM: Capsicum annuum
US-09-864-680A-3

Query Match      11.2%; Score 576; DB 4; Length 905;
Best Local Similarity 24.6%; Pred. No. 3.7e-47;
Matches 218; Conservative 172; Mismatches 310; Indels 186; Gaps 37;

Qy 88 LVGSDSKLLEMDITNANDGPAKVICVGMGLGTALSRKIFSEEDIRKNFPCNAW 147
Db 152 MVRDDQKQLLEDL-TRSYSGEPKVPPIVGMGIGKTTLAKEYV-NDESLRCFDVHAW 209
Qy 148 ITVSQSFRHIELKDMIRQLLPSLSQQLQELQGVVQVHLSYELIELKRYFV 207
Db 210 ATISQOHNKKEILLGLHSTIKMDRVMIGEAE-----LADMLQSLKRRKRLIV 260
Qy 208 LDDLWILHDNWNINEIAPPKNNKGSQIVITNVDLAEKCATASLVYHLDPLQMDAIT 267
Db 261 LDDIWSCEVMDGVR-CPTEDNAGSRILLTRNDEVACVGVENFSLRMSFMDQDESWS 319
Qy 268 LLLKRTKNHEDMESNMQKQWRIKNCGRLEPLAITGAVLATKQ-VSEWEKPYEHL 326
Db 320 -LFKSAAFSSEALP--YEFETVGQIADCHGLPLTIWVAGLLKSKRTIEDMKTVAKDV 376
Qy 327 PSELEINPSLEALRMVMTLGNHLPKPCFLVLSIFPDEFKRNRLVGRWIAEGFVR 386
Db 377 KSFVTDPD-ERCSRVGLSDVHLTSDTKLHFGIFPDESDIPVKNLMSRWNAEGFL- 434
Qy 387 PKVGMTTKDVGESYFNELNRSMT---QSRVGIAGKIKTCRIHDIIRDITVSISROENF 443
Db 435 -KLENDLEGEVEKCLQELAVDRCLVLVSKSRDGT--KIRSKVHDLIYDLCVREVORENI 491
Qy 444 VLLPMGDSGLV-----QENTRHTAFHGSCKTGCLDWSII----- 479
Db 492 FIM-----NDIVLDVSYPECSYLCMYKMQPPKRVGTGEINCYGYLRALLTPVNRQLRD 546
Qy 480 -----RSLAIFGRPKSLAHAVCPD--QLRMLRVLDLEDVTFITQKDFD-----RIA 525
Db 547 HDNNLLKRTHTSVFSFHEPLFYVVKSEVHFLLKLVLELR-----HRQIDGFPREIL 599
Qy 526 LLCHLYLSIGYSSYISLPSRIGKLOGLQTLNMP--STVIAALPSRISKLCILTLRCS 583
Db 600 SLIWLRYLSL-FSYGNFDPVPEICRLNWLQTFIVORFSDIIIPAEIBIWMQLRHLKLP 658
Qy 584 RKFSVDNFSLNHPMKCTNIVCLPKVTPVLSRDRDRAIQIAELHMAKSCWYKSGFKVP 643
Db 659 RPYLPD-----CPSGSV-----DKGRHL----- 676
Qy 644 KGIGKLRDLQVLEVYDVRTSSRAIKELGOLSKLRKLGWMTNGSTKECKILCAAEKLS 703
Db 677 -----DFSNLQTIYSLSPRCTKEVI--WG-IQNVKLGISGKD----- 713
Qy 704 SLQLYYNAAGISDG-----GTLECLDISPPPLRLTLVLYGSLEPMNIEQTHLKKI 759
Db 714 --DYKSRDGLPNNLVYVQLEILSLISVDYSLP--VIISAKAFPAATLKKL-KLERT 768
Qy 760 YLLRSKLKSGKTMILGALPNLWLDLYRKAYLGEKLVFTGAPNRLTSLI-YDLDQLR 818
Db 769 YLSWSYLD-----IAELPNLEVYKLMDDACCAGEWHPIVGMFNRLKLLIKYSF--LK 820
Qy 819 EIREDGSSPOLEKIEIRFCLESGIIGIHLPRKISILGYESKVAGLAQLE-GEVRTH 877
Db 821 FWKATNDNFPVLERIMLRSK-----NLKEIPIEF-----ADIHTLQILREEC 864
Qy 878 PNHPVLRK---REDRSDHDLACDAEGSPVEATEADPLPEQEGESSQ 920
Db 865 P--PKLGESAARIQKEQEDLG-----NNPVDVRI SNPLKESDSDSEE 904

; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-4

Query Match      10.9%; Score 561; DB 3; Length 1240;
Best Local Similarity 23.2%; Pred. No. 2e-45;
Matches 235; Conservative 170; Mismatches 335; Indels 274; Gaps 41;

Qy 69 DSYAEDIRNOSARNVDEAEVLGFSDSKRIEMTDITNANDGPA----KVICVGMGLGK 124
Db 151 DSTKLETRTSTSLIDEDPIFG---RQSETELDRLLSSEGAGSKNITVVPVGMGLGK 207
Qy 125 TALSRIKIFSEEDIRKNFPCNAMITVSQSPHRIELKDMIRQLLPSLSQQLQELQGV 184
Db 208 TTLAKAVY-NDESVKNHFDLKAFCVSEAYNAFRITKGLLQELGSDLDVDDNLNLQVVK- 265
Qy 185 VQVHLSYELIELKRYFVVDLDLW--ILHDWNWINEIAPKNNKGSQIVITVNW 242
Db 266 -----LKERLKEKFLVLDDVNDNYNDELRNVFV--QGDIGSKIIVTRKD 313
Qy 243 DLAEKCATASLVYHLDPLQMDAITLLRKTNNHEDMESNMQKQWRIKNCGRLEPL 302
Db 314 SVALMGMNEQI--SMGNLSTEASWSLQFRAHAFNMDPM-GHSELEEVGRQIAAKCKGLPL 370
Qy 303 AILITGAVLATK-QVSEWEKPYEHLPSLEINPSLEALRMVMTLGNHLPKPCFLYL 361
Db 371 ALKTLAGLRSKSEVEEMKILRSEIWELRDNDILPAL----NLSYNDLPAHLKRCFSFC 426
Qy 362 SIPPEDEIKRNRLVGRWIAEGFVRPKVGMVTKDVGESYFNELINRSNIORSRVGIAGKI 421
Db 427 AIFPKDYPRKEQVIHLWIANGLV-PVEDBIIQDLGNQGFLELSRSSRSLFRVNPSEGI 485
Qy 422 KTC-RHDIIRDITVSISROENFVLLPMGDSGLVQENTRHTAFHGSCKTGCLD----- 475
Db 486 KELFLMHDVLVNDL-AQLASSKLCIRLEESQGSNML-EQCRHLSY--SMVGDDGFEKUTPL 541
Qy 476 --WSIIRSLA-----IFGDRPKSLAHAVCPDQELRVLVDLEDVTFITQKDFDRIA 525
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RESULT 5

US-08-930-996A-4

; Sequence 4, Application US/08930996A

Db 542 YKLEQLTLPTCCSVNYFYNPLTKRVHLNLP--TLRLRLSLUSH--YKMEELPNDLFI 598
Qy 526 LLCHLKLYSGYSSYSLPRSIGKJQLOLQTNMPSTYIAALPSEISKJQLOLTLRCSRK 585
Db 599 KKLRLFLDIS-RTNKRLPDSICVLYNLETLLSSCKLEELPLQMEKLNLR----- 650
Qy 586 FVSDNFSLNHPMKCITWTICLPKVTPLVSRDDRAIQIAELHMAKSCWYKSGVKVPKG 645
Db 651 -----HDSINTWH-----LKMPLH 665
Qy 646 IGLRLDLQVLE---YVDIRTSRAIKELGOLSKL-RKLGWMTNGSTKEKCKILCAAIE 700
Db 666 LSRKLSLOVLGAKFLGVWR-----MEDLGEAQLYGSLSVVKLENVVDREAVKPMR 720
Qy 701 KLSLOLYVNAAGISDGGTLECLDSIS-----SPPLRLTLVLYGSLEEM----- 746
Db 721 EKXHEQL-----SLEWSESISADNSQTERDILDELPHKNIQEVKLIYGRGTN 769
Qy 747 -PNWIEQLTKKLYLRSKLEKGTMLIIGALPNLMVLD-----LYRKAYLG----- 793
Db 770 FPNWADPLFLKVLKLSRCKDCYSLPALGQLFCLKFLSVKGMHGIRVVVTEEPYGRSS 829
Qy 794 -----EKLVEK-----TCAPNLRTLIS----- 811
Db 830 KKPENCKLEKLEFDMTEWKQWALGIGEFPLEKLSIINCPELSLEIPIOFSSLRPRVF 889
Qy 812 -----YD-----LDQLREIRFEDGSS-----PQLEKIE 834
Db 890 GCPVVFDAQVLRSLQSGMKQIEIYIRDCNSVTSFPFSLPTTLTKTIDISGCPKL-KLE 948
Qy 835 IRFCRL-----ESGIIGIHLPRLEISIGYSEKSVAGLAQLEGEVTRTHPNHPVLR 884
Db 949 APVCEMSFLEERSVEECGCVSPFLPTARELRIGCHNVRFLI-----PTATETLH--IR 1002
Qy 885 KREDSDHDLAC-----DAEG-----SPVEVATDPLPEQGE 917
Db 1003 NCENVEKLSMACGGAQLTSLDISGCKKJLCLPELLPSLKLQLTN-CPBIEGE 1055
RESULT 6
US-09-336-946B-4
; Sequence 4, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A P1-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; PRIOR FILING DATE: 1999-06-21
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-336-946B-4
Query Match 10.5%; Score 540; DB 4; Length 928;
Best Local Similarity 25.8%; Pred. No. 1.4e-43;
Matches 206; Conservative 143; Mismatches 312; Indels 136; Gaps 29;
Qy 9 ARSLVGSASIKOASA-----AADETSLILGVEKDIWYLFPHGVGRSGGPPVGMVASGN 62
Db 119 AKXMISSWIALRGLNRRRWIADDEVTLFSARVKE-----AIRQESVHLGRRTSS 170
Qy 63 QSLCAIDSYAEDIRNQARN-----VDEA-----ELVGSDSKRLLEMDITNAN 107
Db 171 RPREEVD---DDREDSAGNERRRFLSLTEGMDAAVHGQLVGRDLSMQKLVRLW---AD 224

Qy 108 DGP-AKVICVVGGLGKTALSRRKIFESB-EDIRKKNFPQNAWITVSFRIELLLKDMIR 165
Db 225 GEPKLKVASTVGGVGKTTTATEFYRLHGRRLDAPDFCRAFVTRPKRQPDMTKILTDMLS 284
Qy 166 QLLGPSSLDQLLOELQKQVVVQVHHLSLEYLIEELKEKRYFVLLDDILWHDWNNWINEIAF 225
Db 285 QL-----RPQHQHSSDVWEVDRLLETIRTHLQDRYFIIEEDLWASSMWDIVSR-GL 336
Qy 226 PKNKKGSQIIVITWNVDLAEKATASLVVYHLDPLQMDAITLLLRKTNKNHDMESNKN 285
Db 337 PDNN-SCSRILITETEPVALACCGYNSEHIKIDPLGDDVSSQLPFSVGVVQGNPEFGH 395
Qy 286 MQKQVERIVNKCRLPLAILITIGAVLATKQVSEWEKFEYHL-----PSELEINPSLEALR 340
Db 396 LTEVSHDMIKKCGGLPLAI-TITARHPKSQLDGMQOMNHQKSLTTSNLRKCNPTLOQMR 454
Qy 341 RMVTLGYNHLPSPHLCPCFLYLSIFPDEFKIKRNLVGRWIAEGFVRPKVGTMTTKDVGESY 400
Db 455 QVNLNLYNNLPCHLCAKCLLYLSIYKEDIIRKANLVQWMAEGFINSIENKWEVAVAGNY 514
Qy 401 FNELINRSMTQSRVGIAGIKICTRIHDIIRDTIVSISROENF-VLLPMGDSGLVQENT 459
Db 515 FDELAVGRGLVQPDVNCNEVLSCVVHHMVLNFTIRCKSIENPFSITLDHSQTTVVRHADKV 574
Qy 460 RHIAFHGSMCKT-----GLDWSIIRSLAIFGDRPKSLAHAVCPDQL-----RMLRVL----- 507
Db 575 RRLSLHFSNAHDTTPLAGRLSQVRSNAFFG-----QVKCMPSIADYRLRLVLLICFW 627
Qy 508 -DLEDVTFLLTKQDFDRIALLCHLYLSIGYSSYSLPRSIGKJQLOLQTNMPSTYIAA 566
Db 628 ADOEKTSY-----DLTSIFELLQRLYDKITGNITV-KLPEKIQLOLHLQLEADARATAV 681
Qy 567 LPSEISKJQLOLTLRCSRKEVSNFSLNHPMKCITWTICLPKVTPLVSRDDRAIQIAEL 626
Db 682 L-LDVIHTQCLLHLRL---VLLD--LLPH-----CHRYIFT----- 711
Qy 627 HMAKSCWYKSGFVKVPKGIGKLRDLQVLYVDIRRTSSRAIKELGOLSKLRKLGVMWNG 686
Db 712 -----SIPKWTGKLNLRILN-IAMVQISQDDLDLTKGLSGSLTALSLLVRT 756
Qy 687 STKECKKILCAJELKSLLOY-LYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEE 745
Db 757 APAQR-----IVAANEFGSLKYFMFV-----CTAFCMTFVEGAMPSVORLNLRFNANE 805
Qy 746 MPNWIEOLTHLKXIYLL 762
Db 806 FKQYDSKETGLEHLVAL 822

RESULT 7

US-08-930-996A-2
; Sequence 2, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE I2 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: Floppy disk


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;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-2

Query Match      10.5%; Score 540; DB 3; Length 1220;
Best Local Similarity 22.9%; Pred. No. 2.3e-43;
Matches 228; Conservative 170; Mismatches 360; Indels 238; Gaps 41;

Qy 70 SYAEDIRNQSARNVDEAELVGFSDSKK-----RLLEMDITNANDGPAKVICVVGNGGLGKT 125
Db 151 STQGETRPTSTSLVDDSGIFGRKNEIENLVGRLISM-DTKRKN--LAVVPVVGWGGWGT 207
Qy 126 ALSRKIPESIEDIRNPPCNWITVSQSFHRIELLDKMIROLQGPSSL--DOLLOELQK 183
Db 208 TLAKAVY-NDERVQHFGLTAMFCVSEAYDAFRIPKGLQOE-IGSTDLKADDNINLQVVK 265
Qy 184 VVV--QVHHLSEYLIIEELKERYFVLLDDLM--ILHDWNWINEAFPPKNNKGSQIVITT 239
Db 266 LKADDNINLQVVKELKGRFLVLLDDVNDWNPEDDLRLNLF--QGDIGSKIIVTT 323
Qy 240 WNVDLAEKCATASLVYHDLFLQNDAITLLLRKTNKNHEDMESNKNMQKMERIVNKCGR 299
Db 324 RKESVALMDSGAI--YMGILSSEDS-WALFKRHSLEHKOPKEHPEEVEVGKQIADKCKG 380
Qy 300 LPLAILTIGAVLATK-QVSEWEKEYEHLPSBL-EINFSLEALRMWTLGVNHLPSHLKPC 357
Db 381 LPLALKALAGMLRSKSEVDWRNT---LRSEIWELPSCNGILPALMLSYNLDPALHLKQC 437
Qy 358 FLYLSIPPEPEIKRNLVGRWIAEGFVRPKVGWTTKDVGESYFENELNRSMTQSRVGI 417
Db 438 LAYCAITPKDYQFKQEVHILWANGLVH-----QFHSNGQYFIERSLSLFEMASEPS 491
Qy 418 AGKIKTCRIHDIIRDITVSISRQENFVLLPMGDSGLVQENTRIHAFHGSMSCKTGLDWS 477
Db 492 ERDVEEFMLHDVNDL-AQIASSNHCIREDNKGSHML-EQCRH-----MSYSIGDGE 543
Qy 478 IIRSLAIFGR-----PKSLAHAVCPQLRMRLVRDLDEDVTFLLITQK 519
Db 544 FEKLKSLFKSEQLRTLLPIDIQFHYSKLSKRVLNLPL-TLRSRLALSHTYQIEVLPN 602
Qy 520 D-PDRIALLCHLKVLS:GYSSISVSLSPRSCKLOGLQTLAMPS-TYIAALPSEISKLQCL 577
Db 603 DLFTKLKL---LRFLDUS-ETSIKLPDPSFVLVNLLETLLSSCEYLEELPLOMEKLINL 658
Qy 578 HTLRCSKRFVSDNPSLNHPMKCIINTTICLPKVFPTPLVSRDDRAIQIAELHMAKSCWYKS 637
Db 659 RHLDISN-----TRRLKIPHLSSL-----KSLQVLVGAKFLVGGWRME 697
Qy 638 FGKVPKGIKGLRDLQVLEYVDIRRTSSRAIKE---LGQLSKRLKGLWMTNGSTYKECKKI 694
Db 698 YLGEAPNLYGSLSTLELENVVDREAVAKMRKNHVEQLSLEWSESISADNSQTER---754
Qy 695 LCAAIEKLSIQLYLVNNAAGISDGGTLECDLSISSPPPLRLTLVLYGSL-EEMPNIWEQL 753
Db 755 -----DILDEL-RPHKNIKAVEITGYRTNFPNWADP 786
Qy 754 THLKKIYLLRSKLKEGKTMILGALPNLMVLDIRKAYLGEKLVFKTKTGAFFNLRTLSIYD 813

;
;
; 787 LFVKLVHLYLRNCKOCYSLPALGQLPCLEFLSI--RGMHGIRVV--TEFYG-RLSKKP 841
; 814 LDOLREIRFED-----GSSPOLEKIEIRFCRLSGLIIGIHLPRLEISLGYE 861
; 842 FNSLVKURFEDPEWKQWHTLGI GEFPTLEKLSKNC-----PELSLEIP 886
; 862 SKVAGLAQLEGEVTRTHENHPVLRKRDRSDHDLACDAEGSPVEATDPLPEQGESSOR 921
; 887 IQFSSSLKRLD-----ICDC-----900
; 922 RDKHSSWFWQVWISS--STIGISGRPCF-----CGCAHLAVPRGAD 961
; 901 --KSVTSFPFSILPTTLKRIKISGCPKLKLEAPVGMFVEYLSVIDCGCVDDDISPEFLPT 958
; 962 LRLPLUSSIASHALDSSLGMCNCFNLTFRSRMLLVP 997
; 959 ARQLSIE-----NCHNVT-----RFLIP 976

RESULT 8
US-09-336-946B-2
; Sequence 2, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Bryant, Barbara S.
; APPLICANT: Valent, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-09-336-946B-2

Query Match      10.5%; Score 539.5; DB 4; Length 928;
Best Local Similarity 26.7%; Pred. No. 1.6e-43;
Matches 194; Conservative 132; Mismatches 282; Indels 119; Gaps 26;

Qy 73 EDTRNQSARN-----VDEA-----ELVGFSDSKKLELMDITNANDGP-AKVICV 116
Db 178 DDDREDSAGNERRRFLSLTFGMDDAVAHVGQLVGRDISMOKLVRWL---ADGEPKLVASI 234
Qy 117 VGMGGGLKTALSRKIPES-EIRKNPPCNWITVSQSFHRIELLDKMIROLQGPSSLQ 175
Db 235 VSGGVGKTLTAEFYRLHGRRLDAPPDCRAFVTRPKPDWTKLTLTMSQL-----R 287
Qy 176 LLQELQGVVVQVHHLSEYLIIEELKERYFVLLDDLMILHDWNWINEAFPPKNNKGSQI 235
Db 288 PQHQHQSSDVWEVDRLLETRTHLQDKRYFIIEEDLWASSMWDIVSR-GLPDNN-SCSRI 345
Qy 236 VIITNVNDLAEKCATASLVTHLDFLQNDAITLLLRKTNKNHEDMESNKNMQKMERIVN 295
Db 346 LITTEIPVALACGYNSEHIIKIDPLGDDVSSQLFFSGVVGQGNFPGHLETVSHDMIK 405
Qy 296 KCGRPLAIIITIGAVLATKQVSEWEKEYEHL-----PSELEINPSLEALRMWTLGVNHL 350
Db 406 KCGLPLAI--TITARHFKSLLDGMQWNNHIOKSLTTSNLUKNPTLOMKQVNLITNNL 464
Qy 351 PSHLKPCFLYLSIPPEPEIKRNLVGRWIAEGFVRPKVGWTTKDVGESYFENELNRSMTI 410
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Qy 411 QRSRVGIAGIKTCRIHDIIRDITVSISRQENF-VLLPMGDSGLVQENTRIHAFHGSMS 469
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RESULT 12

US-09-803-286A-2

; Sequence 2, Application US/09803286A

; Patent No. 666447

; GENERAL INFORMATION:

; APPLICANT: Tankeley, Steven D.

; APPLICANT: Brommonschenkel, Sergio H.

; TITLE OF INVENTION: PLANT GENE CONFERRING RESISTANCE TO TOSPOVIRUSES

; FILE REFERENCE: 19603/3201

; CURRENT APPLICATION NUMBER: US/09/803,286A

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 60/188,356

; PRIOR FILING DATE: 2000-03-10

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1247

; TYPE: PRT

; ORGANISM: Lycopersicon var.

US-09-803-286A-2

Query Match 10.2%; Score 525; DB 4; Length 1247;

Best Local Similarity 24.3%; Pred. No. 7.2e-42;

Matches 206; Conservative 158; Mismatches 318; Indels 164; Gaps 35;

Qy 83 VDEALVGFSDSKRLLEMDITNDNDGPAKVICVVGGLGKLTALSRIESEDIRKNP 142

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Qy 143 PCNAWITVSOFRIELKMIROLLGLPSSLDQLQLQELQGVVQVHLSYELKEK 202

Db 586 DVRAWCIISQYINRRLQLDIFSQTSD-----DNGATVDV--LADMLRRLKMGK 634

Qy 203 RYFVLDLMLTHDNWINEIAPFNKNGKSQIVITWVNDLAEKCATASLVYHLDLQ 262

Db 635 RYLVLDMDCWMDL-RLSFDDGIR-SRIVVTRLEEVGQVKYHTDPYSLPLTT 692

Qy 263 NDAITLLRKTNNHDEMESKNNQKQWVERIVNKGRLPLAILTIGAVLATKQVSE--W- 319

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Db 924 ITTNRAKSINDIFSCISELRLKLDLS--SYIVFSLSLATFKPLNQLKYLAVQAFEFY 981

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RESULT 13

US-09-004-838-11

; Sequence 11, Application US/09004838

; Patent No. 6350933

; GENERAL INFORMATION:

; APPLICANT: Michelmore, Richard W.

; APPLICANT: Meyers, Blake

; TITLE OF INVENTION: Procedures and Materials for

; TITLE OF INVENTION: Confering Pest Resistance in Plants

; NUMBER OF SEQUENCES: 140

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/004,838

; FILING DATE: 09-JAN-1998

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/781,734

; FILING DATE: 10-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Einhorn, Gregory P.

; REGISTRATION NUMBER: 38,440

; REFERENCE/DOCKET NUMBER: 023070-078810US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1402 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: -

; LOCATION: 1..1402

; OTHER INFORMATION: /note= "RLG1a amino acids"

US-09-004-838-11

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GenCore version 5.1.6
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Run on: February 9, 2005, 08:53:28 ; Search time 90.9347 Seconds
(without alignments)
3574.555 Million cell updates/sec

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Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4169.5	81.2	1091	15	US-10-352-179-93
3	4102.5	79.9	1531	16	US-10-437-963-133799
4	3191	62.1	993	16	US-10-437-963-104966
5	2621	51.0	979	15	US-10-352-179-85
6	2613	50.9	974	16	US-10-437-963-143499
7	2379.5	46.3	862	16	US-10-437-963-141086
8	2184	42.5	1007	16	US-10-437-963-110261
9	2170.5	42.3	993	15	US-10-352-179-87
10	2105	41.0	1163	16	US-10-437-963-151916
11	2103.5	40.9	1054	15	US-10-352-179-91
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17	1033	20.1	1251	16	US-10-437-963-156608	Sequence 156608,
18	1020	19.9	981	16	US-10-437-963-149503	Sequence 149503,
19	1005	19.6	916	16	US-10-437-963-167102	Sequence 167102,
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21	987.5	19.2	975	16	US-10-437-963-178601	Sequence 178601,
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23	956	18.6	1011	16	US-10-437-963-134127	Sequence 134127,
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25	944	18.4	1025	16	US-10-437-963-170107	Sequence 170107,
26	932.5	18.2	1205	16	US-10-437-963-190992	Sequence 190992,
27	929	18.1	787	16	US-10-437-963-137268	Sequence 137268,
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34	859.5	16.7	970	16	US-10-437-963-120373	Sequence 120373,
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38	849.5	16.5	933	16	US-10-437-963-181083	Sequence 181083,
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42	814	15.8	936	16	US-10-437-963-185358	Sequence 185358,
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ALIGNMENTS

RESULT 1
US-10-352-179-89
; Sequence 89, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCES: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-89

Query Match	81.8%	Score 4204;	DB 15;	Length 1031;
Best Local Similarity	83.9%	Pred. No. 0;		
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Qy 224 AFPKNKKGSQIVITTNVNDLAECATASLYVHLDFLOMNDATILLARKTNKHEDMESN 283
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RESULT 2
US-10-352-179-93
; Sequence 93, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 93
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-93

Query Match      81.2%; Score 4169.5; DB 15; Length 1091;
Best Local Similarity 79.0%; Pred. No. 0;
Matches 848; Conservative 21; Mismatches 49; Indels 155; Gaps 4;

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RESULT 3
US-10-437-963-139799
; Sequence 139799, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139799
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1.pep
US-10-437-963-139799

Query Match 79.9%; Score 4102.5; DB 16; Length 1531;
Best Local Similarity 89.3%; Pred. No. 0;
Matches 817; Conservative 17; Mismatches 50; Indels 31; Gaps 4;

Qy 57 MVASGNQSLAIDSYAEDIRNQSARNVDEALVCFSDSKKRLLEMDTNDNGPAKVICV 116
Db 1 MVASGNQSLAIDSYAEDIRNQSARNVDEALVCFSDSKKRLLEMDTNDNGPAKVICV 60

Qy 117 VGMGLGKTALSRKIFSEEDIRNFCNAWITVSQSFHRIELDKMIRQLGSPSSLDQL 176
Db 61 VGMGLGKTALSRKIFSEEDIRNFCNAWITVSQSFHRIELDKMIRQLGSPSSLDQL 120

Qy 177 LQELQGVVQVHLSYELIEELKEKRYFVVLDDLWILHDWNWINEIAPPNKKGSQIV 236
Db 121 LQELQGVVQVHLSYELIEELKEKRYFVVLDDLWILHDWNWINEIAPPNKKGSQIV 180

Qy 237 ITTNVNDLAEKATASLYHLDFLOMDAITLLLRKTNKHEDMESKNQKQVRIWVK 296
Db 181 ITTNVNDLAEKATASLYHLDFLOMDAITLLLRKTNKHEDMESKNQKQVRIWVK 240

Qy 297 CGRLPLAILITIGAVLATQVSEWEKFEYHLPSLEINPSLEALRWYTLGVNHLPSHLKP 356
Db 241 CGRLPLAILITIGAVLATQVSEWEKFEYHLPSLEINPSLEALRWYTLGVNHLPSHLKP 300

Qy 357 CFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMWTKDVGESYFNLINRSMIQRSRVG 416
Db 301 CFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMWTKDVGESYFNLINRSMIQRSRVG 360

Qy 417 IAGIKTCRIHDIIRDITVSI SROENFVLLPMGSGSDLVQENTRHIAFHGSMSCKTGLDW 476
Db 361 IAGIKTCRIHDIIRDITVSI SROENFVLLPMGSGSDLVQENTRHIAFHGSMSCKTGLDW 420

Qy 477 SIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLEDVTLITQKDFDRIALIHLKYLISIG 536
Db 421 SIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLEDVTLITQKDFDRIALIHLKYLISIG 480
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Qy 537 YSSISYSLPSIGKLOGLOTLNMPSTYIAALPSEISKLOCLHTLRCSRKVFSDNFSLNHP 596
Db 481 YSSISYSLPSIGKLOGLOTLNMPSTYIAALPSEISKLOCLHTLRCSRKVFSDNFSLNHP 540
Qy 597 MKCITWTICLPKVFTPLVSRDDRAIQIAELHMAKTSWKYKSGVGVKPGIGKLRDLQVLE 656
Db 541 MKCITWTICLPKVFTPLVSRDDRAIQIAELHMAKTSWKYKSGVGVKPGIGKLRDLQVLE 600
Qy 657 YVDIRRTSSRAIKELGOLSKRLKLGWNTNGSTVEKIKLCAAEKLSLQVLYVNA---A 713
Db 601 YVDIRRTSSRAIKELGOLSKRLKLGWNTNGSTVEKIKLCAAEKLSLQVLYVNA---A 660
Qy 714 GISDGGTLECLDSISSPPPLRLTLVLYGSLSEENPWIEQLTHLKKIYLLRSKLEKGTML 773
Db 661 GI1--GTLECLDSISSPPPLRLTLRLNGSLSEENPWIEQLTHLKKIYLLRSKLEKGTML 718
Qy 774 ILGALPNLMVLYLRNAYLGEKLVFKTGAPNLRLLTSIYDLDDQREIRFEDGSSPQLEKI 833
Db 719 ILGALPNLMVLYLRNAYLGEKLVFKTGAPNLRLLTSIYDLDDQREIRFEDGSSPQLEKI 778
Qy 834 EIRFCRLSGIIGIHLPLKIBISLYESKVLGAGLAQLSGEVTRTHNHPVLRKRDRSDHD 893
Db 779 EIGKCRLESIGIIGIHLPLKIBIPITYGSKVAGLQGLEGEVNTNHPVLRKRDRSDHD 838
Qy 894 LACDAEGSPVE-----VEATDPLPEGESSQ-----RDXHSS 927
Db 839 LGABAGSGSIEVQTADPVPDAEGSVTVAVEATDPLPEGESSQSVITLTNDNRNLVG 898
Qy 928 SWFQVNMISISSIGIS 942
Db 899 RWIAGFVRPKVGMT 913

RESULT 4
US-10-437-963-104966
; Sequence 104966, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 104966
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102251C.1.pep
US-10-437-963-104966

Query Match 62.1%; Score 3191; DB 16; Length 993;
Best Local Similarity 66.1%; Pred. No. 7.6e-258;
Matches 657; Conservative 75; Mismatches 122; Indels 140; Gaps 6;

Qy 1 MAETVLSMARSLVGSATSKAASAADETSLLGVKEDIWY----- 40
Db 60 MAETVLSMARSLVGSATSKAASAADETSLLGVKEDIWYKDELKTMQAFPLRAEVNKK 119
Qy 41 -----LF-----RHGV----- 46
Db 120 KDELKTMQAFPLRAEVNKK 179
Qy 47 ---GRSNGPVGWVGWAGNQSCLAIDSYAEDIRNQSARNVDEALVCFSDSKKRLLEMD 103
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Db 180 EVSSRNRYNLVKPDISSNED--DMDCYAEDIRNQSTSNVDETLVGFSDSK----- 229
Qy 104 TNANDGPAKVICVVMGGLGTALSRKIFESEEDIRKNFPCNAMIIVTSQSFRHIELLKD 163
Db 230 -----IRIELLKD 238
Qy 164 IRQLGPSLDQLQELQGVVQVHLSLEYLIELKEKRYFVVLDDLWLHDMNWIN 223
Db 239 IRQFLGNSLDVLQELQGMVVQI PHLSVLYRKKLKEKRYFVVLDDLWLSLDAWNWINDI 298
Qy 224 APPKNNKGSQIVITTNVVDLAEKCATASLYHLDLFLQMDAITLLLRKNTKONHEDNES 283
Db 299 APPKNNKGSRIIVTTTRDVGLAEKCTTSLVYHLEHLQMDAITLLLRKNTKONHEDNES 358
Qy 284 KNNQKMYERIVNKGRLPLAIIITGAVLATKQVSEWEKFEYHLEPSELEINPSEALRMV 343
Db 359 KNNQKIVEQIVNKGRLPLAIIITGAVLATKQVSEWEKFEYHLEPSELEINPSEALRMV 418
Qy 344 TLGYNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMITTKDVGESYFNE 403
Db 419 TLGYNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMITTKDVGESYFNE 478
Qy 404 LNRSMIQRVRGTAGIKTCRIHDIIRDTIVTSISROENFVLLPMGDSGLVQENTRHIA 463
Db 479 LNRSMIQRVRGTAGIKTCRIHDIIRDTIVTSISROENFVLLPMGDSGLVQENTRHIA 538
Qy 464 PHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLDDVTLITQKDFDR 523
Db 539 LHGSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLDDVTLITQKDFDR 598
Qy 524 IALLCHLYLSIG--YSSSIYSLPRSIGKLGQGLQTLNMPSTYIAALPSEISKLOCLHLR 581
Db 599 IALLCHLYLSIG--YSSSIYSLPRSIGKLGQGLQTLNMPSTYIAALPSEISKLOCLHLR 658
Qy 582 CSRKFSVNDPNSLHMPKCIINTNICLPKFTPLVSRDRAIOIAELHMAKTSWYKSGVK 641
Db 659 CTRVSNNNPNSLHMPKCIINTNICLPKFTPLVSRDRAIOIAELHMAKTSWYKSGVK 718
Qy 642 VPKGIGKRLDQVLEYVDIIRTSRAIKELGQSLKRLGVMTNGSKKCKILCAAIEK 701
Db 719 VPKGIGKRLDQVLEYVDIIRTSRAIKELGQSLKRLGVMTNGSKKCKILCAAIEK 778
Qy 702 LSSLYLYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEMPNWIQLTHLKKIYL 761
Db 779 LSSLYLYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEMPNWIQLTHLKKIYL 838
Qy 762 LRSKLEKGTMLILGALPNLMVLDIRKAYLGEKLVFKTGAPNRLTSLIYDLDQLREIR 821
Db 839 LRSKLEKGTMLILGALPNLMVLDIRKAYLGEKLVFKTGAPNRLTSLIYDLDQLREIR 898
Qy 822 FEDGSSPOLEKIEIRFCRLESGIIGIHLPRLEKISLYGSYKAVAGLAQLGEVTRHPNH 881
Db 899 FEDGSSPOLEKIEIRFCRLESGIIGIHLPRLEKISLYGSYKAVAGLAQLGEVTRHPNH 958
Qy 882 VLKREDRSDHDLACDAEGSPVEATDPLPEQE 915
Db 959 VLKREDRSDHDLACDAEGSPVEATDPLPEQE 992
```

RESULT 5

```
US-10-352-179-85
; Sequence 85, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
```

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; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Oryza minuta
; US-10-352-179-85

Query Match 51.0%; Score 2621; DB 15; Length 979;
Best Local Similarity 55.3%; Pred. No. 4.6e-210;
Matches 539; Conservative 134; Mismatches 217; Indels 84; Gaps 6;

Qy 1 MAETVLSMARSLVGSALSAAADSTSLLGVEKDIWYL----- 41
Db 1 MAETVLSMARSLVGSALSAAADSTSLLGVEKDIWYL----- 60
Qy 42 -----PR-HGVGRSNGGPPVGMVASGNQSCLAII----- 68
Db 61 KODLLKWAQVRDLVSYNIEDCLDEFKVVHVESQAKQLMKL---GERHRIAIVOILNLS 117
Qy 69 -----DSYAEDIRNQSARNVDEAEELVGFSDSKRLLEM 101
Db 118 RIEVSNRNTRYSLIKLISSITTEDEDSVLEDAENRSGSNTSESELVGFATKDELLKL 177
Qy 102 IDTNANDGPAKVICVVMGGLGTALSRKIFESEEDIRKNFPCNAMIIVTSQSFRHIELL 161
Db 178 IDVTNDGPAKVICVVMGGLGTALSRKIFESEEDIRKNFPCNAMIIVTSQSFRHIELL 236
Qy 162 DMTRQLLGPSSLDQLQELQGVVQVHLSLEYLIELKEKRYFVVLDDLWLHDMNWIN 221
Db 237 QMTRQLLGPSSLDQLQELQGVVQVHLSLEYLIELKEKRYFVVLDDLWLHDMNWIN 296
Qy 222 EIAPPKNNKGSQIVITTNVVDLAEKCATASLYHLDLFLQMDAITLLLRKNTKONHED 281
Db 297 DTAPPKNNKGSQIVITTNVVDLAEKCATASLYHLDLFLQMDAITLLLRKNTKONHED 356
Qy 282 SNRKMOMQWERIVNKGRLPLAIIITGAVLATKQVSEWEKFEYHLEPSELEINPSEAL 341
Db 357 NDBDLSIVTKLVKRCGYLPLAIIITGAVLATKQVSEWEKFEYHLEPSELEINPSEAL 416
Qy 342 MVTLYGNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMITTKDVGESY 401
Db 417 MVTLYGNHLPKPCFLYLSIFPEDFEIKRNLVGRWIAEGFVRPKVGMITTKDVGESY 476
Qy 402 NELINRSMIQRVRGTAGIKTCRIHDIIRDTIVTSISROENFVLLPMGDSGLVQENT 461
Db 477 NELINRSMIQRVRGTAGIKTCRIHDIIRDTIVTSISROENFVLLPMGDSGLVQENT 536
Qy 462 IAFHSGMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLDDVTLITQ 521
Db 537 LAFHSGMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRMLRVLDLDDVTLITQ 596
Qy 522 DRALLCHLYLSIGYSSSIYSLPRSIGKLGQGLQTLNMPSTYIAALPSEISKLOCL 581
Db 597 RNTGLRHMKYLNFARASTIYTLPRSIGKLGQGLQTLNMPSTYIAALPSEISKLOCL 656
Qy 582 CSRKFSVNDPNSLHMPKCIINTNICLPKFTPLVSRDRAIOIAELHMAKTSWYKSG 640
Db 657 CSRKFSVNDPNSLHMPKCIINTNICLPKFTPLVSRDRAIOIAELHMAKTSWYKSG 716
Qy 641 KVPKIGIKGLDQLVLEYVDIIRTSRAIKELGQSLKRLGVMTNGSKKCKILCAAIE 700
Db 717 RVPKIGIKGLDQLVLEYVDIIRTSRAIKELGQSLKRLGVMTNGSKKCKILCAAIE 776
Qy 701 KLSLYLYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEMPNWIQLTHLKKI 760
Db 777 KLSLYLYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEMPNWIQLTHLKKI 821
Qy 761 LRSKLEKGTMLILGALPNLMVLDIRKAYLGEKLVFKTGAPNRLTSLIYDLDQLREI 820
Db 837 LRSKLEKGTMLILGALPNLMVLDIRKAYLGEKLVFKTGAPNRLTSLIYDLDQLREI 896
Qy 821 RFEDGSSPOLEKIEIRFCRLESGIIGIHLPRLEKISLYGSYKAVAGLAQLGEVTRHPNH 880
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Db 897 RFEGETPTWESIIYGRLESIGIWKLPRLKIIISLEYDGKVAKLVDVQEVNTHPNH 956
Qy 881 PVLKREDSDHDL 894
Db 957 TELQMAEDRSHDL 970

RESULT 6
US-10-437-963-143499
; Sequence 143499, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 143499
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_44401C.1.p
US-10-437-963-143499

Query Match 50.9%; Score 2613; DB 16; Length 974;
Best Local Similarity 55.6%; Pred. No. 2.1e-209;
Matches 539; Conservative 127; Mismatches 226; Indels 78; Gaps 4;

Qy 2 AETVLSMARSLVSGSAISKAASAAADETSLIGVEKDIWYL-----41
Db 3 AETVSNMWSVLGSAVGKASAAADEATLLIGIQEIWIYKDELKTTQAFRAAEVTKK 62
Qy 42 -----FRHGVGRSGPPVGM 57
Db 63 DDLKLVWAEQVRLSYNIEDCLDFKVVHVESQSLAKQLMKLGERHRIAQVIRNLKSRIE 122
Qy 58 VASGNQSLAI-----DSYAEIDRNQSRNVDEALVGFSDSKRLLEMDTN 105
Db 123 VSNRTRYSLIKPISSTTDERDSYLEDARNQSGSNTDESELVGFARTKDELKLDVN 182
Qy 106 ANDGPAKVICVGMGGGLKLTALSRKIFESIEDIRKFPNCAWITVSQSFHRIELLDKDIR 165
Db 183 TNDGPAKVICVGMGGGLKLTALSRKIFESIEDIRKFPNCAWITVSQSFHRIELLDKDIR 241
Qy 166 QLLGPFSSLDQLQLOGVQVHHLSEYILEELKEKRYFVLLDDWLHLDWNNIBAF 225
Db 242 QLLGADSLDLKLFSEKLLVQVQHLADHLVEGLKEKRYFVLLDDWLTDANWHDIAF 301
Qy 226 POKNKGSOIVITWNVDLAKCATASLVTHLDFLQNDAITLLRTKNKHEDMESKN 285
Db 302 PKINRGSRRIITRDAGLAGRCTSESLIYHLEPLHTDDAIHLLAKTNIRLEDMDENED 361
Qy 286 MOKMVERIVNKGRLPLAILTIGAVLATKOVSEKEFVHLPSELEINPSLEALRRMVTL 345
Db 362 LGSIVTKLVKRCGYLPLAILTIGILATKIMEMGKFTRELPSLEINPSLEALRRMVTL 421
Qy 346 GYNHLPKPCFLYLSIFPEDFEIKNRLVGRWIAEGFVRPKVGMTTKDVGESYFNELI 405
Db 422 SYNHLPKPCFLYLSIFPEDFEIQGRVLDWIAEGFVRATDVGNIEDVGNHSFNELI 481
Qy 406 NRSMIQSRVGIACKIKTCRIHDIIRDITVISISQENFVLLPMGSGSDLVQENTRHIAFH 465

Db 482 NRSIQPSKYSTDGVKRCRIHDIRDIIYVISREENFVLLTREKITVVAESIRHLAPH 541
Qy 466 GSMCKTGLDWSIIRSLAIFGDRPKSLAHAVCPDQLRMLRVLDLEDVTFITQKDFRIA 525
Db 542 GSKCKICLENHLSVTLFGDRPVGRTPALCSPQFRMLRVLDLEDKAFKFTQNDIRNIG 601
Qy 526 LLCHLYLSIGYSSISYSLPRSIGKLOGIQTANPSTYIAALPSEISKLOCLHLTRCSRK 585
Db 602 LLRHMYLNPARASTIYTLPRSIGKLOCLQILNNREANISALATTEVTKJQNLRLCSRR 661
Qy 586 FVSDNFS-LNHPMKCTINTCLPKVFTPLVSRDRAIQIAELHMAKSCWYKSGVGVPK 644
Db 662 SGSCYFSIIDNPKELMTWCLPNVFLTSINFSDRVKLIPEICMSCSTRSDTKGVVR 721
Qy 645 GIGKLRDLQVLEVYDRIIRTSRAIKELQIGLSKRLKLGVMGTNGSTKCKIKLCAAEIKLSS 704
Db 722 GIDNLKELQILEVVDINRTSRKAIEELGELIQLRKLSTVTGATNKKYQIFCAAEIKLSS 781
Qy 705 LOVLYNNAAGISDGTLECLDSISSPPPLARTLVLYGSLSEMPNWIQLTHLKKIYLLRS 764
Db 782 LQSLRVDAEGFSDGTLEWLSIACPPFPFLKRLKLSLADTPNWFNGLKOLVXKCLSR 841
Qy 765 KLKEGKTMILGALPNLWLDLYRKAYLGKLVFKTGAFNLRITLSIYDLDQLEIRIFED 824
Db 842 GLKDGKTMELGALPNLWLVLYNAYADEKMTFRCTFPNLRCLDIYLLKQLEIRIFE 901
Qy 825 GSSPOLEKIEIRFCRESGIIGIHLPRLEISIGYKSVAGLQLEGEVTRTHNHPVLR 884
Db 902 GTSPTMESIEIYGRLESIGIIGKHLPRLEISIGYKSVAGLQLEGEVTRTHNHPVLR 961
Qy 885 KREDSDHDL 894
Db 962 MAEDRSHDL 971

RESULT 7
US-10-437-963-141086
; Sequence 141086, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141086
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42224C.1.p
US-10-437-963-141086

Query Match 46.3%; Score 2379.5; DB 16; Length 862;
Best Local Similarity 51.4%; Pred. No. 6.6e-190;
Matches 508; Conservative 109; Mismatches 158; Indels 213; Gaps 10;

Qy 1 MATVLSMARSLVSGSAISKAASAAADETSLIGVEKDIWYL-----41
Db 1 MTDTVLSTAKSLVGSASVSAABKQVLLGVQKEIFIKDELQRIQAFMAAEPSKK 60
Qy 42 -----FRHGVG-----47
Db 61 SILLKVVQVQVRLSDYDIEDCLDEFTVHVSSQTLRSQMLKDRHRIAQIRNLRTREE 120


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Qy 48 -----RSGGPGVGMVAGSQSLAIDS---YAEDIRNQSARNVDABELVGFSDSKRL 98
Db 121 VSTENIRYN-----LIENDLTCTTDERNLFMEDIRNQSANNIEADLVGFGPKREL 173
Qy 99 LEMIDTWNADGPAKVICVGMGGGLGKTALSRSKIPESEDIRKNFPCNAWITVSOSFHRIE 159
Db 174 LDLDIVHANTGPTVEWCVGMGGGLGKTITARKIYESKEDIKAFNSCCAWITVSQSFVRLE 233
Qy 159 LKDMIRQLCPSSLDQLLOELQGVVVQVHLSLEYLIELKEKRYFVVLDDLWILHDWN 218
Db 234 LKDLMMKLFGEVLLKQKMLEGK-VPOVDLASYLRTELNERR----- 277
Qy 219 WINEIAPFNKKKGSQIVITVWNVDLAEKCATASLVYHLDPLQNDAITLLLRKTNKHE 278
Db 278 -----NNKGSWIVITRVDGLAKECTSELLIYQLKPLEISYAKELLRRKANKTTE 328
Qy 279 DMESKNMKNQKVERIVNKGRLPLAIIITIGAVLTKQVSEWEKPYEHLPSLEINPBLEA 338
Db 329 DIESDKKMSDITIKVKKCGYLPLAIIITIGVLAKEIREWETFYSQIPSELESNPLEA 388
Qy 339 LRMMVTLGYNHLPSHLKPCFLYLSIPDEPEIKENRLVGRWIAAGFVRPKVGMTTKDVG 398
Db 389 MRRIVTLSYNPLSHLKQCFYLSIPDEFEINRRL----- 425
Qy 399 SYFNELINRSMIQRSRVGIAGKIKTCRIHDIIRDTIVTSIQROENFVLLPMGDGSDLVQEN 458
Db 426 ----- 425
Qy 459 TRHIAFHGSMC-KTGLDWSIIRSLAIFGDRPKSLAHAVCDQRLMLRVLDLVDVTLIT 517
Db 426 -----GSKYCKISIPDWSIIRSLTFAERPAEVLHSHVCSSQLRMLRVLDLDAQFTIT 478
Qy 518 QKDFDRALILCHLVLSI---GYSSSYSLPRSIGKLOGLQTLNMPSTYIAALPSEISKL 574
Db 479 QNDVNNIVLLCHLYLRARIYNNASYISLPSKISGRDLGQLTLDLSTNLTPTQITKL 538
Qy 575 QCLHTLRCRSKFVSDNLSNHPMKICTNTICLPKVFTPLVSRDDRAIQIAELHMAKSCW 634
Db 539 RSLRSKCMQYDSSFT-----TCLDTYTLCLPMIFTPSVSTSDRAEKIANHLATKSF 593
Qy 635 YKSGFVKVPKGIGKRLDQVLEYDIIRTSSRAIKELGQSLKRLGVMWNGSTKECKKI 694
Db 594 SKSNGVVKPGICRLRLDQILGVVDIIRTSRVVKELGQSLKRLVVTGKSTKLKEI 653
Qy 695 LCAAEKLSLOYLYVNAAGISDGTLECLDSISSPPLIARTLVYGSLEEMPNWIEQLT 754
Db 654 LYTAIQKLYLSQSLHMDAVGCTGTLECLDSVSSPPPLTLTLRLNGSLEELPNWIERLT 713
Qy 755 HLKKIYLLRSKLKGGKTMILGALPNLMVLVDLYRKAYLGEKLVKPGTGAFFNLRTLSYDL 814
Db 714 HLRFYLLRTYKLKGGKTMILGALPNLMLLHFCNAYLGEKLVKPGTGAFFNLRTLVFNL 773
Qy 815 DQLEIRFEDGSSPOLEKIEIRFCRLESIGIIGIHLPRLKEISLGYSKVAGLAQLEGEV 874
Db 774 DQORDIRFEDGSSPOLEKIEIGRCLSSGIIGIHLPRLKEISVEYKGVAMLAQLEGEV 833
Qy 875 RTHPNHVLKREDRSDHDLACDAEGSP 902
Db 834 NAHNPFCVLRWMDRSDHDLAGNAKGP 861
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RESULT 8

US-10-437-963-110261

; Sequence 110261, Application US/10437963
; Publication No. US20040123343A1

GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 110261
; LENGTH: 1007
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14340C.1.pep
US-10-437-963-110261

Query Match 42.5%; Score 2184; DB 16; Length 1007;

Best Local Similarity 48.2%; Pred. No. 2.1e-173;

Matches 488; Conservative 143; Mismatches 279; Indels 102; Gaps 16;

Qy 1 MAETVLSMARSLSVSAISKAAASAAADETSLLLGVKDIWYL----- 41
Db 1 MAETALSMAARMGLGALSAASAAAGEMSLLMGVQKEINFWDELKTQAFLIAAETMKK 60

Qy 42 -----FRHGVGRSNGGPVVG-----MVASGNQSCV----- 66
Db 61 KDLALLKVAQOV-RSLSYDIEDCLEEPVHVHGNQSLQLQTLNLKDRHRIAVKIRNLKSRL 119

Qy 67 -----AIDSVAEDIRNQSARNVDABELVGFSDSKRLEMDT 104
Db 120 EYVSSRNTRYNSIKMEANNTFDEIES-MEDVRNHSRNSIDEAKLVGFDTPCKEELDKINM 178

Qy 105 NANDGP-AKVICVVGGMGLKKTALSRKIPESEDIRKNFPCNAWITVSQSFPHRIELKDM 163
Db 179 DANDDDHRCVLCVGMGGGLKTLVXKIFESKEDIINNPHRAWIVVQSFSMIEMLKDM 238

Qy 164 IROLGPFSSLDQLLOELQGVVVQVHLSLEYLIELKEKRYFVVLDDLWILHDWNWINEI 223
Db 239 ISQLLGHE-----LKRPEGK-PIRAHDLGTHLADGLKELRYFVVDLWNTDHWIREF 293

Qy 224 AFPKNKKGQIVITVWNVDLAEKCATASLVYHLDPLQNDAITLLLRKTNKHEDMESN 283
Db 294 ALPSKNKRSRVITVTRLDGVANACTTEPFVYKLLLETCALDILLRKNKESKEDMKND 353

Qy 284 KMKQKVERIVNKGRLPLAIIITIGAVLTKQVSEWEKPYEHLPSLEINPS--LEALRR 341
Db 354 NNKLSIVTVQVKCGCLPLAIIITIGAMFANKPSKVEEMCRQLPSELENPPSGVEAIR 413

Qy 342 MVTLYGNHLPSHLKPCFLYLSIPDEPEIKRNLVGRWIAAGFVRPKVGMTTKDVGSSYF 401
Db 414 VVTLSYGHLPKPCVLYLSIPDEIEIKRHLVNRWVAEGLVRAVRVGMTISDVGSYF 473

Qy 402 NELINRSMIQRSRVGTAGKIKTCRIHDIIRDTIVTSIQROENFVLLPMGDGSDLVQENTRH 461
Db 474 DELISRSMIQRSRVNMEGHVKSCRVDHIMRDIIVTSIKSEENFVYSTGDNVSTVIVEKFRH 533

Qy 462 IAFHGSCKTGLDWSIIRSLAIFGD--RPKSLAHAVCPDQLRMLRVLDLVDVTLITQ 518
Db 534 LSCHGNYPIVGMDFSRVSLTVFGEFDQRPMLVGSSICSAQFTMLRVLDLENVFSVTQ 593

Qy 519 KDFDRIALLCHLYLS--IGYSSSYSLPRSIGKLOGLQTLNMPSTYIAALPSEISKLOQC 576
Db 594 KDINKIGLLRHLRYLNTHTRRRSTIYALPSSIGKQLQNLQVLDIRSEISTLPTDISKLLM 653

Qy 577 LHTLRCRSK--FVSDNFSLNHPMKICTNTICLPKVFTPLVSRDDRAIQIAELHMAKSCW 634
Db 654 LRILRCSKGPWFYFYFDPDEPKCKLHTRMLMLTLPVGSAAARNYTIHELHAYSSH 713

Qy 635 YKSGFVKVPKGIGKRLDQVLEYDIIRTSSRAIKELGQSLKRLGVMWNGSTKECKKI 694
Db 714 SETPGVRVPTGISKLKELQVLEVVDLKTLSKAIEELGELRWLQKLRVSTKGADKKRKT 773

Qy 695 LCAAIEKLSLOYLYVNAAGISDGTLECLDSIS-SPPPLLRTLVLYGSLEEMPNWIEQL 753

Db 774 LCEAIEKLSSQSLCVYEGYFITGTEWLGPCNFSPPLLRKULHGRIRVMPDPSFNL 833
Qy 754 THLKXVLLRSLKREGKTMJLILGALPNLMLVLDLYRKAYLGEKLVFKTGAPFNRLTSLYD 813
Db 834 KQLRKIFLRLSEL-DGRAIEILGTLPNMLMLNDGRAVGNELAFKKHEFPNKLRLSM 892
Qy 814 LDQLREIRPEGSGSPQLEKIBIRFCRLBSGIIIGIHLPRKLEISLGYESKVAGLAQLEGE 873
Db 893 LSELRGIRFERDALPHERMEIECQLRSGIVGIKHLEQLNEISLGCD--VAGLDLLEQE 950
Qy 874 VRTHPNHVLKRDRSDHDLACDA-----EGSPVEVEATDPLPBGESQ 920
Db 951 VKAHPKTPALRLQDRSKIDIGLPVLTGDEGSNVEEAKESVHDDAGESSQ 1002

RESULT 9
US-10-352-179-87
; Sequence 87, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; PRIOR FILING DATE: 2003-01-27
; PRIORITY APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 87
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-352-179-87

Query Match 42.3%; Score 2170.5; DB 15; Length 993;
Best Local Similarity 49.1%; Pred. No. 2.7e-172;
Matches 478; Conservative 155; Mismatches 236; Indels 105; Gaps 17;
Qy 1 MAETVLSNARSLSVCSATSKAASAADETSLLGVKDIWYL-----PRGVCGRSN 50
Db 1 MTETVSNAMSLVGSARVASSASSQEMSLIGVQNEIFIKBELKTMQAFRAAEVRKD 60
Qy 51 GGPVVGVWAS-----GNQS-----C-----LAI----- 68
Db 61 QDELVKVWAEQVRDLAYDIEDCLOEPFAHVHGHQSLQSLKLCRHRIAVQIRNLKORVE 120
Qy 69 -----DSYABDIRNQARNVDEALVGFSDSKRLLEMDTN 105
Db 121 EVSNRMRYNLKSVPSSTDDSQSNMELIRYQTAHYVNESELVGFDPVKKEILELVSS 180
Qy 106 ANDGPAKVICVVGGLGKLTALSKRIPESIEDIRNFPNCNWIIVSOFRIELKKMIR 165
Db 181 EN-AEAQTIWTVGGGLGKTTLAKKVYES-SDVSSKFPRAWITVRSFNKOLLKNMK 238
Qy 166 QLIGPSSLDQLLQELQGVVVVHLSLEYLTELKERYFVVLDLMLHDNNWINEIAP 225
Db 239 QLIGEDSLKKLLDE-HKEVIVKRNLTDLHKNLGRGRYFLVLDLMTQAWDCIKETSW 297
Qy 226 PKNKKGSIQVITWTVNDLAEKATASLVYHLDLQWMDATLLLRKTNKKNHEDMESKN 285
Db 298 -GNNMGSRVVVTRNKNLAGGST-SPVYCLKTLKEDATKLLRKTGRSLHDIKQD- 354
Qy 286 MQKVRIVNKCGRPLAILTIGAVLATKQVSEVEKFEYHLPSELEINPSLEALRRVMTL 345
Db 355 MKEIFEKILKCGGLPLAIIITIGAVLEKGOIKWEIILYAQLPSELESNPFAEPMKKVVTL 414
Qy 346 GYNHLPKLCFLYLSIFPEDFEIKRNLVGRMTAEGFVRPKVGMITTKOVGESYFVELI 405
Db 415 SYNLPKPCFLYLCIFPEDFDIQRKRLVHRVIAEGFTNARGGVGVVDVAQKYFDELI 474

Qy 406 NRSMQBSRVGIAGKIKTCRIHDIIRDTIVSISROENFVLLPMGDSGLDVOENTRHIAFH 465
Db 475 NRSMQBSRVDIIEGNIKSCRVHIDMRDMISIGREENFVYLMGDDGTSVVEENIRHLVHH 534
Qy 466 GSMCKT-GLDWSIIRSLAIFG-DRPKSLAHAVCPDQLRMLRVLDLEDVFLITQKDFDR 523
Db 535 DTSKCSNIGMDWHSVRSLTLPFGRPKGLSPFPQPKMLRVLDLQDVFKGTMQKDIGK 594
Qy 524 IALLCHLKYSIGVSSYSPLRSIGKLOGLQTLNMPSTYIAALPSEISKLOCLHTLRCS 583
Db 595 IGLRLHKYVNIHGSHSIYALPRCIGKLDCLTLDTSVITELPTEISKLSCLILRCR 654
Qy 584 RKFDVNFSLNHPMKCITNTICLPKFTPLVSRDDRAIQIAELHMAKTSCHYK---SFGV 640
Db 655 GRPNSGDFNLNDPKDCLIAFSCPLPMAATDS-DERNKIIAELHVGGSQSPNGGTGYV 713
Qy 641 KVPKGIGKRLDQVLEVYDVRTSSRAIKELGOLSKRLKLGVMNTGSTKCKCKILCAIE 700
Db 714 RVPAGIKVLRQLQVLETVINDINTSSKSVBELGELIQURKLSVTVQGTKECKILCTAIQ 773
Qy 701 KLSLOYLYVNAAGISDGGTLECLDSISSPPPLRLTLVLYGSLEEMPNWIEQLTHLKIIY 760
Db 774 KLTSLKTLVNAHGPLDGTGLEWLSHSILPS-LRIIRLIGYMKEMPNWPRELQKLVKIH 832
Qy 761 LLRSKLEGTMLILGALPNLMLVLDLYRKAYLGEKLVFKTGAPFNRLTSLIYDLDQREI 820
Db 833 LONSLEEDKTMETGELPNMLLFLSWRA-----VLIRNQQLKEV 875
Qy 821 RFEDGSSPQLEKIEIRFCLESIGIIGIHLPRKLEISLGYESKVAGLAQLEGEVTRHPNH 880
Db 876 RFEEGTSPMWERIDIRECRUTSGIAGIKHLPRLKEISLEYSKAVVRLQGLEVEGTHPNR 935
Qy 881 PVLRKREDRSDHDL 894
Db 936 PMLRFGERSHDL 949

RESULT 10
US-10-437-963-151916
; Sequence 151916, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 151916
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52015C.1.pel
US-10-437-963-151916

Query Match 41.0%; Score 2105; DB 16; Length 1163;
Best Local Similarity 52.2%; Pred. No. 1.1e-166;
Matches 448; Conservative 143; Mismatches 247; Indels 20; Gaps 11;
Qy 73 EDIRNQSARNVDAELVGFSDSKRLLEMDTNANDGPAKVICVVGGLGKLTALSKRIF 132
Db 113 EMTRYQAHYVDEAKLVGFGPKKEIKMI-SGSEDEVQTIWIVGAGGLKTLAKKVY 171
Qy 133 ESEDIRKNFPNCNWIIVTSQSFRHIELLKOMIRQLLGPSSLDQLLQELQGVVVVQHLS 192

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Db 172 ES-SNITSMPCRAWITVSQSFVMDLLKQKGLGKESLDNLFITYK-EVKIKENNL 229
Qy 193 EYLIEELKEXYFVVLDDLLHDDNNINETAFFNNKKGSOIVITVWVDLAEKCATAS 252
Db 230 DHLKEWLNRKRYFLVLDLSTKAWCDLKPLW-GNNREGSRLVVTTRNRDLAEG-SSSP 287
Qy 253 LVYHLDLQWMDATLLLRKTNKHEDWESNKNQKQVVERIVNKCGRPLAIIITIGAVLA 312
Db 288 LVYPLQTLHREDATKLLAKTNKSLCDINKD-GNNETFEKILKCGGLPLAIIITIGLLA 346
Qy 313 TKQVSEWEKYEHLPSELEINPSLEALRRMVTLYGNHLPKPCFLYLSIFPDDFIKR 372
Db 347 AKDVKEWDGLYAQIPSELENNPSEVMRQVLAISKYLPKPCFLYLSIFPDDFIQR 406
Qy 373 NRVLRGRIAGFVPKVGMTTKDGESEYFNELINRSMIQSRVGIAGKIKTCRTHDIIRD 432
Db 407 KRLVRYIAEGFIRARDGVSIVDAIKYFNDLINRSLMQPSRVNMEGTIKSCRVDHIIRD 466
Qy 433 ITVYSIRQENFVLLPMGDGSLDVOENTRHIAFHGSMCKTGLDWSIIRSLAIFGDRPKSL 492
Db 467 IMISIRBEKFKVCRIDKETCLMBENIHVAFYNSNSEITAMDLANQVRSITVFGERHEL 526
Qy 493 AHAVCPQLRLRLVLDLEDVTFITQKDFRIALLCHLYLSI-----GYSSSIY 542
Db 527 TPLLCSQVRLRLVLDLFGQVRFMTQKEMDHIWSVLHLKYNIRCDYNLPNSSCY-SKIY 585
Qy 543 SLPRSIGKLOGLQTLNMPSTYIALPSEISKLOCLHTLRCSRKPVSNFSLNHPMKITN 602
Db 586 RIPSISGKLOGLRLVLDISNTCITSPTTEICELRSNLITLCRTEYEFPPSPKPIQCLFA 645
Qy 603 TICLPKVFPTLVSRDRAIQIAELHMAATKSCWYKSGVGVKPGKIGKLRDLQVLEYVDIRR 662
Db 646 LSCIP-VTMALADSDQRHEITAEHLMACSTWFTCGVRVPMRLGNLQQLGYVDIRL 704
Qy 663 TSSRAIKELGOLSKRLKLGVTNSTRKCKILCAAIEKLSLQLYLVNAAGISDGGTLE 722
Db 705 TSSKAVKELGELSQKXLRINGATQKCKVLAIEKLSLQSLRINAFDVSSLRNLE 764
Qy 723 CLDSISSPPPLRLTVLYGSLEMPNWEIQTLHKYILRLSKLKEGKTMILGALPNLM 782
Db 765 WLHYISSPPPLKNTLLEGCIKEI-DWLREFTLVKHLFGSKLKEGKTVQILGELENLM 823
Qy 783 VLDLYRKAYLGEKLVFKTGAPPNRLTSLVDOLREIRPDDGSSPOLEKIEIRFCLES 842
Db 824 VLQRWGAIVGVKLLFRAEAPPKRLKLEIRFLEDLRMRFEERTSPQWETIEISHCLES 883
Qy 843 GIIGIHLPLRLKEISLGYESKVAGLAQLEGVTRTHPNHPVLRKREDSDHDLACDARGSP 902
Db 884 GIIGIKHLPLKLEISLRWNCVAVRLQGLEBVKANPNRPVLLYNDPFSKHDLGDTQSGSG 943
Qy 903 VEVEATDPLPQREGSSQ 920
Db 944 TPVEANEP-PRNVGESSQ 960

RESULT 11
US-10-352-179-91
; Sequence 91, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 1054
```

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; TYPE: PRT
; ORGANISM: Oryza minuta
US-10-352-179-91

Query Match      40.9%; Score 2103.5; DB 15; Length 1054;
Best Local Similarity 45.9%; Pred. No. 1.2e-166;
Matches 480; Conservative 131; Mismatches 244; Indels 191; Gaps 25;

Qy 1 MAETVLSMARSLVSGATSKAASAAADSTSLLGVEKDIWYL----- 41
Db 1 MADTVLSIAKSLVGSASVAVAAAKMMLGQVKEINFIKDELOIQIAFLIAEASKK 60
Qy 42 -----FRHGVGRSNGG----- 57
Db 61 SILLKVVVQVRDLSDYIEDCLDEFTVHVGSQNLRSQMLKDKDRHRTAIQIRNLRIEE 120
Qy 58 VASGN-----QSCLAIDS---YABDIRNSARNVDEAEIVGFSDSKRLLEMDITN 105
Db 121 VSTRNIRYNLIENDLTCTTTDERNLFMEDIRNQ-ANNIEEADLVGFGSPKRELLDLIDVH 179
Qy 106 ANDGPAKVICVWGCGIGKLTALSRKIPESIEDIRKPPPCNAWITVSOPHRIELLDKDIR 165
Db 180 ANDGPTKVCVWGCGIGKTTIARKIYESKEDIKFNCCCAWITVSQFVRVELLDKLMV 239
Qy 166 QLLGPSLDDLLOELQGVVQVHHLSYLIIEBKERYFVVLDDLLWILHWNWINEIAF 225
Db 240 KLFGEVVKRLRELEKQ-VPOVDDLASYLRTLNERRYFVVLNDVWSTDSWKWINSIAP 298
Qy 226 P-KNNKKGSIIVTTNVDLAEKATASLYHLDFTLOMNDAILLLLRKTNKHEDMESNK 284
Db 299 PRNNNKGSRVITVTRDVGLTKECTSELLIYQLKPLEINTAKELLERKANKAIGDMESDK 358
Qy 285 NMQKQVERIVNKCGRPLAIIITIGAVLATQVSEWEKPYEHLSELEINPSLEALRRMVT 344
Db 359 -MSDIITKIIKCGYPLAIIITIGVLSKREIWEFTYQISELESENPLEAMRIVT 417
Qy 345 LGYNHLPKPCFLYLSIFPEDFEIKRNLVRGWIAEGFVRKPVGMTTKDVGESEYFNE 404
Db 418 LSNYLPKPCFLYLSIFPEDFEIKRNLVRGWIAEGFVRKPVGMTTKDVGESEYFNE 477
Qy 405 INRSMIQRSGVGIAGIKTCRIHDIITVTSIRQENFVLLPMGDGSLVQENTRIHAF 464
Db 478 INRSMIQRSGVGIAGIKTCRIHDIITVTSIRQENFVLLPMGDGSLVQENTRIHAF 537
Qy 465 HGSWSC-KTGLDWSIIRSLAIFGDRPKSLAHAVCPDOLRLVLDLEDVTFITQKDFDR 523
Db 538 HGSYCESTLSDWSIIRSLAIFGDRPKSLAHAVCPDOLRLVLDLEDVTFITQKDFDR 597
Qy 524 IALLCHLYLSIG-----YSSSIYSLPRS-----IGKLOGLQTLNMPSTYIALPSE 570
Db 598 IVLLCHLYLSIG-----YSSSIYSLPRS-----IGKLOGLQTLNMPSTYIALPSE 648
Qy 571 ISKLQCLHTLRCSRKFVSDNFSNLNHPMKITNTICLPKVFPTLVSRDRAIQIAELHMA 630
Db 649 ---LRSLSRLCMKEYPSSSLTTT-----LTNTLCPLMIFTFPFVSTSDRSETIAKLHMA 700
Qy 631 KSCWYKSGVGVKPGKI-----GKLRDLQVLEYVDIRTSRAIKELGOLSKRLKGVWNTG 686
Db 701 KGFRSKNGVGVKPGKICNKKTRLTNIGGSGYKD--QSNQRV-----G 740
Qy 687 STKECKKILCAAIEKLSLQLYLVNAAGISDGGTLECLDSI-SSPPPLRLTLVLYGSLEE 745
Db 741 AVQAEEIEMC-----GNKGIHKGK-----MDTLYSYPEALFFTISCECCGE 782
Qy 746 MPNWEIQLTHKKIYLLRS-----KLKEGKTMILGALPNLMVLD--LYRKAYLGEK 795
Db 783 FRYW---NTSVYRFYFISSTPDTQVERKSGDALDAHAAPDEVQLMEEQTKRHHVGV-- 837
Qy 796 LVFKTGAPNRLTSLIYDLQDLREIREPDDGSSPOLEKIEIRFCR----- 839
Db 838 ---TCGVAQPHGPLSPFCPLPWGEASIQNSKNTIFDQFGAAKKGIDIGRLNLVKGDR 894
Qy 840 ---LSSGIIGIHLPLRLKEISLGYESKVAGLAQLEGVTRTHPNHPVLRKREDSDHDLA 895
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Db 895 NIQLESGIVGIHLPRLKEISLGYGSKVARLQLEGEVTRHPNHPVLNRDSDHDLA 954
Qy 896 CDAEGSPVEATDPLPQEGESSQR 921
Db 955 CDAEGSPVEATDPVRAHSCRSQR 980

RESULT 12

US-10-437-963-177336
; Sequence 177336, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 177336
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_74999C.1.pap
US-10-437-963-177336

Query Match 31.4%; Score 1615; DB 16; Length 812;
Best Local Similarity 43.7%; Pred. No. 7.4e-126;
Matches 401; Conservative 84; Mismatches 197; Indels 236; Gaps 23;
Qy 54 VVGVMASGNSCLASIDSAEDIRNQSARNVDEALVGFSDSKRLLEMDITNANDGPAKV 113
Db 52 LVEPISSGTED--DMSYAEIDRNSARNVDEALVGFSDSKRLLEMDITNANDGPAKV 109
Qy 114 ICVVGMGGLGKTLASRKIFESSEDIRNFPNCNMITVQSFPRIELKMDIRQLLGPSSL 173
Db 110 ICVVGMGGLGKTLASRKIFESSEDIRNFPNCNMITVQSFPRIELKMDIRQLLGPSSL 169
Qy 174 DOLLOELQGVVQVHHLSEYLIIEELKEKYP-VVLDLMLLHDWNINEIAPFPKNNKG 232
Db 170 DQLLOELQGVVQVHHLSEYLIIEELKEKRNFSVVGRLIHFRFQQLSTVSLPLDPA 229
Qy 233 SQIVITVNVNVDLAEKCATASL-----VYHLD-----FLOWNDAI----- 266
Db 230 LPPKLTGVCAAATSATGRLELGIHLPRLKEISLGYGSKVARLQLEGEVCAHPK 289
Qy 267 -TLRLKTNKHNDESNKMN-----QKVRIVNKCGR--LPLAI----- 304
Db 290 HPVLQWMDRSYDLGRHSSWFDQVISSIGISGRPMLPASVAPSRGADLRHPLFS 349
Qy 305 -----LTIGAVLATKQVSEWEKFEYHLPSLEINPSLEALRMYTLGNHLPK 356
Db 350 IASQLFARMSRACVHGDRIDEEWILYAQLPSLGCNPSLAAMKVKVALSYNLPESHVPK 409
Qy 357 CFLYLSIFPEDFETKRNRLVGRWTAEGFVRPKVGMVTKKDGESYFNELINRMIQRSGV 416
Db 410 CFLYLCIFPEDFQVRKRLVHRWTAEGFVRK-----GGFWD----- 448
Qy 417 IAGKIKTCRIHDIIRDITVISROENFVLLPMGDGSDLVQENRTHIAFHGSMCKTGLDW 476
Db 449 -----GDG-ELRKE----- 456
Qy 477 SIIRSLAIFGDRPKSLAHAVCPDQRLMLRVLDLSDVTLITQKDPDRIALLCCHKYLSIG 536

Db 457 -----LPPQYQL--- 463
Qy 537 YSSSIYSLPSIGKLOGLQTNMPESTYIAALPSEISKLOCLHTLRCSRKPFVSDNPSLNP 596
Db 464 -----GRDRRQGSYYDLDTN-----RKERVLLLS----- 488
Qy 597 MKCITNTICLPKVFTPLVSRDDRAIQIAELHMAKTSCKYK-SFGVKVPKGIKGLRDLQVL 655
Db 489 -----CPLMA--LSDSDNHRRLITDLHTGSSSHWRHXDGVRVPRGINKLUKVL 539
Qy 656 EYVDIRRTSRAIKELQGLSKRLKLGVTNGSTKEKCKILCAAIEKLSLSLYLVNA-AG 714
Db 540 EIVDIAVTDSKAQELGELNQLRKLKSVTKGNSKKCKILCAAIEKLTSPKSLYVDGDHG 599
Qy 715 ISDGTLECLDSISSPPPLRLTLVYGSLEMPNWIIEQLTHLKKIYLLRSLKKEGKTMLI 774
Db 600 YSLDGTLECLDSISHPPS-LKSLRLKGCIKETPNWPRELKHVLKVIYLYKSHL-NGDTMEI 657
Qy 775 LGALPNLMVLDLYRKAYLGEKLVKTCGAFNRLTSLIYDLDOLREIFEDGSSPOLEKIE 834
Db 658 LGELHNLMDLHFRWYAYVGEKLVFIEGAFQNLKLVVETEDKLEVRFEGETSPOMEWIE 717
Qy 835 IRFCRLSEGGIIGIHLPRLEISLGYGSKVAGLAQLEGEVTRHPNHPVLNRKREDSHD 894
Db 718 ICHCELISGIVGVKHLPRLEIGL-KSAKVRLQLEGEVDTTHNRPILRLSEKRSYHDL 776
Qy 895 ACDAEGSPVEATD-PL 911
Db 777 G-ETHVSVEVEVADEPL 793

RESULT 13

US-10-437-963-171923
; Sequence 171923, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171923
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(926)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70107C.1.pap
US-10-437-963-171923

Query Match 30.5%; Score 1565; DB 16; Length 926;
Best Local Similarity 37.0%; Pred. No. 1.4e-121;
Matches 380; Conservative 144; Mismatches 260; Indels 244; Gaps 17;
Qy 1 MAETVLSMARSLVGSISAASAAADETSLLLGVKDIW-----YLFPHGVGRSNG 51
Db 1 MAETVLSMARSLVGNATKAGEAABASISLLGVNKEIKTKLTILNFPNWL-----SNT 54
Qy 52 GP-----VVG 57
Db 55 HPHPPKKTLLVPSDELKTWQAPLMTABEMKKPRLLKAWVEQVRLDSFDIEDCLAEFM 114

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